

799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096

CGTCCAGTCA	TTAGCGCCAA	AGAAGGGAGC	GATCCAAGCT	CTCTAGCTTA	CAACACCATA	60
GAAAGCGCGA	TCGCTAAAAA	TATAGATGAA	GTTTTTATAG	ACACCGCCGG	GAGGTTGCAC	120
AACCAGACCA	ACCTCAAAAA	CGAGCTTTCT	AAAATCGCGC	ACACCTGCTC	TAAAGTTTTA	180
AAAGACGCCC	CCTTTTACAA	ATTCTTATT	TTAGACGGCA	CGCAAGGGAG	TTCTGGGCTA	240
ACGCAAGCGA	AGATTTTCCA	TGAGACTTTG	GCGCTAGATG	GCGTGATTAT	GACTAAGCTT	300
GATGGCACTT	CTAAGGGCGG	AGCGATTTTA	AGCGTGCTGT	ATGAGTTGAA	ATTACCCATT	360
CTTTATTIAG	GAATGGGCGA	AAAAGAAGAC	GATTTGATCG	CTTTTGATGA	AGAACGCTTT	420
ATAGAAGATT	TGTTTGATGC	GGTGTGTTGTG	GAACAA			456

(2) INFORMATION FOR SEQ ID NO:1097:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic).
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097

AATTTAAGGA	TTATAACCAT	TAAACGATT	TTTAGAGATT	TTTGTAAGA	ACGCTTGAAA	60
AGGGCTAAAT	CAAAAAATAA	AGTCAGGGAT	AAATTGGCTT	GCAAGCTTTT	GTTTGGAAA	120
CTCAAAGATT	ATCAAAATAT	TTTATTGTAT	AGCCCATTAG	GGCATGAGCT	TGACATTAGG	180
CCTTTGATTT	TGAAGTTAAG	ACAAAAAAT	AAGCGCGTGT	GGTTGCCTAA	AAGCATCAAA	240
AAAGGCGCTC	ATTTTCTAA	AGAGGGTTTT	ACTATCGCGC	CCTTTAGGTT	GCCATTAAAG	300
CGTTTGGGGT	GGTTTGATGA	GCCGAGTTTG	TCGCGCTATT	ATAAGCGGGA	ATTGGATTGT	360
ATTGTCTGTC	CGATTTTAGG	AATGGATACA	AGCTTTAGGC	GCGTGGGTTT	TGGGCTAGGC	420
ATGTATGATA	GGAGTTTACC	CCAATTATTC	AAAAAGCAAC	TAAAACGCCC	CTTAGTCATA	480
TTTGTAAGTA	GGGAGTTAGC	GCTGGCTAAT	GGTATTCTTA	CAGACGCTTA	TGACATTGAA	540
GCAAATCTTT	ACATGAATGC	TCGTATCGTT	ATGAAGAATA	ATAAAAGGAA	ACATTATGAG	600
CAGCGGGTTA	ATTTACATTT	CATTAGAAGT	CTTGGTAGCG	TGTTTGATCA	CCGCTCTAAT	660
CATGTATTAT	GTGATGAAAA	AGATCTATTA	CGC			693

(2) INFORMATION FOR SEQ ID NO:1098:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

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800

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098

AGAATAATAA	AAGGAAACAT	TATGAGCAGC	GGGTTAATTT	ACATTTTCATT	AGAAGTCTTG	60
GTAGCGTGTT	TGATCACCGC	TCTAATCATG	TATTATGTGA	TGAAAAAGAT	CTATTACGCT	120
AGAGGGCAAG	CCATTTTAAA	AGGCGCTTCA	GCCAAAGCTA	AATTAATGGA	ATTTCAAGCG	180
AAATCTTTTCG	TGGAAGCTGA	AGAAATGCGC	ATGAAAAGCC	AAGAATGCAA	GTTGCAACAG	240
CAATATGAAA	ATAAGAATTT	GCAACTCCAA	ACCCATTTTG	ATAAAAAAGA	AGCGCATTTG	300
AAGCATTTAG	AAGCGCAGCA	CAAAGAATTT	GTAAGAGATG	AAAAACGCTA	TTTGGAAGAAG	360
GAAAAAAAAG	AGCTTGAAAA	AGAACGCCAA	ATTTTAGAAC	AAGAGAGGGA	AAATTTTAAA	420
AAACAGCGCG	CCATTTGTAA	AGAAGCTCAA	GCCAAAGCGC	TAGATGCGAT	GCTCAATTAC	480
ATGGCTTATA	CCAAAGATGA	AATTTAAAGC	ATGATCTTAG	AGCAATTAGA	ACAGGAACTA	540
GAAGCGCAAA	AGAGCGCCTT	GATCAGGCGT	TATGAAGAAG	AAGCCTTTAT	TATGTGTTTA	600

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099

ATAAGGTCAT	CAATGACAC	CCAAACCACC	CAAACACCAT	GGCACTCAA	CACCAGACGG	60
CCAAAACCCA	CCCCTAAACC	CATTAAAAAA	GAGGCTAAAA	AGGCTAAAGA	GAAAACAAC	120
AAGCATGCGC	ATTCAAAGCA	TGCGCACTCT	CCATTGAACG	AAAGGAGCGC	TAAAAAAGAA	180
ATTCCTAAAA	AAGAAATCCC	TAAAAAAGAA	ATCCCTAAAA	AAGAAATCCC	TAAAAAAGAA	240
ATCCCTAAAA	AAGAAATCCC	TAAAAAAGAA	ATCCCTAAAA	AAGAAATCCC	TAAAAAAGAA	300
GCAGAAAATG	AGAGTAAGAA	CCAAATCTTT	ATAGCAGAAA	AAAATGATAC	TTGGATCAAA	360
ACCAAGCGCA	AAAAACACAA	AAAGATCGTT	TTGGACGCTG	GGCATGGGGG	GAAAGATTGC	420
GGGGCGATGA	GCGCGAATTT	GGTGTGTGAA	AAGGACATTG	TTTTAGAAGT	GGTGAAGTTT	480
TTGCATAAAG	AGCTTAAAAA	AAGAGGCTAT	AGCGTTTAT	TGACAAGGGA	TAAGGACATT	540
TACATTGATT	TAGTGGCCCG	AACGGAATTA	GCCAATAAAA	AAGGGGCGGA	TTTATTCATC	600
TCAGTGCAATG	CCAAATTCAT	CCCTAAACGC	TCCACCTCTA	ACGCCCATGG	CATAGAGACT	660
TATTTTTTAT	CCACCGCAAG	GAGTGAAAGG	GCTAGGAAAG	TGGCTGAGCA	AGAAAATAAA	720
GACGATGTGA	ATTTAATGGA	CTATTTTTCT	AAAAGTTTGT	TTTTAAATTC	ATTGAACACG	780
CAGCGATTGA	TCGTCTCCAA	CAAATTAGCG	ATTGACGTGC	AATACGGCAT	GCTCCAAAGT	840
GTCCGCAAAA	ATTACCCTGA	TGTGGTGGAT	GGGGGTGTTA	GGGAGGGGCC	TTTTTGGGTG	900
TTAGCCGGGG	CTTTAATGCC	TTCAATTTTA	ATAGAAATTG	GTTATAATTC	CCATGCCGATA	960
GAATCTAAAC	GCATCCAAAG	CAAACCGTAT	CAAAAAATCT	TGGCTAAGGG	CATTGCTGAT	1020
GGCAATGATA	GTTTCTTCAG	CAAGAATGAT				1050

(2) INFORMATION FOR SEQ ID NO:1100:

801

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...558
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100

AGAGTATCTA	TGAATGTCAA	AAAAAAGGGA	AAGCCACAAA	GTGGAAAGAT	TGATAGGGTG	60
GATTGTTTGG	AGAAACTTGG	GAAAGAAAAC	ACTACTTTTT	TAAGCAGTAT	AGCTATGGGG	120
AGCATTGGTC	AATTAGCGAT	CCCCATTCCCT	GGAGTTGGAG	TGCTCATTGG	GGGCTTTGTG	180
GGTGGGGTGA	TGAGTAAAC	TTTTTATGAT	GTCTCGCTAA	CGATTTTCAA	AGAGGCTAAA	240
TTAGCGCGTC	AAAGGCGTAT	TGAGATTGAA	AAAGAATGCC	GTGAGAGTAT	CAGACAGTTA	300
GAGATGTATC	AAAATCAATT	TAATGAAGTG	TTTGAGCGGT	ATTTTCATGG	GACTATAAAA	360
TTCTTTAATG	AAAGTTTGA	TGAGCTGGAG	AGGGCGCTTT	GTGCGGGCGA	TGCGGATTTG	420
GCTATAGCAG	TCAATAACAA	GATCCAAGAG	GGGATGGGTC	AAGAGTTGCT	GTTTGACAAT	480
AAGCAAGAGT	GCTGGGAATT	TATCACTAGC	CGTAAAGAGG	GTTGGAATTT	CGTCACTAGC	540
CGTGGAAAAA	CAGAAATT					558

(2) INFORMATION FOR SEQ ID NO:1101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1086 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1086
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101

AAGAGGGATC	AAATGGCCGA	AGAAGAAAAG	ACCGAACTCC	CTAGCGCGAA	AAAAATCCAA	60
AAAGCCAGAG	AAGAAGGCAA	TGTCCCTAAA	AGCATGGAAG	TGGTGGGGTT	TTTAGGGTTA	120
TTGGCTGGGC	TAATGAGTAT	TTTGTTTTTT	TTTATATGGT	GGGTGGATGG	CTTTAGCGAG	180
ATGTATCGCC	ATGTGTTGAA	AGATTCTCTC	CTAGATTTTA	GCAAAGAAAG	CGTTCAAGAG	240
CTGTTTAACC	AGCTGGCTAA	AGACACTTTT	TTATTGCTTT	TGCCTGTTTT	AATCATTTTA	300
ATGGTGGTGG	CGTTTTTGTG	TAATGTCTTG	CAATTGGCTT	GGCTCTTTGC	CCCTAAAGTC	360
ATTGAGCCTA	AATTTTCTAA	AATCAACCCT	ATCAATGGCG	TCAAAAACCT	TTTTTCTTTA	420
AAAAAGATCC	TTGATGGGAG	TTTGATCACT	TTAAAAGTTT	TTTATAGCTT	TTTTCTGGGG	480
TTTTTCATCT	TTTCCTTATT	TTTAGGGGAA	TTAAACCATG	CGGCTCTTTT	GAATTTGCAA	540

802

GGCCAGTTGT	TGTGGTTTAA	AAGCAAGGCG	TTATGGCTCA	TTTCTTCGCT	TTTATTTTAA	600
TTTTTTGTCT	TGGCTTTTGT	GGATTTAATC	ATCAAACGCC	GCCAATACAC	TAACTCTTTA	660
AAAATGACTA	AACAAGAAGT	TAAGGACGAA	TACAAACAGC	AAGAAGGAAA	CCCAGAAATC	720
AAAGCCAAAA	TCGCCAGAT	GATGGTAAAA	AACGCCACGA	ATAAAATGAT	GCAAGAAATC	780
CCCAAATCCA	ATGTCGTGGT	GACTAACCCCT	ACCCATTATG	CCGTCGCTCT	CAAATTTGAT	840
GAAGAACACC	CTGTGCCTGT	GGTAGTGGCT	AAAGGCACGG	ATTATTTAGC	CATTAGGATT	900
AAGGGTATCG	CCAGAGAGCA	TGACATAGAA	ATTATAGAAA	ATAAAACGCT	CGCTAGAGAG	960
CTTTATAGAG	ACGTGAAATT	GAACGCCACC	ATACCAGAAG	AATTGTTTGA	AGCGGTAGCG	1020
ATTGTCTTCG	CTCAAGTGGC	TAAATTAGAG	CAAGAACGCC	AAAAACAAAA	GATCATTAAA	1080
CCTCTT						1086

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102

GAAATACTA	TGCAAGATTT	ACAACATTTT	AAAAATGATA	TTACGCTCAT	TCTGTCTAAA	60
GACAGATTAG	ATACTTATGA	CAGCCTAGAG	CAATACAAAG	AAAATTTAAA	ACTCATTTCT	120
TTCATCACGC	CTAAAATCTC	TAACTTAGAG	ATTATTTTAC	GCAACGCTTT	AGACTATTGC	180
TTAACCCAAA	TTAAGGGGAG	CGAATGGGTG	TTTAATGAAA	ATTCTTTAAC	AGATTTAATT	240
AACGAACAAA	AAGAAAAGAA	AAAAGAAATC	ACGCATTCTT	TAATCTTATC	TAAAATGTCT	300
TTAGGGGCAG	TGGTTAGGCT	TATTTTGT	TATAAGTTAG	AGGGGGTAAT	ATTAGATTTG	360
AGAGCGTATC	GTTTGAGAGC	TTATTATCAC	GAAAATAAAG	ATACCTTGCT	TATTAAAGGC	420
AAAAAACGCC	TTCTTTACAA	TTATATTAAA	GCCCATATTG	CTTTAAACTT	GCTATGGACA	480
ATTAGAAATC	GCACGTATCA	TTGGGAAAAT	TTACTCAAAA	TCCAACCGAA	CAACCGCCCA	540
CAA						543

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

803

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103

GCTAATGCAT	GCGAAAAAAG	GATTTTTCATG	CTGCTTTGCG	CGGGAAGGAA	TGAGACTTTA	60
AAAAAAGCGG	TGCCTATTGG	TGTGGGCTTG	ATAGAGAGCG	CGATCAATTT	AACGAGAATG	120
TGCCTTAAAA	ACCTTGATAC	AGAAAGCCTT	ATTTTATAG	GGAGCGCGGG	GAGTTATAGC	180
CCAGAAACGG	AGATTTTGAG	CGTGTGTTGAA	AGCATTGAAG	GCTATCAAAT	TGAAGAGAGT	240
TTTAGCCATT	TAAACAGCTA	CACGCCTTTG	GATAATTICA	TTCCATAGA	AACTAAAGAG	300
CAGGCTCTTT	TTGAAAGGGT	GCGTGTGAAT	AGCAGTAACT	ACATCCACAC	CAGCGAAATG	360
TTTGCTAAAA	AAATGGTTCA	AAAGGGCGTT	TTATTAGAAA	ACATGGAGTT	TTTAGCGTC	420
TTAAGCGTGG	CTAAAATTTT	TTCTTTAAAG	GCTAAAGGGA	TTTTTTGCGT	GAGCAATCAT	480
GTAGGGCTTA	ACGCGCATAA	GGAATTTAAA	GAAAACCACG	CCAAAGTCAA	ACAGATTCTA	540
GAAAACATCA	TTGATAGTTT	GATAGTT				567

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104

TTTTAATGAG	TTTTATAAGC	TTGCAATCGC	CTCTTGCGCA	GAACCCCTAA	GAGTGAGTAT	60
AGAATTTGTG	GATTTGCCTA	AAAAAATCAT	CCGTTTTCCG	GCCCATGATT	TGAAAGTGGG	120
GGAGTTTGGT	TTTGTGGTTA	CTCAACTTTC	AGATTATGAA	ATCGTTAATT	CTGAAGTGGT	180
CATTATTGCT	GTTGAAAATG	GCGTCGCAAC	GGCTAAATTC	AAAGCGTTTG	AGTCGATGAA	240
ACAAAGCCAT	TTACCCACTC	CAAGAATGGT	CGCTAAAAAA	GGGGATTAG	TCTATTTTCA	300
GCAATTTAAC	AACCAAGCGT	TTTGTATCGC	TCCTAATGAT	GAACCTCTATG	AGCAAATCAG	360
AGCGACTAAC	ACCGATATTA	ATTTCATTAG	CTCTGATTTC	TTGGTTACTT	TTTTGAATGG	420
GTTTGACCCA	AAAATCGCTA	ATTTAAGGAA	AGCGTGCAAT	GTTTATAGCG	TGGGGGTGAT	480
TTATATTGTA	ACCACCAACA	CGCTCAATAT	TTTAAGTTGT	GAGAGTTTTC	AAATTTTAGA	540
AAAAAGAGAG	CTGGATACAA	GCGGCGTTAC	TAAAACTTCC	ACGCCGTTTT	TTTCTAGGGT	600
TGAGGGCATT	GATGCAGGCA	CGCTAGGGAA	ACTTTTTTCA	GGCAGTCAAT	CTAAAAATTA	660
CTTCGCTTAC	TATGACGCTT	TAGTGAAAAA	AGAAAAACGA	AAAGAAGTAA	GGATTGAAAA	720
GAAAGAAGAA	AGGATTGATG	CTAGAGAAAA	TAAACGAGAA	ATCAAGCAAG	AAGCCATTAA	780
AGAGCCTAAA	AAAGCCAATC	AAGGCACAGA	AAACGCTCCC	ACTTTAGAA	AGAAAACTA	840
CCAAAAAGCA	GAGCGAAAAT	TTGACGCTAA	AGAAGAAAGG	CGTCGTTC	GAGATGAAAG	900
GAAAAAACT	AAAGCCACCA	AAAAGGCTAT	GGAATTTGAA	CAAAGAGCGA	GAGAACATCA	960
AGAAAGAGAT	GAAAAAGAGC	TTGAAGAAAG	AAGAAAGCT	TTAGAAATGA	ATAAGAAG	1018

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

804

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105

GGAGAAACAA	CAATGAAACT	GAGAGCAAGT	GTTTTAATCG	GTGTGGCAAT	TCTGTGCTTA	60
ATTTTAAGTG	CGTGCACTAA	CTATGCGAAA	AAAGTGGTGA	AACAAAAGAA	CCATGTTTAT	120
ACGCCTGTGT	ATAATGAACT	GATAGAGAAG	TATAGTGAGA	TCCCCTTAAA	TGACAAACTC	180
AAAGACACAC	CAITTCATGGT	GCAAGTGAAG	TTGCCAAATT	ACAAGGACTA	TTTGTTGGAT	240
AATAAACCAAG	TTGTACTAAC	TTTCAAACCT	GTTCCACCATT	CTAAAAAGAT	TACGCTCATA	300
GGCGATGCCA	ATAAGATCCT	CCAATACAAG	AATTACTTCC	AAGCTAACGG	GGCAAGATCT	360
GACATTGATT	TTTACTTGCA	ACCCACTTTG	AATCAAAAGG	GTGTGGTGAT	GATAGCGAGT	420
AACTACAATG	ATAATCCCAA	CAACAAAGAA	AAACCACAGA	CCTTTGATGT	GTGCAAGGA	480
AGTCAGCCAA	TGCTAGGAGC	TAACACAAAA	AACCTGCATG	GCTATGATGT	GAGTGGAGCA	540
AACAACAAGC	AAGTGATCAA	TGAAGTGGCA	AGAGAAAAAG	CTCAGCTAGA	AAAAATCAAT	600
CAGTATTACA	AGACTCTCTT	GCAAGACAAG	GAACAAGAAT	ATACCACTAG	GAAAAATAAC	660
CAACGAGAAA	TTTTAGAAAC	ATTGAGTAAT	CGTGCAGGTT	ATCAAATGAG	GCAGAATGTG	720
ATTAGTTCTG	AGATTTTTTA	GAATGGCAAC	TTGAACATGC	AAGCCAAAGA	AGAAGAAGTT	780
AGGGAGAAGC	TACAAGAAGA	AAGAGAGAAT	GAATACTTGC	GCAATCAAAT	CAGAAGTTTG	840
CTCAGTGGTA	AG					852

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106

AGTTATTGTC	AAATGAAAAC	ACTCGTGAAA	AATACCATAT	ATTCTTTTTT	GCTATTGTCT	60
GTTTTGATGG	CAGAAGATAT	AACAAGCGGC	TTAAAGCAAC	TGGATAACAC	CTACCAAGAG	120
ACCAACCAAC	AGTGCTCTCA	AAACCTAGAT	GAGATTTTTT	CAACCACTAG	CCCTAGCGCT	180
AATAATAAAA	TAGGTCAAGA	AGATGCTCTA	AACATCAAAA	AAGCGGCCAT	TGCTTTGAGA	240
GGAGATTTAG	CGTTATTGAA	AGCCAAATTT	GAAGCGAATG	AGTTATTTTT	CATCTCAGAA	300
GATGTGATTT	TTAAGACTTA	TATGTCTAGC	CCTGAACTTT	TATTAACCTA	TATGAAAATC	360
AATCCCTTAG	ACCAAAAGAC	TGCTGAGCAA	CAATGCGGAA	TATCCGATAA	AGTTTTAGTT	420
CTTTATGTG	AGGGGAAGCT	GAAAATCGAG	CAAGAAAAAC	AAAATATAAG	AGAGCGTTTA	480

805

GAAACTTCTC	TAAAGGCATA	TCAGAGCAAC	ATTGGAGGTA	CAGCTTCCTT	AATCACTGCT	540
TCACAGACGC	TTGTAGAAAG	CCTAAAAAAT	AAAAATTTCA	TCAAAGGAAT	CAAAAAGCTT	600
ATGTTAGCTC	ACAACAAGGT	CTTTTAAAT	TATTTAGAGG	AGTTGGACGC	ATTAGAAAGA	660
TCCCTAGAAC	AAAGTAAGCG	ACAATACCTA	CAAGAAAGGC	AATCAAGTAA	GATCATTGTT	720
AAA						723

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107

ATAAATAAGA	ACATGTTTAA	TATTAAAAGG	ACTTTTTTAA	TAACGATCAT	AAGTTTTTTT	60
CTCATTGTTT	CTAATTGGTT	GAAAGCTATT	GATTTGCCCA	TTGTTTCAAA	TCTCAAAATT	120
TACCAAACAG	TTTATTGCAT	GCTGATACCG	AGTTATGTTT	TAACCAACAA	AAGTTTGTGA	180
GATATTTTGA	CAGGCTATAC	ATCTATTGGT	GCATCAGGGA	GTGGAAAGAG	TTCAGGGCAG	240
GGTGTGATCG	AAGCGCTTAG	CACACCATTA	GCCACAAGTT	TAGCCGCTAG	CAATCTGGTG	300
AAATATTTGA	ATACTTTAGG	TCCTTTATGG	GGATCGGCGT	GGGCAAGTGT	TGCTACAGCT	360
ATACAAGGTT	TIGCTCTAAC	GCCATCAAGT	GGCTGTAATT	TTGGTTGGAA	CGCATTGATA	420
AATAAAAACA	TAGATGTATC	CATGGATAGC	GTACTAGACA	ATTTGAGCAA	CAAGATTGAG	480
AATTTTACCA	AAGGCGGTGT	TGAGGACAAT	GTGAAAGGCA	ATATTCTTTT	ACAAATAATT	540
GGCTCAATAA	CCGCTCAAGC	TTCTACGAAT	ATTACAGCTG	ATGGTTTAAAT	TTGGCTGATT	600
GGTAAAGAAT	CTACTGCAAA	TAAACTGCAA	AACAACACTA	TAGCCATGCT	TGCTTTTGCC	660
GCATTAGAAT	CTGTTGTCAA	AGGAGCGGAC	GCTGCTGTTT	TTCCTGCATA	TGGTGTAGTC	720
AATCTGCCTG	ATATTATCAT	AGGGCAAGGG	TCATATCTTG	ATTTTGTTC	TTACCTAATT	780
TATATTGTTT	TTGGGATTIT	TGTTTTTATT	TCTTTTATGA	AATTGAGAGA	TATTTCAAAC	840
GGCATTGAGA	TAAACATAGG	TTTTGAATAC	ATGCGATTGG	TTGGGGGGAC	ATTATTCAAA	900
ATGGCGATGG	TCTCTTTTAT	CGCCTATGCA	GGTTTIGGTT	ATCTTTTATA	AATCTCTTAT	960
TCTATTTATT	TTGGTTTAGC	AGGTGCTTTT	GGGCTGAATC	AAGTTCCTTT	TTGGGCTTTA	1020
GATTTAGTGC	TGAATTACAC	TGTTAATTCA	ATTTTACCTG	CGGTAAGAGC	TGTTTTTTCT	1080
AATGTTGGCA	ACAACGCTCC	TAGTTTGTTA	CAAGGCTTGC	AAGTGGCAGG	TATTTCTTTA	1140
TTGCTATTTT	TTATGCAAGT	AACTATCATT	ATGAGAATAA	GCACTGTTGT	TGTGAAACCT	1200
TTGATAGCGG	GGGCTTTTAG	CGGTATTGTT	TTCCCTATTG	CAGTATGTTT	GATCGTGCTA	1260
GATTGGTTCA	AAGATTCTAT	GAAAAACATA	TTGATATGGT	TTATTAATAA	TCTGTTTATC	1320
TTGTTTCTAG	CTATTCTTAT	TTTGCTCTTT	GGTGTTTTGG	CATTATTGGC	ATTCAATTTG	1380
ACCATAACGC	CCTCTGTTGC	TATACAAAAC	ATCAATCAAG	GGGGATTGGG	TATCGATTCA	1440
ACTATTGCGA	GTTTGATCAC	TCTATTTATT	TTAAAAGGTT	TCATAGAGAC	GATTATTGAG	1500
AGCGTCAATG	CGATCGTTAA	CACCATTTTC	AGCTCTGTCT	CTATGGATGG	TAGCAGAATG	1560
GATAGAGAAA	GAGATGCCTT	AATGGTGCGA	AGAGTTGGTG	GATCTATGTT	TAAAGGA	1617

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

806

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...768
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108

CTCCATAGAA	TTATCTCCTG	CGATAGCGCT	TGGAGGACTA	ATCTTGTGTG	GCGGACCAAT	60
AAAGCCTTGT	ATCAATTCAT	TTTGAGGATA	GCCCAAAAAG	ACAATTTTGC	TTCAGCGTAT	120
CTAACAGTCA	AATTAGAATA	CCCACAAAGA	CACGAAGTCT	CTAGCGTTAT	TGAAGAGGAA	180
TTAAAAAAGA	GAGAAGAAGC	AAAGAGGCAG	AGAGAATTGA	TCAAGCAAGA	AAATCTCAAC	240
ACCACAGCCT	ACATCAATAG	AGTAATGATG	GCGAGCAATG	AACAGATTAT	CAACAAAGAA	300
AAAATAAGAG	AAGAAAAACA	AAAAATTATA	CTAGATCAAG	CAAAGGCGCT	AGAGACCCAA	360
TATGTGCATA	ATGCGTTAAA	AAGAAACCTT	GTGCCTAGAA	ACTACAATTA	CTACCAAGCG	420
CCTGAAAAAC	GCTCTAAACA	TATTATGCCC	TCTGAAATTT	TIGATGATGG	CACATTCACT	480
TATTTTGGTT	TCAAAAACAT	CACTCTCCAA	CCTGCTATTT	TGTGGTTCA	ACCTGATGGG	540
AAATTGAGCA	TGACTGATGC	CGCCATTGAT	CCTAACATGA	CTAATTCAGG	ATTGAGATGG	600
TATAGAGTTA	ATGAAATGTC	AGAGAAGTTT	AAGCTCATT	AAGACAAAGC	CCTTGTAACA	660
GTGATCAATA	AAGGCTATGG	GAAAAATCCA	TTGACAAAAA	ATTACAATAT	CAAAAACTAT	720
GGTGAATTGG	AGCGTGTGAT	TAAAAGCTC	CCTCTTGTC	GAGATAAA		768

(2) INFORMATION FOR SEQ ID NO:1109:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109

ACTAGTTCTT	TCAAAACCAA	AATGAAACGA	CCGATCAGCA	AATTGAAACA	AAACTTTTTT	60
CAATTCAAAC	ATTCTTTCAA	CAAACATTTA	GATAAGTACA	GCCTTTATTA	TAGGCTGTTC	120
AATATCAGCT	CTATCGTTAT	AGGTTTTTTT	ATAGCGCTTT	TTTCTTATGG	GGCAGGGGTG	180
ATTTTAGTTT	ATCCAATATT	ATTCTTGTTT	GCTCTTATAA	TAAACCTAG	CTTTTTTTAT	240
TACACTACTT	ATCTTTTGCT	ACTCGTTTCT	CTCAGCATAA	TAAGCAAATA	CTATCTCCTA	300
AGCCACGCAA	ATTCACAAT	GAAGCTAATC	ATGCTTATGA	CTCAATGGCA	AAATTGGTTC	360
TTA						363

(2) INFORMATION FOR SEQ ID NO:1110:

SUBSTITUTE SHEET (RULE 26)

807

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110

GTATGCTATT GTGAAATGCT TCCTACTAAA ACACGCATTA GAGATCCGAA CAAGCAAGAA	60
CTTACACAAC CAAAAATAAA AGGATTGAGT ATGGGAAAAA TTTTAGCTTC TTTGTTGGGT	120
GGCGGAACAA ATCTTTTAC AGGTTTATCC AGTGATTGT TTTCTATGAT ATTAAATTTT	180
TTGTTCTTCC TGATGTTAAT GATGGGACTT AATGAAGCAT TAGGGAAAAA ATTTAACTTG	240
CCTATGGACA ATATCAAGAA TTTTATGGCA GAAGTGCTGA AGAATGGATT CGATAGTATC	300
AAAAACATGG GATCTGCTTT GGTGGTAAT GGTTTGGTA GCAGCAAATC AGACAAAACC	360
ACTAATAAAA TGAGTGTCCT ACAAGTAAGA CTC	393

(2) INFORMATION FOR SEQ ID NO:1111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 891 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...891
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111

GAGGAATTGT TGATGGGGCA GGCATTTTTT AAAAAAATTG TTGGCTGTTT CTGTCTTGGT	60
TATTTATTTT TATCTAGCGC AATAGAAGCA GTAGCACTTG ACATTAAGAA TTTTAATCGT	120
GGTAGGGTGA AAGTGGTGAA TAAGAAGATT GCTTATTTGG GAGATGAAAA ACCTATTACG	180
ATTTGGACTT CATTAGACAA TGTTACCGTG ATCCAACCTG AAAAAAGATGA AACTATTTCT	240
TACATCACAA CAGGTTTCAA TAAAGGTTGG AGTATTGTGC CTAATTCCTAA TCATATATTC	300
ATCAACCTA AATCGGTAAA AAGTAATCTC ATGTTTGAAA AAGAAGCAGT GAATTTTGCC	360
CTAATGACAA GAGATTACCA AGAATTTTAA AAGACAAAAA AACTTATCGT AGATGCGCCT	420
GACCCTAAAG AATTAGAAGA ACAAAAAAAA GCTCTAGAAA AAGAAAAAGA AGCTAAAGAA	480
CAGGCGCAA AGGCACAAA AGATAAAGA GAAAAAGAA AGGAGGAGCG TGCAAAAAAT	540
AGAGCCAATT TAGAAAACT CACTAACGCT ATGAGTAACC CACAAAATTT GAGCAATAAC	600
AAAAATCTTA GCGAATTGAT CAAGCAACAG AGAGAAAATG AATTAGACCA AATGGAACGA	660

808

CTAGAGGACA	TGCAAGAGCA	GGCTCAAGCT	AACGCACTCA	AACAAATTGA	AGAGCTCAAC	720
AAGAAACAAG	CTGAAGAGGC	AGTTAGGCAA	AGAGCCAAGG	ATAAAATCAG	TATTAAGACA	780
GATAAATCTC	AAAAAAGCCC	CGAGGATAAC	TCCATAGAAT	TATCTCTGTC	GATAGCGCTT	840
GGAGGACTAA	TCTTGTTGTG	CGGACCAATA	AAGCCTTGTA	TCAATTCATT	T	891

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112

AGCTGTCGCA	TGTTAGGGAA	AAAAACGAA	GAAGTCTTGA	TGATGAAAA	TTTGGTTGGG	60
GGTGTGATAG	CCCTTGATAG	ATTGGCAAAA	CTCAATAAGG	CCAATAGGAC	TTTCAAAAGG	120
GCTTTTATC	TCTCTATGGT	GCTCAATGTC	GCCGCTGTAA	CGAGTATTGT	GATGATGATG	180
CCTTTGAAGA	AAACAGATAT	ATTTGTTTAT	GGCATTGATC	GATACACAGG	AGAATTTAAA	240
ATCGTCAAAC	GCTCCGATGC	TAGGCAAATC	GTCAATTCTG	AAGCCGTTGT	GGATAGTGCA	300
ACTTCAAAAT	TTGTCTCATT	GCTGTTTGGT	TATAGCAAAA	ATTCTTTGAG	GGATCGCAAG	360
GATCAACTAA	TGCAGTATTG	CGATGTGAGT	TTCCAAACCC	AAGCAATGAG	AATGTTCAAT	420
GAAAAATATCA	GACAATTTCGT	AGATAAAGTC	CGAGCAGAAG	CTATCATTAG	CTCCAACATA	480
CAAAGAGAAA	AAGTCAAAAA	TAGTCCCTTA	ACGAGATTAA	CATTTTTCAT	TACCATCAAA	540
ATCAGCCTTG	ATACAATGGA	AAATTATGAA	TATATCACTA	AAAAACAAGT	AACTATTTAT	600
TATGATTTTG	CTAGAGGTAA	CTCTTCTCAA	GAAAACTTTA	TCATCAACCC	TTTTGGCTTC	660
AAAGTGTTTG	ACATTCAAAT	CACGGATTTA	CAAAACGAAC	AGACAGTAAG	CGAAATTTTG	720
AGAAAGATTA	AAGAAGTGGA	ATCAAAAAAT	AAGSCATTAA	ATAAA		765

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...750

809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113

AAGCGCCTAA	TTCAAAGAGA	TGAGACAATC	GCAACTCAGA	GAGAGAATGG	TATAATATCA	60
AAACAATTTT	TCAATTTAAT	TCTTGAAAGG	AGTTTCATGA	ACGATACAAC	AGAGCACCAT	120
GGATCCAATC	CGCTAAACGC	CCCACCACCT	AGCAACTCAC	AGAGCAACGA	TCTCTTAAAT	180
TTGCTAGACT	CGTTATATCC	TAAAGGGAGT	TTAGGGGAAC	AAAGATTTC	CGAAGCTTTA	240
AAGAATCAAG	AAGAGTTGAA	AAATATCCTA	ATAGAAATAG	AAAAGCTACC	GCAAGAAAAA	300
AGGTATGAAC	TTCTGATGCA	GATAGGACAA	GCCAAACAGA	GAATAATGGA	AGCATACGCT	360
CATTCATTCT	TAGGATATAT	AGGGGGACTA	GAGCATCTGT	TAGGATTGTG	TATGGGTGGG	420
ATATTTGTTT	TGTTTGCAAT	CTATTTTGTA	TTTTTAAGAA	CTAGCAAAAA	CACAGAGCTA	480
GTGGAAAGTC	TAAAAACAAA	ATTAAAACTT	CAGTATTTT	ACTATGCCTT	TGGTGTGGGT	540
GCGGTTTTGT	TTTTTGGATT	AGAAACAATT	AGATCGATTT	ATGAAGTATA	TATCTTAGGA	600
ATTGGTAGCA	CTAACGACAA	GGTGCTCTTT	GTTTTGAAAA	ACATTTCCTT	CATAGGTATG	660
GGCTATTTGA	TTTATAAAGT	TATTAAAGTT	ATTGGTATAA	AAAATTTTAT	CAATGGTCTT	720
TTGCGTTCAA	AGAAACAAGG	CGGTGCAGAA				750

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114

GGTTACAAAA	ACTATAAGAT	GCTTGCAAAA	ATCGTTTTTA	GCTCATGGT	TGCGTTTGGA	60
GTTTTGTTCG	CTAATGTGGA	GCAGTTTGTT	TCATTTTTCA	ACGAGATAAA	AAAAGAACAA	120
GAAGAAGTGG	CCGCAAAAGA	AGACGCTCTT	AAAGCTCGCA	AGAAGCTCTT	AAACAATACG	180
CATGATTTCT	TAGAAGACTT	GGTTTTTAGA	AAACAAAAAA	TCAAAGAGCT	TGTGGATTAC	240
AGAGCTAAAG	TTCTTTTAGA	TTTAGAAAAA	AAGTACAAAA	AAGAAAAAGA	GGCTCTAGAG	300
AAAGAGACAA	GAGGTAAAT	CCTTACTGCT	AAGTCAAAGG	CTTATGGTGA	TCTAGAGCAA	360
GCCTTAAAAG	ATAACCTCT	TTATAAGAAA	CTTCTTCCTA	ACCCTTATGC	TTATGTTTTA	420
AACCAAGAAA	CATTCACGCA	AGAAGATAAG	GAGCGTTTGA	GTTATTACTA	CCCCCAAGTG	480
AAAACGAGCA	GTATTTTTAA	AAAAACTACC	GCTACCACTA	AAGATAAGGC	TCAGGCTTTG	540
CTTCAAATGG	GTGTGTTTTT	TTTAGATGAA	GAGCAAAACA	AAAAAGCGAG	CCGATTAGCT	600
TTATCTTACA	AGCAAGCGAT	TGAAGAATAT	TCCAATAACA	TTTCTAATTT	ATTGAGCAGA	660
AAAGAATTGG	ATAATATAGA	TTATTACTTG	CAGCTTGAAA	GAAACAAATT	TGACTCCAAA	720
GCAAAAGATA	TTGCTCAAAA	AGCCACCAAC	ACGCTTATTT	TTAACTCGGA	ACGCTTGGCG	780
TTTAGCATGG	CGATTGATAA	GATCAATGAG	AAATACTTAA	GGGGCTATGA	AGCTTTTTCT	840
AACCTGTTGA	AAAATGTCAA	AGATGATGTG	GAGTTGAATA	CTTTGACTAA	AACTTCACC	900
AATCAAAAAT	TGAGTTTCGC	ACAAAAACAA	AAATTGTGTT	TGTTGGTTTT	AGACAGCTTC	960
AATTTTGATA	CCCAATCCAA	AAAACTTATA	TTAAAAAAGA	CTAATGAATA	CAATATCTTC	1020
GTAGATAGCG	ATCCTATGAT	GAGCGACAAA	ACAACATATG	AAAAAGAACA	CTACAAGATA	1080
TTTAATTTCT	TCAAAACAGT	GGTTTCTGCA	TACCGGAACA	ATGTTGCCAA	GAATAACCCC	1140
TTTGAA						1146

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

810

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115

AAATTTAGTG	AAGTATATTT	TATAATGAAA	ACTAAGGCAG	GCTTTGTAGC	TCTTATAGGC	60
AAACCAAACG	CTGGAAAAAG	CACTCTTTTA	AACACTTTAT	TAAACGCTCA	TTTAGCCCTT	120
GTTTCGCATA	AGGCTAATGC	GACTAGAAAA	TTGATGAAAT	GCATCGTGCC	TTTTAAAGAC	180
AAAGAAGGGT	ATGAGAGCCA	AATCATTTTT	TTAGACACTC	CAGGGCTCCA	TCATCAAGAA	240
AAATTACTCA	ACCAAGTCAT	GCTCTCACAG	GCTTTAAAAG	CGATGGGCGA	TGCTGAATTG	300
CGCGTTTTTT	TGCCTTCTGT	GCATGATGAT	TTGAAAGGGT	ATGAAGAGTT	TTTGAGTTTG	360
TGCCAAAAAC	CCCATATCTT	GGCTTTGAGT	AAGATTGACA	CAGCCACGCA	TAAGCAGGTT	420
TTACAAAAAT	TACAAGAGTA	TCAAAAATAT	TCATCGCAAT	TTTTAGCTCT	AGTGCCTTTG	480
AGTGCGAAAA	AATCTCAAAA	TTTAAACGCG	CTTTTAGAAT	GCATCAGTAA	GCATTTAAGC	540
CCTAGCGCAT	GGCTTTTTGA	AAAGGATTTG	ATGAGCGATG	AAAAAATGCG	CGATATTTAT	600
AAGGAAATCA	TTAGGGAGAG	TTTGTTTGAT	TTTTTGAGCG	ATGAAATCCC	TTATGAAAGC	660
GATGTGATGA	TTGATAAATT	TATAGAAGAA	GAACGCATAG	ACAAGGTGTA	TGCGCGCATT	720
ATCGTAGAAA	AAGAAAGCCA	AAAAAAATC	GTGATAGGTA	AAAACGGGGT	GAATATCAAA	780
CGCATCGGGA	CTAACGCGCG	ATTGAAAATG	CAAGAAGTGG	GCGAAAAAAA	GGTTTTTTTA	840
AACTTGCAAG	TGATCGCTCA	AAAATCATGG	AGTAAGGAAG	AAAAAAGCTT	GCAAAAACTA	900
GGCTATATCT	ATCAAAGGAA	TAGGGAT				927

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1176 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116

TTTCTGTCTC	TAAGTCTCAT	AGAAAGGGAC	TTGAAACTA	TGGCAAAGAT	ATTAAACCT	60
AATTTAGATA	GAGATGAGTT	AAACACACTT	TATAAGGCAA	ATCTTGCTTA	TGCTAAAAAC	120
ACGCATGAGC	ATTATTTCAA	ATTTAAAAAA	GATGTAGACT	ACAACTCTT	TAATCCTAGC	180
ATTATGCATG	AGCAATGTTT	TATAAGCTTT	GTAGGCGGAC	AAGGAGCTAA	AAGATTATTA	240

SUBSTITUTE SHEET (RULE 26)

811

TACATACTCT	ACAAGCTCGC	ATTTAATGCT	AAGTCTAATA	AGATTGCCCT	AGATAGACAT	300
TACGCCAAA	TGTTTTTGCA	AGTTGTAGCA	AGAAGCTCTAA	TAAAGAATGT	CAATATATTA	360
GAAGAGCAAG	GTTTTATTGA	AGTCATTAAA	GGAAAACAAA	GATACTTGTA	TGTGTATCTT	420
AAAGATTACA	GAGAATTAGA	ATGCTTAGTG	AAGAGCAAGA	TGGCTAAGTA	TGTGATGTAT	480
TTAAGACAAT	TCCTTGATTA	TTTGGATAGA	AAAAGGCGTT	ATGGCTTTGA	TTTACGCCTT	540
AAAAACCTAG	CCTTTGCTAA	GACCAAAGAA	AGCTTACCCA	GACATTTAAA	CGATAAAGAC	600
TTAAAGAGTT	TTTTAAAAAC	ACTCTTAGAC	TATAAGCCAG	CTACAAGCTT	TGAAAAACGC	660
AATAAGTGTA	TTCTACTTAT	TGTAATACTT	GGGGGACTTA	GAAAATGCGA	AGTGTTAAAC	720
ATAGAATTAA	AACACATTCA	AGTAGAAGAG	CAAACTACT	CTATTTTAAT	TCAAGGTAAA	780
GGTAGAAAAG	AGAGAAAAGC	TTATATTAAA	AAGAGTTTGT	TAGAACCAAG	CTTGAATGCT	840
TGGATTAGTG	ATGATTACAG	ACTAAAATAT	TTCAATGGAG	CATATCTCTT	TAAAAAGGAT	900
AAGCAAAAT	CACAAATTC	TTTAACGCTT	TATAATTTTA	TCCCCTTAAT	CTTTAAATTA	960
GCCCAATCA	AACATTACAA	ACAATATGGC	ACAGGCTTAC	ATCTATTTAG	GCATAGTTTT	1020
GCAACACTCA	TTTATCAAGA	AACCAAGAC	TTAGTTTTAA	CTTCAAGGGC	GTTAGGGCAT	1080
AGCTCCTTAC	TCCTACTTAA	GATTTATATT	CATACCACAC	AAGAGCATAA	CAAGAAAGTG	1140
GCTCTTGTGT	TTGATAGTTT	GATAGAGAAC	AAGAAG			1176

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117

AAAAGAAAGG	AACATTGCAT	GAAAAATTTA	AGGCATTTTA	GAAAGCTTAT	CGCCTTTTTA	60
GGTTTTTCAC	CTCTTTTATT	ACAAGCGGAT	ATGACTACCT	TTTTTAATTC	CATTGAACAA	120
CAGCTACTA	GCCCTACGGC	TAAAGGCATT	TTAATGGTTA	TTTTTTTAGG	ACTTGCTATT	180
TTTATATGGA	AAACTTAGA	TAGATGGAAA	GAAATTTTAA	TGACCGTGCT	TGCTTTAAAA	240
GAAGTCCCCA	TGCAATTAGT	TGCTATTTCA	GTTTCTAATC	TCAAAGAAAT	CAGCTCCAAA	300
GAAAAATTTT	TTTGGCTCAA	TGCTAAGAGT	TTTTTACTCT	CAGGATTGTG	GCCTTTTATT	360
ATGATACCTT	GGCTAGATAT	ATTGAACTCT	TTTGTGCTTT	ATGTGTGCTT	TCTCTTAATT	420
TTTAGCATAG	CGGAGTTCCT	TGATGAAGAT	ATAAGTGACA	TTTTAATCGC	TCATTCCAAA	480
ATTAAACCA	AAGCTAATTC	ATTTTACGCT				510

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

812

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118

AAGTCTCGCA	ACTTTAGCTA	TAATCAAACA	GAAAAAATTT	GGGAAAACCA	CTTTAACTTA	60
TTTTCAGTAG	GAATAGGCAT	GGCAGAAGAA	CAAGAAAATA	CCGCGCAACA	ACCCCAAAAA	120
AAAAGCAAAG	CCCTTTTATT	TGTCATTATT	GGAAGCGTGC	TAGTGATGCT	TTTATTGGTG	180
GGGGTGATTA	TCATGCTGCT	TATGGGGAAT	AAGGAAGAAT	CTAAAGAAAA	CGCTTCTAAA	240
AACACCCAAG	AAGTCCAAGC	TAATCCTATG	GCGAACAAAG	ATCAAGAAGC	CAAAGAAGGC	300
TCTAATATCC	AGCAATATTT	GGTGCTTGGG	CCTTTGTATG	CGATTGATGC	GCCTTTTGCG	360
GTGAATTGG	TCTCTCAAAA	TGCAGACGCG	TACCTTAAGG	CTTCTATTTT	GCTAGAATTG	420
AGCAATGAAA	AGCTTTTGAA	TGAAGTCAAG	GTAAAGACA	CGGCGATTAA	GGACACGATT	480
ATAGAAATTC	TATCGTCTAA	AAGCGTGGAA	GAAGTGCTTA	CTAACAAAGG	CAAAAACAAG	540
CTTAAAGATG	AAATTAAGAG	CCATTTGAAT	TCGTTTTTGA	TTGATGGCTT	TATTAAAAAT	600
GTCTTTTTC	CTGATTTTCA	TATCCAA				627

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119

GGAAGCATGA	TGACGGAAAT	GGAATTAAAG	CTCATTAAAA	TAGACACAAG	CCATTATTTT	60
GAAAAAAAAC	CAGGCTTGGG	GGAGAGAATG	GATTATGCGG	GTGTTTGTTA	TTATAATAAA	120
TTCCAAAGAG	TGAATGCCAT	GCTCACAAGC	TCGCTCATTC	AAAAGCATT	GAAAAGGGAG	180
ATAGAAATCG	CGCACAACCT	CATTTTTCGT	AACGATAAGG	TGGAAAACAT	CGTGTTTGAT	240
TATAATGGGA	GGAATCCGGA	GCGTTTTTAT	CATAAGGCGC	AGTTATTGCT	TCGTGAGGAA	300
GGTTTTATGA	ATTTTACCGC	TTATAACACG	AAGACGCCAG	GGCATTGCA	TTTGTATGTG	360
CATAAGGGGC	ATACGGAATT	AGGCGAGGGT	GAAAGGCTGA	TTAAACTTT	ATCCATGAAA	420
TTAGCGCAAG	GTTTGCCTAA	AGAATGGAGG	GTTTTCCCTA	GCAATGAATG	GCCTAAGGAA	480
TTTAATATTT	TAGCTTTTACC	TTATGAAGTG	TTTGCAAAAG	AGCGCGGGAG	CTCTTGGGCG	540
AAGCATTTA						549

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

813

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120

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CCATTTTGA AAGGATTTT GATGTCAGAA AAAGAAAGAC TGAATGAAGT GATCTTAGAA      60
GAAGAGAATA ATGGGAGTGG TACTAAAAAG GTGTTTTTGA TCGTGGCCAT AGCCATTATC      120
ATTTTGCGCG TGCTTTTAAT GGTGTTTTGG AAAAGCACCA GAGTCGCTCC TAAAGAGACT      180
TTTTTACAAA CCGATAGTGG CATGCAAAAA ATAGGCAACA CTAAAGATGA GAAAAAAGAC      240
GATGAGTTTG AAAGCTTGAA TATGGATTCT CCCAAACAAG AAGACAAGTT AGACAAAGTG      300
GTGGATAATA TTAAAAACA AGAGAGTGAA AATTCTATGC CCATTCAAAC CGATCAAGCT      360
CAAATGGAGA TGAACAACAC AGAAGAAAA CAAGAATCTC AAAAGAATT AAAAGCTGTT      420
GAGCCTATTC CCATGAGCAC TCAAAAAGAA TCTCAGGCTG TGGCTAAAAA AGAAACCCCC      480
CATAAAAAGC CTAAAGTAGC GCCAAAAGAT AAAGAAGCGC ATAAAGATAA AGCTAAGCAT      540
GCAGCTAAAG AGCCAAAAGT CAAAAAAGAA GCTCGTAAAG AAGTTTCTAA GAAAGCTAAT      600
TCTAAACCAA ATCTTACTAA AGGGCATTAT TTGCAAGTGG GGGTTTTTGC GCACACGCCC      660
AACAAAGCCT TTTTACAAGA GTTAAATCAA TTCCCCATA AAATTGAAGA TAGGGGGGCT      720
ACTAAACGCT ACCTCATAGG CCCTTATAAG AGCAAGCAAG AAGCCTTAAT GCATGCCGAT      780
GAAGTCAGCA AGAAGATGAC TAAACCGGTT GTCATAGAAG TGC GG      825

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(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121

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TCAAGGCTTC AAAAAGCCAT AATTAAAGA GTTGAGATGT TGGAAAACT GATTGAAAGA      60
GTGTTGTTTG CCACTCGTTG GTTGCTAGCC CCTTTATGCA TTGCCATGTC GTTAGTGTTG      120
GTGGTTTTAG GCTATGTGTT CATGAAAGAG TTGTGGCACA TGCTCAGCCA TTTAGACACC      180
ATTAGTGAAG CCGATTGTTT TTTATCAGCC TTAGGTTTAG TGGATTGTTT GTTCATGGCC      240
GGGCTTGTTT TGATGGTGCT GCTCGCCAGT TATGAAAGCT TTGTTTCTAA ATTAGACAAG      300
GTGGATGCTA CGGAAATCAC TTGGCTAAAA CACACAGATT TTAACGCTTT AAAATTAAAG      360
GTTTCCCTCT CCAATGTAGC CATTTCGGCG ATTTTCTTGC TCAAACGCTA CATGAGTTTA      420
GAAGACGTTT TATCCAGTAT TCCTAAAGAC ACGCCCCTAT CGCATAACCC TATTTTTTGG      480
CAAGTGGTGA TCCATTGTTT GTTTGTGTGT TCAGCGCTGT TAACCGCTGT TACCAATAAC      540
ATCGCTTTTT CGCAGAAAGA AAGGCAT

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814

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122

GGTTTGA	ACT	ATATTG	ATTT	GGCGTT	ACTT	GTGGTAG	TGG	TAGCCTT	TGG	GATTAG	GGGG	60
TTTTAT	CATG	GCTTC	GTGAG	TGAAAT	AGCA	GCGACT	TTGG	GGATT	GTGCT	TGGCG	TTTAT	120
TTGGCG	TCTC	GCTATT	TCTGT	GGCTGT	TGGG	AATTTA	TTTT	CAGAG	CATTT	GTATG	ATTTA	180
AGAAAT	GAAA	CCATG	ACCAA	TCTCAT	TGGT	TTTTTA	CTGG	TGTTG	GCGTC	CATTG	GGGTG	240
TTTTTT	TTAG	CTCTG	GAGT	GTTGCT	AGGC	AAGAT	GTTAG	TCTTT	AGCGG	TCTAG	GCATT	300
ATAGAC	AAGG	CGTTA	GGGTT	TATTTT	TTTCA	TGTTT	GAGA	CTTTT	TTAGT	GCTTT	CTTTC	360
ATCCTT	TATG	CGCTC	TCTAA	AATGG	ATTTA	ATGAA	AGACG	CTAAC	GCCTA	TTTGA	AAGAA	420
AAGAGC	GCTA	TTTTC	CCAC	CATGA	AAAGC	GTCG	CTAGTA	AGATC	ATGCG	CCTTG	ATGGC	480
GTCAAA	CATG	TGGAG	AAAAA	CCTTA	AAGAC	AACCT	TGAAG	AAATG	AGCGA	TGAAG	TTAAA	540
AATAAA	AGGAT	CTATT	GATAA	CGCAA	AAGAA	TCTTT	TAAATA	AGGCT	ACGGA	TAAGG	GCCTA	600
GAAGCT	TTTAA	AAGAA	AAGGC	TAAAG	ATTTG	CCTAA	AAACA	TGCTA	GAGCC	AAAAC	ACAAT	660
AAACCA	CAACC	AAACCA	CAACC	AATCC	CAACC	CCATC	TAAATA	AAGA	ACCCCT	A		711

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123

AGCTTAT	TGGG	TTGAAA	ACCC	TATATT	ACTA	TCACACT	CAC	AAGTCT	ATAG	CCCCCA	AAGA	60
TGCTGG	TTTT	TTAAA	ACCC	TAGAA	CAGC	GCTTT	TGCTT	TGGGTT	TTTTT	CGTGG	GGGCG	120
TTATTG	TTTT	ACTGG	TGCG	TTTA	AGGCTT	TCGCAT	TCGG	ATTTC	ACTTA	TTTATT	TGCCC	180

815

TTAATCATTG	TTTTAGTAGC	GTTAGTTTAT	GGGGTTTTAT	TTTATTTGTT	GCTCTATTTT	240
GAAAACCCCT	ACTTCAGGCT	TTTGAGTTTT	TTAGGCTCTA	GTTTTATCCA	CCCTTTTGGA	300
TTTGATTGGT	TAGTCCCGGA	TAGCTTTTTT	TCTTATAGCG	TGTTTAGGGT	GGATAAATTA	360
TCTTTAGGGC	TTATTTTTTT	AGCTTGCATT	TTTTTGAGCG	CTCAAAATCT	TAAAAAATAC	420
AGAATGATAG	GGGTTTTTAT	GCTGCTTGGC	GCGTTGGATT	TTCATTTTTT	TAAAAATAAGC	480
GATTTAAAAG	AGGTTGGAAA	TATTGAATTA	GTCTCTACAA	GAACGCCCCA	AGATTTGAAA	540
TTTGACTCAA	ATTACCTTAA	TAATATTGAA	AACAACATTC	TTAAAGAAAT	CAAACTCGCT	600
CAAAGCAAGC	AAAAAACCTT	GATTGTTTTT	CCAGAGACCG	CTTACCCTAT	CGCTTTAGAA	660
AACTCCCCTT	TTAAAACCCA	ACTAGAAGAT	TTAAGCGCCA	AGATCGCCAT	TTTAATAGGG	720
ACATTGCGCG	CTCAAGGCTA	TAGCCTTTAT	AACAGCTCGT	TTTTATTTTC	TAAAAAAAAGC	780
GTTCAAATCG	CTGATAAAGT	GATCTTAGCC	CCCTTTGGCG	AGATAATGCC	TTTACCGGAG	840
TTTCTTCAAA	AACCCCTTGA	AAAGCTCTTT	TTTGGCGAGA	GCGCTTATTT	ATACCGCAAC	900
GCTCCCCATT	TCAGCGATTT	TACATTAGAC	GATTTCACTT	TTGCCCCCTT	GATTTGCTAT	960
GAAGGCACCT	CCAAACCCGC	TTATTCAAGC	AGCCCTTCAA	AAGTTTTTAT	CCTAATGAGC	1020
AATAACGCAT	GGTTTAGCCC	AAGCATTGAA	CCCACCTTAC	AAAGAACGCT	TTTAAAATAC	1080
TACGCAAGGC	GTTATGATAA	AATCATCTTG	CACAGCGCGA	ACTTTTCAAC	TTCTTACATT	1140
TTAAGCCCTA	GCTTATTGGG	CGATATTCTT	TTTAGGAAAC	GATCA		1185

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124

GAAACGATCA	TGATTAAAGC	GATTGATATT	TCTCATGCTT	TTGAAAAACC	TCTTTATAAT	60
GGCGTGAATT	TGCGCATTAA	ACCCAAAGAA	AGCCTGGCGA	TTTTAGGCGT	GAGCGGGAGC	120
GGTAAAAGCA	CGCTTTTAAAG	CCATTTGGCC	ACCATGCTAA	AACCGGATAG	CGGAACAGTC	180
AGTTTGTTAG	AACACCAAGA	TATTTATGCC	CTAAATTTCA	AAAAGCTTTT	GGAATTGCGG	240
CGCTTAAAAG	TGGGCATCGT	TTTTCAATCG	CATTACCTTT	TTAAGGGTTT	TAGCGCTTTA	300
GAAAACTTGC	AAGTCGCTTC	AATCCTAGCC	AAGCAAGAAA	TAAATCATT	CCTTTTAGAA	360
CAATTAGGCA	TAGCCACAC	CCTAAAACAA	GGCGTGGCG	AATTGAGCGG	CGGCCAGCAA	420
CAACGCTTAA	GCATCGCCAG	AGTGCTTTCT	AAAAAACCCC	AAATCATTAT	CGCTGATGAA	480
CCCACCGGGA	ATTTAGACAC	CACTAGCGCT	AATCAAGTCA	TCAGCATGCT	GCAAAATTAC	540
ATTACAGAAA	ACGAAGGGGC	GTTAGTCTTA	GCCACGCATG	ATGAGCATT	AGCCTTCACT	600
TGCTCTCAAG	TCTATCGCCT	AGAAAAAGAA	TCTTTGATTA	AGGAAAAA		648

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

816

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125

TCGCTCGCCC CTAAATTAAA AGCGTTTTTT AAGGTAGCGT TATCCTGTAA GGCGGTGATA	60
AAAATCACAG GCGTAGAGAT TAAAAAATCG TTTTIGATGC GCTTGAATAA TTCCAAGCTA	120
TTCAATTCAG GCACTTGACG GTCTAAAAGC AAGAGGTTAA AGCGCTCAAC AGAGAGCCTT	180
TCA	183

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126

TTTGCCTTGC ATAAAAAGT TCTGTTGGCT TTAAGTGCCA GCTTGATTG CCAAGAGTCT	60
TTGTTGCTA AGGATAAAGA CTACACTTTG GGCAAGGTTT CTACTGCCGG TAAAAAGGAT	120
AGATCTGACT ATTCTGGGCA GGTCAATTTG GGTATAGCG GGATTACCGC GCCTAAGAGT	180
TGGCAAGATG AAGAAGTGAA AAAATACACA GGAAGCCGCA CCGTGATCTC TAACAAAGCG	240
CTCACCCAAC AAGCTAACCA AAGCATTGAA GAAGCTTTAC AGAATGTCCC CCGTCTGCAA	300
ATTAGGAATG CCACAGGTGT GGGGGCTATG CCTACTATCC AAATCCGTGG CTTTGGAGCG	360
GGGGGTTTCA GGCATAGCGA TGGGACGCTC ATGTTAGTTA ATGGTATPCC TGTATTATATG	420
GCCCCCTTACG CTCACATTGA GCTAGACATT TTCCCTGTTA CCTTTCAAGC CATTGATCGC	480
ATTGATGTGA TCAAAGGTGG AGGCAGCGTG CAATATGGGC CTAACACTTA TGGGGGTATT	540
GTCAATATCA TCACTAAACC TATCCCTAAT CAATGGGAAA ACCAAGCGGC TGAAAGGATC	600
ACTTATTGGG CTAAGGCTAG AAACGCTGGG TTTGCCGCTC CCCCTGATAA AACCAGCGAT	660
CCTTCTTTCA TCAAGTCTTT AGGCAACAAC CTCCTCTATA ACACATTATG GAGGAGCGGA	720
GGGATGATCA ATAAGCATGT GGGTATCCAA GCGCAAGCTA ACTGGGTTAG AGGCCAAGGC	780
TTTAGGGACA ATAGCCCTC TAGTATTTCA AACTATTGGC TGGATGGGGT CTATGACATC	840
AATGAAAGCA ATGGGATTAA AGCCTATTAC CAATACTACG ATTTTGCTAT CGCCCAACCG	900

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

817

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127

GTGTCAATAC	TAGTTATAAT	AGAACCTTAC	ACTTTTTACA	AAAGGGAGGA	GAGTGTCAATG	60
TTGGGGAGCG	TCAAAAAAGC	GGTTTTTAGG	GTTTGTGTT	TGGGGGCGTT	GTGTTTATGC	120
GGGGGGTTAA	TGGCAGAGCA	AGATCCTAAA	GAGCTTATAT	TTTCAGGTAT	AACTATTTAC	180
ACGGATAAAA	ATTTCTACTAG	AGCTAAGAAA	TATTTTGAAA	AAGCTTGCAA	ATCAAACGAT	240
GCTGATGGCT	GTGCAATCTT	AAGAGAGGTT	TATTCTAGTG	GTAAGCCAT	AGCGAGAGAA	300
AACGCAAGAG	AGAGCATTGA	AAAAGCTCTT	GAACACACCG	CTACTGCTAA	AGTTTGTAAG	360
TTAAACGATG	CTGAAAAATG	CAAGGACTTA	GCAGAGTTTT	ATTTTAATGT	AAACGATCTT	420
AAAAATGCTT	TAGAATATTA	CTCTAAATCT	TGTAAGTTAA	ATAATGTTGA	AGGGTGTATG	480
CTGTCAGCAA	CTTTTATATA	CGATATGATA	AAGGGTTTGA	AAAAAGATAA	AAAAGATCTA	540
GAATATTATT	CTAAAGCTTG	CGAGTTAAAT	AACGGTGGAG	GGTGTTCCTA	ATTAGGAGGG	600
GATTATTTTT	TTGGTGAAGG	CGTAACAAAA	GATTTCAAAA	AAGCTTTTGA	ATATTCTGCC	660
AAAGCTTGTC	AGTTGAACGA	TGCTAAAGGG	TGTTACGCTC	TAGCAGCGTT	TTATAATGAG	720
GGTAAAGGCG	TGGCAAAGGA	TGAAAAGCAA	ACGACAGAAA	ACCTTGAAAA	GAGTTGCAAG	780
CTAGGATTAA	AAGAAGCATG	CGATATTCTC	AAAGAACAAA	AACAA		825

(2) INFORMATION FOR SEQ ID NO:1128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...417
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128

ACCCGCAAAT	CATCAGCATC	CATGTCAGAA	AATGAAAAAC	ACCCCATAG	GGTGTGCAA	60
CTCATTAAAA	GTTCAAGCAT	CACGCCAGGC	ATTGTCCTAA	ACCCCCACAC	GCATGAAGAA	120
AGTATTAAAT	ACTTGCTAGA	AAGCGTGGGG	CTAGTGCTTT	TAATGAGCGT	GAATCCGGGC	180
TTTGGCGGGC	AGAAGTTTTT	AGATCTAGTG	CTAGAAAAAGT	GCTTGAAAGT	TAAAGAACTG	240
ATCAAACGCT	ACAACCCTAG	CTGTCTTTTA	GAAGTGGATG	GGGGCGTGAA	TGATAAAAAAT	300
ATCTTTGAAC	TCCAACAAGC	GGGCGTGGAT	GTGGTGTTT	CAGGGAGTTA	TATTTTGAAG	360
TCCAAGATC	GTAAGCTGGC	TATTGAAGGC	TTACAGAATG	TCAGACAACC	TCTTGCA	417

818

(2) INFORMATION FOR SEQ ID NO:1129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129

AAACTTTTAA	GAGTTTACA	TAAGATGATT	AAAAAGCGG	CTAAAACCCC	TTTTTTTAAA	60
ATTTTGTTC	AAGCTTTAAG	CTACAATATA	CGCATGAAAG	ATTTAAACAA	GACTATCGGC	120
GTGTTTGTGC	GGCCCACTCA	TCATCAAAAC	GCTCTTTTAA	AAGAGCTAGA	GCAGGCTAAA	180
GAATGGGTTT	TAACGCTTTT	AGAAGATGAG	GGGTTTGAAA	GCTTTATGAT	TGATAGCCTT	240
GATGGGGCAA	AAGATGCACA	ATTGATAAAA	AAAGCTTACG	CGTTTTTGTG	TTTAGGAGGC	300
GATGGCACGA	TTTTAGGGGC	TTTAAGAATG	ACGCATGCTC	ACAATAAGCC	ATGCTTTGGG	360
GTGAGGATTG	GGAATTTAGG	GTTTTTGAGC	GCGGTTGAAT	TGAACGGGTT	GAAAGATTTT	420
TTACAAGATC	TCAAGCAAAA	CAGGATCAAA	TTAGAAGAGC	ATTTGGCTTT	GGAGGGCCGT	480
ATTGAAACA	CTTCTTTTAA	TGCGATCAAT	GAAATCGTGA	TCGCTAAAAA	AAAAGCTTTA	540
GGGGTTTTAG	ACATCAAAGC	GTGCGCGGGC	CATACGCCCT	TTAACACTTA	TAAAGGCGAT	600
GGGCTTATCA	TTGCCACGCC	CCTAGGCTCA	ACCGCTTATA	ATTTGAGCGC	TCATGGGCCC	660
ATTGTGCATG	CTTTAAGCCA	AAGCTATATT	TTAACGCCCT	TGTGCGATTT	TTCTTTAACG	720
CAACGCCCTT	TAGTGTTAGG	GGCGGAATTT	TGCTTGAGTT	TTTGCGCTCA	TGAAGACGCT	780
CTTGTGGTTA	TTGATGGGCA	AGCCACCTAC	GATTTAAAAG	CCAACCAACC	CCTATACATT	840
CAAAAAAGCC	CCACGACCAC	CAAGCTCTTA	CAAAAAAAT	CAAGGGATTA	TTTTAAAGTG	900
CTTAAAGAAA	AGCTGTTATG	GGGGGAAAGC	CCTAACAAAA	AAAGA		945

(2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130

CGCTACAATA	CCCCCATGCA	AAAAAAGATT	TTTTTACTAG	AAGACGATTA	CCTTTTAAGC	60
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819

GAGAGTATCA	AGGAGTCTT	GGAGCATTTA	GGCTATGAAG	TGTTTTGCGC	TTTTAACGGG	120
AAAGAGGCTC	ATGAAAGGCT	CTCTGTTGAG	CGCTTTAAAC	TCCTTGCTTT	AGACGTGCAA	180
GTGCCTGAAA	TGAATAGCTT	GGAATTATTC	AAGCGCATCA	AAAACGATTT	TTTAATCTCT	240
ACGCCTGTGA	TTTTTATCAC	CGCCTTACAG	GATAACGCTA	CCTTAAAAAA	CGCTTTTAAT	300
TTAGGGGCGA	GCGATTATTT	GAAAAAGCCT	TTTGATTGGG	ACGAATTGGA	AGCGCGCATT	360
AAAAGGTTTT	TCAATGATGA	TCCGATAGAA	ATCATGCTTA	ACATTTTTTTA	CCACCAACAC	420
GCTTTGAACG	TTAAAGGGAA	AAAGGAAATC	TTAGCGCCCA	AAACCGCCCA	ACTTTTAGAA	480
TATTTTTTAG	AGCATAAAGG	GCAAAATCAT	AGCTCTCAAG	CGTTAGAAAA	CAACTTATGG	540
GAGCAAGCGA	TTGATGATTC	CACCTTACGC	ACTTACATTA	AAGTGTGCG	CAAGCTTTTG	600
GGTAAAAATT	GCATAGAAAC	GCATAAGGGG	GTGGGCTATC	GCTTTAACCC	ACTA	654

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131

TGTGGCGCTA	ATCGCTCAAA	AGGGCGTGGA	GGTTTTAGTT	CAAAATGCGC	GGGCGCGAAT	60
AGCGGTTATA	GTAACGAAGC	GTATGAAAGC	GTGGGGGCTA	AAATCGTGGA	TTCTAAAACG	120
GCGTGGGGGC	AGGATTGGT	GGTCAAATGC	AAAGAGCCTT	TAGAGCATGA	ATACCCTTTG	180
CTCAAAGAAA	AAGCGACTCT	GTTTAGTTAT	TTGGATTTAG	CGTATCAAAA	AAGCTTGTGT	240
GAAATGTTTA	TTAATAAAAA	AATCACTTCT	ATTTGCACTG	AAACCATTCG	CGGGCCTAAA	300
AACGACTACC	CTATTTTAGC	GCCTATGAGC	GTGGTGGCTG	GGAGGTGGC	TGCGCATTTA	360
GTCCAGCATT	ATTTACTGGC	TTTAGAGCAT	GTTAAAGGGT	TTATGGGTAA	GGGGGTCATG	420
CTAGGGGGTT	TGTCGGGTGC	GCAAAGGGCT	AAAATCGTCG	TAATTGGAGG	CGGTGTGGTT	480
GGCATGGAGA	GCGCGAAAGT	CCTAAGCCAA	ATGGGGGCTA	AAGTAACGAT	TTTAGAATTA	540
GACTACGCTA	AATTACAAA	CCACCCTTAT	TATCATTTGT	ATGATTTAGA	AGTCTTAAGC	600
GTGAATGAAG	CCAATATCAT	TCAAGCCTTA	AACGGGGCGG	TGGGGCTAGT	GGGAGCGGTG	660
CTGTTACAG	CGAGCCAAAC	CCCTAAAGTG	ATCTTAAGAA	GGCATTAAAA	ATACATGCAG	720
ACACAAGGGG	TAGTCATTGA	TGTGGCTTGC	AGTTTAGGGG	GGTGCATAAG	AGCCATACGC	780
CAAGCAAGCC	ATTCTAACCC	GGTGATGTG	GAAGAAAGTT	TGTTGCATTA	TGGCGTGCCG	840
AACATGCCAG	GGATTGTTCG	TAAAACGAGC	TCTACGGCTT	ATAGCCATGC	GAGTGTGCCG	900
TATTTGTTGT	ATTATTTAGA	GCATGGCTTG	AAGGGTTTTT	TAACAGCCAA	CACTAAAATC	960
GTGGCGAACA	CGCTTGAGG	CTTGAGCGCT	TATAACGGCT	ATATCACCCA	AGAAGGCATC	1020
GCTAAAGCGT	TCAATCTGGC	GTTCAAATCG	CCTTTAGAAA	TTTTAAAGGA	GCTT	1074

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

820

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132

AAGGGTAAAA	GGGTAAAAAA	CATGCGAGAT	TTCAATAACA	TTCAAATCAC	ACGCTTAAAA	60
GTGCGTAAAA	ATGCCGTTTT	TGAAAAACTG	GATCTGGAGT	TTAAAGATGG	CTTGAGCGCG	120
ATTAGTGGGG	CTAGTGGGGT	GGGGAAAAGC	GTCCTTATTG	CGAGCCTTTT	AGGGGCGTTT	180
GGGCTTAAAG	AGAGCAACGC	TTCAAACATT	GAAGTGAAT	TGATCGCGCC	TTTTTTAGAC	240
ACGGAAGAAT	ACGGCATT	TTAGAGAAGAT	GAGCATGAAC	CCTTAGTTAT	TAGCGTGATT	300
AAAAAAGAAA	AAACACGCTA	TTTTTTAAAC	CAAACAAGCC	TATCTAAAAA	CACGCTCAAA	360
GCGTTATTAA	AGGGGCTTAT	TAAACGCTTA	TCTAACGACA	GATTCAGCCA	GAATGAAC	420
AACGATATTT	TAATGCTCTC	CTTATTAGAT	GGCTATATCC	AAAATAAAAA	TAGGCGTTTA	480
GCCCCCTTT						489

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133

TCAAATCATA	AAAGGGTTTT	TATGGATTAC	AAACGTTTTA	AAGGCAAGCA	TGCGAACATC	60
GTTATAGAAA	TCATCAGTCT	TTTAGAAAAA	GGGGTTAAAA	AAGCCCAAGA	GATTTTAGAA	120
AAGCCGGACG	CTGGGAGTTA	CACTCAGTTA	GAAAACAGCA	GCGGGGATAC	GCCTATTAAA	180
GCGGATTTAG	CCCTAGATAA	GTTTTTAGAG	GAAACTTTTT	TGAGTTTAGA	GAATGTGAAA	240
AGCGTTTTTA	GCGAAGAAAA	AGAAACGCCT	GTTACTAAAG	AAAACGGCTC	TTATTTGATC	300
GCTTATGACC	CCCTAGATGG	GAGTTCAGTG	ATGGAGGCGA	ATTTCTTAGT	AGGCACGATT	360
ATAGGGGTTT	ATGAAAAGGA	TTATAAGCGG	CAAAATTTAG	TTGCAAGCCT	TTATGTGGTT	420
TTTGGGCATA	AAATAGAATT	GGTGGTGGCT	TTAGAAGAAG	TTTATCGTTA	CGCTTTTTAT	480
CAAAACAAGT	TTCATTTTAT	AGAAACCATC	GTTTTAGAAA	ATAAGGGTAA	AATCATCGCT	540
AGCGGAGGCA	ATCAAAAGGA	TTTTTCTTTG	GGCTTAAAAA	AGGCTTTAGA	AGGGTTTTTT	600
GCAGAAAATT	ACCGCTTGCG	ATACTCAGGA	TCTATGGTGG	CTGATGTCCA	TCATGTGTTG	660
GTTAAAAAGG	GCGGAATGTT	TTCTACCCG	CAAAAGAAAT	TGCGAAAGCT	TTTTGAAGTC	720
TTTCCTTTAG	CCTTGATGGT	TGAAAAAGCT	AAAGGGGAAG	CGTTTTATTT	TGATAAGGGG	780
GTTAAAAAGC	GTTTGCTAGA	TCAAAGCGTA	GAAAGCTACC	ATGAAAAAAG	CGAATGCTAT	840
TTAGCCAGCC	CGCATGAAGC	TCAGATTTTA	GAAAAACATT	TAAAGGGAGA	A	891

(2) INFORMATION FOR SEQ ID NO:1134:

SUBSTITUTE SHEET (RULE 26)

821

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134

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ACTTTTTTAA TTATTTTTTG GGTATCTTTT TTAAGAATTA AGCATTATGT TAAGGAATTA      60
TCCATGAAAA AATTTTTTTC TCAATCTTTG TTAGCTCTTA TTATCTCTAT GAATGCGGTA      120
TCTGGCATGG ATGGTAATGG CGTTTTTTTA GGGGCGGGTT ATTTGCAAGG ACAGGCGCAA      180
ATGCATGCGG ATATTAAATC TCAAAAACAA GCCACCAACG CTACGATCAA AGGCTTTGAC      240
GCGCTCTTGG GGTATCAATT TTCTTTTGAA AAACACTTTG GCTTACGCCT TTATGGGTTT      300
TTTGACTACG CTCATGCCAA TTCTATTAAG CTTAAAAACC CTAATAATAA TAGCGAAGCG      360
GCGCAAGTGG CTAGTCAAAT TCTTGGGAAA CAAGAAATCA ATCGTTTAAAC AAACATTGCC      420
GATCCCAGAA CTTTTGAGCC GAACATGCTC ACTTATGGGG GGGCTATGGA CGTGATGGTT      480
AATGTCATCA ATAACGGCAT CATGAGTTTG GGGGCTTTTG GCGGGATACA ATTGGCCGGC      540
AATTCATGGC TTATGGCGAC ACCGAGCTTT GAGGGCATTG TAGTGGAACA AGCCCTTGTT      600
AGCAAGAAAG CCACTTCTTT CCAATTTTTA TTCAATGTGG GGGCTCGCTT AAGGATCTTA      660
AAACATTCTA GCATTGAAGC GGGCGTGAAA TTCCCATGTC TAAAGAAAAA CCCCTACATC      720
ACTGCAAAAA ATTTGGATAT AGGGTTTAGG CGCGTGATTG CGTGGTATGT GAATTACGTG      780
TTCACCTTTC

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(2) INFORMATION FOR SEQ ID NO:1135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135

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TGGATTGACG CTAAAAAATA AGAAGAAGCC ATCATTCAAG GCTACACTAT CATTGATCCA      60
AGCACCGTTA TTGCGACGCA CACCAGCGAA TTAGTGAAAA AATACGCTGA AGATTTTATC      120
ACCAAAGATG AAGTGAAATC CCTTTTAGAG CGCTTGGCTA AAGACTATCC TACGATTGTA      180
GAAGAGAGTA AAAAAATCCC CACCGGTGCG ATCCGCTCAG TCTTGCAAGC CTTGTTGCAT      240

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SUBSTITUTE SHEET (RULE 26)

822

GAAAAAATCC	CCATTAAGGA	CATGCTCACT	ATTTTGAAAA	CGATTACTGA	TATTGCTCCA	300
TTGGTTCAAA	ACGATGTGAA	TATCTTAACC	GAACAAGTGA	GGGCGAGGCT	TTCTAGGGTG	360
ATCACCAACG	CTTTTAAATC	TGAAGACGGG	CGTTTGAAAT	TTTTAACCTT	TTCTACCGAT	420
AGCGAACAAT	TTTGCTCAA	TAAATTGCGA	GAAAAATGGCA	CCTCTAAGAG	CTTATTACTC	480
AATGTGGGCG	AATTGCAAAA	ACTCATTGAA	GGGGTTTCTG	AAGAGGCTAT	GAAAGTCTTG	540
CAAAAAGGGA	TCGCTCCGGT	GATTTTGATT	GTAGAGCCTA	ATTTAAGAAA	AGCCCTTTCT	600
AATCAAATGG	AGCAGGCTAG	GATTGATGTG	GTCTGTCTAA	GCCATGCGGA	ATTAGATCCT	660
AACTCTAATT	TTGAAGCCTT	AGGCACGATC	CACATTAAC	TT		702

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136

AAAAAAAGA	CCCTAAACAT	TTCACAATTA	GGAAAAACCA	TGCATGTTGC	TTGTCTTTTG	60
GCTTTAGGGG	ATAACCTCAT	CACGCTTAGC	CTTTTAAAG	AAATCGCTTC	CAAACAGCAA	120
CAGTCCCTTA	AAATCCTAGG	CACTCATTG	ACTTTAAAA	TCGCCAAGCT	TTTAGAATGC	180
GAAAAACATT	TTGAAATCAT	TCCTGTTTT	GAAATATCC	CTGCTTTT	TGACCTTAAA	240
AAACAAGGCG	TTTTTTGGGC	GATGAAGGAT	TTTTTATGGT	TATTAAAAGC	AATTAAAAAA	300
CATCAAATCA	AACGTTTGAT	TTTAGAAAA	CAAGATTTTA	GAAGTTTTCT	TTTATCCCAA	360
TTTGTTCCTA	TAACCACTCC	AAATAAGAA	ATTAAAAACG	TTTATCAAAA	CCGCCAGGAG	420
TTGTTTTCTC	AAATTTATGG	GCATGTTTT	GATAACCCTC	CATATCCCAT	GAGTTTAAAA	480
AACCCCAAAA	AGATTTTGAT	CAACCCTTTC	ACAAGAGAAA	ATGATAGGAA	TATTTCTTTA	540
GAGCATTTAA	AAATCGTTTT	AAAACFCTTA	AAACCCTTTT	GTGTTACGCT	TTTAGATTTT	600
GAAGAACGAT	ACGCTTTTTT	AAAAGACAGA	GTGCTCATT	ATCGCGCTAA	AACCAGTTTA	660
GAAGAAGTTA	AAAACCTGAT	TTTAGAAAGC	GATTGTGATA	TAGGGGGGGA	TTCTGTTTTG	720
ATCCATTG	CTTACTATTT	AAAGAAAAAT	TATTTTATCT	TTTTTTATAG	GGATAATGAC	780
GATTTTCATGC	CGCCTAATAG	TGGGAATGAG	AATTTCCCTAA	AAGCCCATAA	AAGCCATTTT	840
ATAGAACAGG	ATTTAGCCAA	AAAATTCCGC	CATTTGGGGC	TATTA		885

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

823

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137

AACACACAGC	GCCAAACACT	CCCCCTAGTC	AAGTCCCGCC	CACACCCCCT	AGTCAAAATT	60
TACCTAAAAC	AAATGTGTGG	AATGGGGTTT	ATTGGCTTCA	AAACAAAAC	TACTCAAACA	120
AAGGCATTTA	TTATATTGAT	CCCAATCTTT	CAGGACAGAG	CGGTCAAAGC	GGCAACACGC	180
TCAGCACCTA	TACAGCTAAT	TTGT				204

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...4239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138

ACGCTAATAT	CAATTTTCAG	CGCAAGCCAG	GCTGATTTTG	GAGGCAACAC	GACTATTGAT	60
ACAGCAAGCT	TTAATTTTGA	CAGCGCAAGT	TCATTGAATT	TTAATAACCT	TACGGCTAAT	120
GGGGCGTTAA	ATTTTAATGG	TTATGCGCCC	TCTTTAACTA	AGGCTTTAAT	GAATGTCAGC	180
GGGCAGTTTG	TTTTAGGGAA	TAATGGGGAT	ATTAATTAT	CTGACATCAA	TATCTTTGAC	240
AACATCACAA	AATCTGTAAC	TTACAACATC	TTAAACGCTC	AAAAAGGGAT	TACTGGCATT	300
AGTGGGGCTA	ATGGCTATGA	AAAAATCCTT	TTTTATGGCA	TGAAAATCCA	AAACGCTACC	360
TATAGCGATA	ATAACAACAT	CCAAACTTGG	TCGTTTATAA	ACCTCTCAA	TTCTTCTCAA	420
ATCATTCAAG	AGAGCATTAA	AAATGGGGAT	CTAACCATAG	AAGTTTTAAA	TAACCCTAAC	480
TCGGCTTCCA	ACACTATTTT	TAATATCGCT	CCTGAGCTTT	ATAATTACCA	AGATTCTAAG	540
CAAAATCCTA	CCGGCTATAG	CTATGATTAT	AGCGACAATC	AAGCAGGCAC	TTATTACTTG	600
ACAAGCAACA	TTAAGGTCT	TTTCAACCCT	AAAGGCTCTC	AAACGCCTCA	AACCCACGGC	660
ACTTATAGCC	CATTTAACCA	GCCTTTGAAT	AGTTTGAATA	TCTACAATAA	GGGTTTTTCT	720
AGCGAGAATT	TAAAACGCT	TTTAGGGATC	CTTTCTCAA	ATTCCGCCAC	CTTAAAAGAA	780
ATGATGAAT	CCAACCAACT	AGACAATATC	ACTAACATTA	ATGAAGTGTT	GCAACTCTTA	840
GATAAGATTA	AAATCACCCA	AGCGCAAAAG	CAAGCGCTCC	TAGAAACGAT	CAACCATTG	900
ACTGACAACA	TCAATCAAAC	CTTTAATAAC	GGGAATCTCG	TTATAGGCGC	TACCCAAGAT	960
AATGTTACAA	ACTCTACTAG	CTCTATATGG	TTTGGGGGCA	ATGGCTATAG	CAGCCCTTGC	1020
CGCGTAGATA	CGGCCACTTG	TTCTTCTTTT	AGAAACACTT	ACTTGGGGCA	ATTATTAGGC	1080
TCAACTTCCC	CTTATTTAGG	CTACATTAA	GCTGATTTTA	AAGCTAAAAG	CATTTATATT	1140
ACCGGGACAA	TTGGAAGTAG	TAACGCTTTT	GAAAGCGGAG	GGAGCGCGGA	TGTAACCTTT	1200
CAAAGCGCTA	ATAACTTAGT	GTTGAATAAA	GCTAACATAG	AAGCTCAAGC	CACAGACAAT	1260
ATCTTTAATC	TTTTGGGTCA	AGAAGGGATT	GATAAAATCT	TTAATCAGGG	GAATTTAGCG	1320
AATGTTCTTA	GTCAAATGGC	TATGGAAAAA	ATCAAGCAAG	CCGGCGGTTT	AGGGAACTTT	1380
ATAGAAAACG	CTCTAAGCCC	TTTGAGTAAG	GCAATTACCCG	CTAGCTTGCA	AGATGAAACC	1440
TTAGGCCAAC	TTATAGGTCA	AAATAACTTA	GATGATTTAT	TGAATAATAG	TGGAGTCATG	1500
AATGAAATCC	AAAACATTAT	CAGTCAAAAA	CTAAGCATTT	TTGGCAATTT	TGTTACCCCA	1560
TCCATCATAG	AAAACCTACCT	TGCTAAGCAG	TCTTTAAAAA	GCATGCTAGA	CGATAAAGGG	1620
CTTTTGAATT	TTATCGGTGG	GTATATAGAC	GCTTCTGAAT	TAAGCTCTAT	TTTAGGCGTG	1680

SUBSTITUTE SHEET (RULE 26)

824

ATTTTAAAGG	ATATTACTAA	CCCCCTACA	AGCCTGCAAA	AAGACATTGG	TGTGGTAGCG	1740
AACGACTTGT	TGAACGAGTT	TTTAGGACAA	GATGTTGTCA	AAAAGCTAGA	AAGTCAAGGC	1800
TTGGTGAGTA	ATATCATCAA	TAATGTTATT	TCTCAAGCGG	GGTTGAGCGG	CGTTTATAAT	1860
CAAGGTTTAG	GGAGCGTGTT	GCCGCCCTCT	TTACAAAACG	CGCTCAAAGA	AAACGATTTA	1920
GGCACTCTTT	TATCGCCTAG	AGGCTTGCCAT	GATTTTGGC	AAAAAGGGTA	TTTTAACTTT	1980
TTAAGCAATG	GCTATGTTTT	TGTCAATAAC	AGCTCTTTTA	GTAACGCTAC	TGGGGGTAGT	2040
TTGAATTTTG	TCGCAACAA	GTCTATTATC	TTTAATGGCG	ATAATACGAT	TGACTTTAGC	2100
AAGTATCAAG	GCGCATTGAT	TTTTGCTTCT	AATGGTGTTT	CTAATATCAA	TATCACCACC	2160
CTAAACGCCA	CTAATGGCTT	AAGCCTTAAT	GCGGGTTTGA	ATAATGTGAG	CGTTCAAAAA	2220
GGAGAAATTT	GTATCAATTT	AGCCAATTGC	CCTACAACCA	AAAACAGCTC	TCCTGCAAAC	2280
TCTAGCGTAA	CCCCCACTAA	TGAGTCTTTA	AGCGTGCACG	CTAATAATTT	CACTTTCTTA	2340
GGCACAAATCA	TCCTAATGG	GGCTATTGAT	TTGTCTCAAG	TAACAAATAA	TAGCGTTATA	2400
GGCACGCTCA	ATCTCAATGA	AAATGCGACC	TTGCAAGCTA	ATAATTTAAC	GATCACCAC	2460
GCTTTTAAACA	ACGCTCTTAA	CTCTACGGCT	AATAATTGATG	GTAATTTTAC	CTTAAACCAA	2520
CAAGCGACTT	TAAGCACTAA	CGCTAGTGGT	TTGAATGTCA	TGGGGAATTT	TAATAGCTAT	2580
GGCGATTTGG	TGTTTAACCT	CAGTCATTCA	GTTAGTCATG	CTATTATCAA	TACTCAAGGC	2640
ACAGCGACGA	TCATGGCCAA	TAATAACCCCT	TTGATCCAAT	TCAACGCTTC	TTCACAGAA	2700
TGGGTACTT	ACACGCTGAT	TGATAGCGCT	AAAGCCATTT	ATTACGGGTA	TAACAACCAA	2760
ATCACAGGAG	GCAAGTAGCCT	GGATAATTAC	CCTAAGCTTT	ATGCGCTCAT	TGATATTAA	2820
GGCAAGCACA	TGGTGATGAC	TGACAACGGC	TTAACCTATA	ACGGGCAAGC	CGTGAGCGTT	2880
AAAGATGGCG	GTTTAGTTGT	AGGCTTTAAG	GACTCTCAAA	ATCAATACAT	TTACACTTCC	2940
ATTCCTTTATA	ATAAAGTGAA	AATCGCTGTT	TCTAATGATC	CTATCAATAA	CCCACAAGCC	3000
CCCACCTTAA	AACAATATAT	CGCTCAAAAT	CAGGGCGTTC	AAAGCGTGGA	TAGCATCGAT	3060
CAAGCTGGGG	GAAATCAAGC	GATTAATTGG	CTCAATAAAA	TCTTTGAAAC	TAAAGGAAGC	3120
CCTTTATTTCG	CTCCCTATTA	TCTAGAGAGC	CACTCCACAA	AAGATTTAAC	CACGATCGCT	3180
GGAGATATTG	CTAACACTTT	AGAAGTCATC	GCTAACCCCTA	ATTTTAAAAA	TGACGCCACT	3240
AATATTTTAC	AGATCAACAC	CTACACGCAG	CAAATGAGTC	GTTTAGCCAA	GCTCTCTGAC	3300
ACTTCAACTT	TCGCCCCGTT	TGATTTCTTA	GAACGCTTAG	AAGCCCTTAA	AAACAAGCGA	3360
TTGCGTGATG	CGATCCCTAA	CGCTATGGAT	GTGATTTTAA	AATACTCTCA	AAGGAATAGA	3420
GTTAAAAATA	ATGTGTGGGC	GACAGGAGTT	GGAGGGGCTA	GTTTCATTAG	TGGAGGTACT	3480
GGAACTTTAT	ATGGTATCAA	TGTAGGGTAT	GATAGGTTTA	TTAAGGGCGT	GATTGTGGGA	3540
GGTTATGCCG	CTTATGGGTA	TAGCGGGTTC	CATGCAAAACA	TCACTCAATC	AGGCTCTAGC	3600
AATGTCAATG	TGGGCGTTTA	TAGCCGAGCG	TTTATCAAAA	GAAGCGAGCT	AACCATGAGC	3660
TTGAATGAGA	CTTGGGGGATA	CAATAAAACT	TTTATCAACT	CCTATGACCC	CCTACTCTCA	3720
ATCATCAATC	AGTCTTACAG	ATACGACACT	TGGACGACTG	ACGCTAAAAT	CAATTATGGC	3780
TATGATTTCA	TGTTTAAAGA	TAAAAGCGTT	ATTTTAAAC	CCCAAGTAGG	CTTAAGCTAT	3840
TATTACATTG	GTTTGTCTGG	TTTAAGGGGC	ATTATGGATG	ATCCTATTTA	CAACCAATTC	3900
AGAGCCAATG	CTGACCCTAA	TAAAAAATCC	GTTCTAACGA	TCAATTTTGC	CCTAGAAAGT	3960
CGGCATTATT	CTCAATAAAA	CTCTTATTAT	TTTGTGATTG	CGGATGTGGG	CAGAGACTTA	4020
TTCAATTAAT	CTATGGGGGA	TAAAATGGTG	CGTTTCATCG	GTAATAACAC	CCTAAGCTAT	4080
AGAGATGGTG	GCAGATACAA	CACTTTTGCT	AGCATTTATCA	CAGGCGGGGA	GATAAGATTG	4140
TTCAAAACCT	TTTATGTGAA	TGCGGGCATA	GGGGCTAGGT	TTGGGCTTGA	TTATAAAGAT	4200
ATTAATATTA	CCGGAATAT	TGGTATGCGC	TATGCTTTT			4239

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

SUBSTITUTE SHEET (RULE 26)

825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139

AGGGATAACA	TGGAGCTTAT	TTTAGGCTCT	CAATCCAGCG	CTAGGGCGAA	TCTTTTAAAA	60
GAGCATGGGA	TTAAGTTTGA	ACAAAAAGCG	CTCTATTTTG	ATGAAGAAAG	CCTAAAAACC	120
ACAGACCCTA	GGGAGTTTGT	CTATTTGGCG	TGCAAGGGGA	AATTAGAAAA	AGCTAAAGAG	180
TTACTTGCGA	ATAATTGCGC	TATCGTGGTG	GCTGATAGCG	TGGTGAGCGT	GGGTAATCGC	240
ATGCAACGAA	AAGCTAAAAA	CAAGCGAGAA	GCCCTTGAAT	TTTTAAAACG	CCAAAATGGC	300
AATGAAATAG	AGGTTTTAAC	TTGCTCTGCA	TTGATTTC	CTGTGTTGGA	ATGGCTGGAT	360
CTATCGGTTT	TTAGAGCGCG	TTTAAAGGCG	TTTGATTGCA	GCGAAATAGA	AAAATATTTA	420
GAGAGCGGTT	TATGGCAAGG	AAGTGCGGGC	TGTGTGCGTT	TAGAGGACTT	TCATAAGCCT	480
TATATTAAAA	GCTCAAGCAA	GAATTTAAGC	GTGGGGTTGG	GGCTGAATGT	GGAAGGCTTG	540
TTAGGGGCAC	TAAAATTAGG	GGTTAAACTT	TCATTATTA			579

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140

AGAATGGCTC	TTTTTGTTTC	AAAGAGTAAG	ATGTTAGAAA	CTTATGCACT	TAAAAGTGGG	60
GCTGTTTTTA	TCTCTGATGC	GCAITTTTTG	CCCAAAAGCC	CTCATTTAAT	CCATACGCTT	120
AAAGAACTTT	TAAGCGCCAA	ACCCCGCAA	GTCTTTTTCA	TGGGCGATAT	TTTCCATGTT	180
CTTGTTGGGCT	ATTACCCCT	AGATAAAGAG	CAGCAAAAAA	TCATTGATTT	AATCCATGGC	240
TTGAGCGAAA	TTTCAAGT	CTTTTACTTT	GAAGGCAACC	ATGATTTTTT	CATGCGTTTT	300
GTATTTCAAT	CCAAAGTAAT	GGTTTTGAG	CGCCAAAACC	AACCCGCATT	ATTCCAGTAT	360
GATAACAAAC	GCTTTTTGCT	AGCCCATGGG	GATTTATTCA	TCATAAAGC	GTATGAATTT	420
TACATCACGC	AGCTCACTTC	CACTTGGGCT	AGATTTTTTT	TAACTTTTTT	AAATTTATTA	480
AGTTTTAAAA	CCTTATACCC	TTTT				504

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

826

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141

AATGATGATG	AGAATAAAGT	AATTGAATTA	AAAACAAGGA	ATAACATGCG	CATCGTATTT	60
ATGGGAACGC	CTAGTTTTCG	TGAAGTGATC	TTAAGGGCGT	TGGTTGAAAA	TGAAGATAAA	120
AAGATAGAAG	TGGTGGGGCT	ATTCACTCAA	AGGGACAAAC	CTTTTGGGCG	CAAAAAAGAA	180
TTGAAAGCCC	CAGAGACTAA	AACATACATT	TTAGAAAATC	ATTTAAATAT	TCCCATTTC	240
CAGCCGCAAA	GTTTGAAAGA	GCCTGAAGTT	CAAATCTTAA	AAGGTTTGAA	GCCTGATTTT	300
ATCGTGGTGG	TGGCTTATGG	TAAGATTTTG	CCTAAAGAGG	TTTAAACCAT	CGCTCCTTGC	360
ATTAATTTGC	ATGCGTCGTT	ATTGCCCCAA	TACAGGGGGG	CTTCGCCCAT	TCATGAGATG	420
ATACTCAATG	ACGATAGGAT	TTATGGCATA	AGCACCATGC	TTATGGATT	GGAATTGGAT	480
AGCGGGGATA	TTTTAGAAAG	CGCTTCTTTT	TTAAGAGAAG	ATTATTTGGA	TTTAGACGCT	540
TTAAGTTTAA	AATTAGCGCG	CATGGGGGCG	ACTCTGCTTC	TTTCAACGCT	CAAAAATTTT	600
CATTCCATCA	CAAGAAAGCC	TCAAGATCAC	ATGCAGGCTA	GTTTTTGTA	AAAAATCGCC	660
AAGGCCGATG	GGTTAGTGGG	TTTTAAAGAC	GCTAAAAACT	TGTTTTTAAA	ATCGCTTGCG	720
TTTAAATCTT	GGCCAGAAAT	CTTTTGTAG	AATAGCCTTA	AACTTTTAGA	ACTGGAGTTA	780
GTGGAGAATG	AAAAGAGCCA	CAAGGAAGGC	GAGATTTTAG	CAATTGATGA	AAGAGGCGTT	840
CTTGTAGGTT	GTTTGAAAGG	CAGCGTGCCT	ATAGCAAGGT	TGCAAGCGGT	GGGTAAAAAG	900
CCTTTGAAAG	CGAAGGATTA	TTGAATGGC	AGGCGTTTGA	AAGTGGGCGG	TATTCTAACA	960

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142

AAAAGCACAA	GGAAAACAAT	AATGGAAGCG	CAATTACGAT	TTACGGGTGT	TGGAGGGCAA	60
GGCGTGTGT	TAGCGGGAGA	GATTTTAGCT	GAGGCTAAGA	TCGTGAGCGG	GGGCTATGGC	120
ACTAAGACTT	CCACCTACAC	TTCCGAAGTG	CGTGGAGGTC	CCACTAAAGT	GGATATTTTG	180
TTAGATAAAG	ATGAAATTAT	TTTCCCTTAT	GCTAAAGAGG	GCGAGATTGA	TTTCATGCTT	240
TCAGTCGCTC	AAATCAGCTA	CAACCACTTT	AAAAGCGACA	TTAAAAAAGG	CGGTATCGTT	300
GTCATGATC	CCAACTAGT	AACCCCCACT	AAAGAAGATG	AGGAAAAATA	CCAGCTTTAT	360
AAAATCCCTA	TCATTAGTAT	CGCTAAAGAT	GAAGTGGGTA	ACATTATCAC	GCAATCTGTG	420
GTGGCGTTAG	CCATTACCGT	GGAGCTGACT	AAATGCGTGG	AAGAAAAATAT	CGTTCTAGAT	480
ACCATGCTTA	AAAAGTTCC	CTGCAAAAGT	CGC			513

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

827

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143

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GCATGTTTAA AACAAGAAAA TATTACTAAT ACGCAGATAT TGCATATCGG TGATAATTCT      60
TGGGCAGATG ACGCTATGCC TAAAAGTTTA GGCATAGCAA CGCTATTTAG AAAAAGCGTG      120
TTGAAACAAT TAGAAGAAGT TTTTCCTAAA TACAAAACAT TTAATCCAAC CAGTGTGCG      180
CAAAGTTTFA TTTTAGGATC TTTATGCGTT TTTTATAAAA ATTATATTCA AAAACATGAA      240
AAATTTGATT ATTGGTTTCT TTTAGGAGCG ATGCAGGCAG GAATTGCAGC CGTTGCTTAT      300
TGCCAGTTTA TCTATAAGGA GATTCACAAA AGAAATATTG ATACTTTAGT GTTTGTTGCG      360
CGAGATGGTT ATTTATGCA AAAAATTTTT AATATTTTAT ATCCAAATTC ATATAAAACT      420
ACTTATGTCT ATGCTCCCAG AATTTTAAAA AAAGCGGTAT TTTTAGAAGT CGTAGAGGGC      480
GAGAGTTTGG AAATTTTGGC TATTTTAGAA GGCGAAGAAG AAGTTAAAAA GAAGCAAATC      540
ACCACCAACC AACAGGCGTA TGTATATCTC TATAGCAATT TTGAACATTG CCGCCATTTA      600
GCGTTAAAT GTTTAGATAA TTACAGAAAA TACTTGTTTT CATCAAATTT AGAAGGAAAT      660
ATCGCTATTG TAGATACGAT TACTTTAGGC TATTCCTCGC AAGGGTTAAT CCAAAAAGCT      720
TTAAATAAAG AAGTTTTTGG GTGCTATGTG GATCTCCTAA GAATTTTAAA TTATGATTGC      780
GTGAGTTTCT TACCTTTTTT ACACCCCTAA CCCGTTTATT TTCATAATTG GGATTTTATG      840
GAGTTTTTGC TAACAAGCCC TGAATACCCT ATTTTAAATG TAGAAAATGG CGTTCCAATC      900
TATCAAAAAG ACGTTTCATC TTGTGAAAAA CACCGCTCTA AAGCTTATGA AAAAATAGTA      960
GAAGGGGCTG TTGGATATGC TTCATATTTT AAAGAAAGTC AAATTTCTTT AGACATTCAT     1020
GATGTGATAG AATGGGTGAA TTTCTTCATT GACAATCCTA GTATTCAAGA TCAAGAGCAA     1080
TTCAGACAAA TTTATTTTCT TCCAGACGCG ACGCATAAAA ACGCTCTGCC CTGTGTTTGC     1140
AACGATGTTT CTTTGTGTGC TTGTATTTTA AAGCCTTCAC AAAGTTATAG CGTATTAATA     1200
AGGAGTCTTA GGACAAACAA GCAAGAGAGG TTGTTTAAAA TATTGTCTCT AATTAAAAAA     1260
ATCTATGGGA AGTTAAAAAA GAAA                                     1284

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(2) INFORMATION FOR SEQ ID NO:1144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1125
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144

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GGGTTATTAG CTTGTTTGCT GGTCTTACTC AATCTAAAGA TTACGCCGAA TTGATGTGG      60

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828

CCTTTAGATA	TTATTGTGGT	TGTGGCATGG	GTGTTATGGG	GGGTTAATAT	GTTTGGGAGC	120
ATGAGCGTTA	GAAGAGAGAA	TACTATTTAT	GTGTCCTTGT	GGTATTACAT	CGCTACTTAT	180
GTGGGTATAG	CGGTGATGTA	TATCTTCAAT	AACCTTTCTA	TCCCCACCTA	TTTTGTGCGT	240
GATATGGGGA	GCGTTTGGCA	TTCTATTTCT	ATGTATTTCAG	GCAGTAATGA	TGCGCTCATT	300
CAATGGTGGT	GGGGGCATAA	TGCGGTGCGT	TTTGTCTTTA	CGAGTGGGGT	GATTGGCACC	360
ATTTATTATT	TCCTGCCTAA	AGAGAGCGGC	CAGCCTATCT	TTTCTTACAA	ACTCACTTTG	420
TTTTCTTTTT	GGAGTTTGAT	GTTTGTTTAT	ATTTGGGCGG	GCGGGCACCA	TTTGATCTAT	480
TCCACCGTGC	CTGATTGGGT	ACAAACCCTT	TCTAGCGTGT	TTTCAGTGGT	GTTGATCTTG	540
CCTTCGTGGG	GGACAGCGAT	TAACATGCTT	TTAACGATGA	GAGGCCAATG	GCACCAGCTC	600
AAAGAAAGCC	CTTTGATCAA	GTTTTTAGTT	TTAGCCTCAA	CTTTCTACAT	GCTTTCCACG	660
CTAGAGGGCT	CCATTCAAGC	CATTAAAAGC	GTGAACGCCT	TAGCCCACTT	CACCGATTGG	720
ATTATAGGGC	ATGTGCATGA	CGGCGTGCTT	GGGTGGGTAG	GCTTCACTTT	GATTGCCAGC	780
ATGTATCACA	TGACCCCTAG	GCTTTTCAAA	AGAGAGATCT	ATTCAGGAAG	ACTTGTGGAT	840
TTCCAAATTT	GGATCATGAC	TTTAGGGATT	GTGCTTTACT	TTTCGTCCAT	GTGGATTGCA	900
GGGATCACGC	AAGGGATGAT	GTGGAGGGAT	GTGGATCAAT	ACGGGAATCT	CACTTACCAA	960
TTCAATTGACA	CGGTTAAGGC	GCTAATCCCT	TATTACAATA	TTAGAGGCGT	TGGGGGTCTT	1020
ATGTATTTTA	TTGGATTTAT	TATTTTGTCT	TACAATATCT	TTATGACAAT	CACGGCAGGC	1080
AAAAAATTAG	AGCGTGAGCC	CAATTACGCC	ACGCCTATGG	CCAGA		1125

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145

GGTTTTGATG	ACGATATGGA	AATTAGAAAC	ATCAAAGAGT	TTGAAAAAGC	TTCCAAAAAA	60
CTCCAAAAAG	ACACTTTTAA	GATCGCTCTC	GCTCTTTTGT	TCCTCATTTG	CGCCGCTTTG	120
CTCGCTCTCA	TTTTTGGGCA	GGCTAATTCT	AAGGGATTGT	TGCTCATCTT	TGCGGCCGTG	180
ATTGGGGGGT	ATATGGCGAT	GAATATTGGC	GCGAACGATG	TGTCTAATAA	TGTCGGCCCCG	240
TCCGTAGGCT	CTAAAGCCAT	TAGCATGGGT	GGGGCGAATT	TGATCGCTGC	GGTTTGTGAA	300
ATGCTAGGAG	CGATCATTGC	TGGGGGGGAA	GTGGTTTCTA	CGATTAAAGG	CCGTATCGTT	360
TCGCCTGAAT	TTATTAACGA	TGCGCATGTT	TTCAATTAATG	TCATGTTGGC	TAGCCTTTTG	420
AGTGGGGCGT	TATGGTTGCA	TGTAGCCACT	TTAATAGGCG	CTCCCGTTTC	CACTTCGCAC	480
TCCGTAGTGG	GAGGGATTAT	GGGGGCTGGA	ATGGCAGCAG	CTGGAATGTC	TGCTATCAAT	540
TGGCATTTTT	TATCCGGCAT	TGTGGCTAGT	TGGGTAATCT	CGCCTTTAAT	GGGGGCTTTG	600
ATAGCCATGT	TTTTTTTAA	GCTCATTAAA	AAGACTATCG	CTTATAAAGA	AGATAAAAAG	660
AGCGCGGCTT	TAAAGGTCGT	GCCTTATTTG	GTGGCGTTGA	TGAGCTTAGC	CTTTAGCTGG	720
TATTTGATCG	TGAAGGTTTT	AAAACGCCTC	TATGCGGTGG	GTTTTGAAAT	CCAGCTCGCT	780
TGCGGTTGTG	TCCTTGCCTC	TTTGATTTTT	ATCCTTTTTA	AAAGATTGTG	GTTAAAAAAA	840
GCCCCGCAAT	TAGAAAATAG	CCACGAAAGC	GTCAATGAGC	TTTTTAATGT	CCCTTTGATT	900
TTT						903

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs

SUBSTITUTE SHEET (RULE 26)

829

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146

AGAATGAAGC	TTAAAAAAC	CCTGACTTAT	CAACACCACG	CCTATTCTTT	TTTAAGCGAT	60
AACACGAATG	AAGTTTTAGA	AAACCCCTAA	GAAATCCTTT	TTGTCAAAAC	GCCTTTAAAC	120
GAAAAATACG	CCCCTTTAAT	CGCAGAAAAA	AACCTGGCTA	TTTTGGATTT	TAACGAGCTT	180
AAAAACTACT	TTGATTTTAA	GATTAAGATT	GTAGGGATTA	CAGGCACTAA	TGGTAAAACG	240
ACCACAGCGA	GCTTGATGTA	TTCTTGCTC	TTAGATTTGA	ATAAAAAGAC	CGCTCTTTTA	300
GGCACAAGAG	GGTTTTTTAT	CGACGACAAA	CACATCAAAG	AAAAGGGCTT	GACCACGCCC	360
ACTCTTTTAG	AGCTTTATAG	CGATTTGGAA	GAAGCGATT	GTTTAAAATG	CGAATACTTC	420
ATTATGGAGG	TGAGCTCCCA	TGCGATTGTC	CAAAAACGCA	TGCTGGGCT	TGATTTGCGT	480
CTTAAAATTC	TCACCAATAT	CACAAGCGAT	CATTTAGATT	TCCATCAAAA	TATAGAAAAT	540
TACAGGGACG	CTAAAAACAG	CTTTTTTAA	GATGAGGGCT	TAAAAGTCAT	CAACAGAGAT	600
GAAACAAACG	CCCTTTTTTA	CCCCATTAA	GCGCGCACT	ACGCACTGGA	TAAAAAGCG	660
CATTGGAATG	TTCAAGCCTT	TTCGCTCAAC	CCTTCCATTA	GCGCGTCTTT	ATGCTACCAA	720
CACGATTTAA	GAGATCCCAA	TCTTAAAGAA	ACCGCCCTGA	TCCATTCCCC	CCTTTTAGGG	780
CGTTACAACC	TTTATAATAT	TTAGCGGGC	GTTTTAGGGG	TTAAATTGCT	CACTCAATTG	840
CCTTTAGAAA	CGATCGCACC	GTTATTGGAA	AACTTTTATG	GGGTAAAGGG	GCGTTTGGAA	900
ATTGTACATT	CTAAACCTTT	AGTGGTCGTG	GATTTTGCCC	ACACAACAGA	CGGCATGCAA	960
CAAGTTTTTG	AAAGCTTTAA	AAATCAAAAG	ATCACCGCTC	TTTTTGGGGC	AGGGGGCGAT	1020
AGGGATAAAA	CCAAGCGCCC	TAAAATGGGA	GCGATAGCGA	GTTGTTACGC	GCATCAAATC	1080
ATCTTAACCT	CAGACAATCC	TAGAAGCGAA	AACGAAGAAG	ACATCATTA	GGATATTTTA	1140
AAAGGCATCA	ATAATTCTTC	TAAAGTCATT	GTAAGAAAAG	ACCGAAAAAA	GGCCATTTTA	1200
AACGCTTTAG	AAAAATTTAA	AGACGATGAG	GTGTTGTTGA	TTTTAGGCAA	GGGCGATGAA	1260
AACATTCAAA	TCTTTAAAGA	CAAAACGATT	TTTTTT			1296

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 981 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147

SUBSTITUTE SHEET (RULE 26)

830

AGATTATTAT	CTCAATTTAA	AACAAGGATA	AACATGCAAG	AATTCAGTTT	GTGGTGCGAT	60
TTTATAGAAA	GGGATTTTTT	AGAAAACGAT	TTTTTAAAGC	TCATCAATAA	GGGGGCTATT	120
TGCGGGGCGA	CGAGTAACCC	TAGTTTGTTT	TGCGAAGCGA	TCACAAAAG	CGCGTTTAT	180
CAAGATGAAA	TCGCTAAACT	CAAAGGCAAA	AAAGCTAAAG	AAATTTATGA	AACTCTGGCA	240
CTAAAGGATA	TTTTACAAGC	CTCTAGCGCG	TTAATGCCTT	TGTATGAAAA	AGACCCTAAC	300
AACGGCTACA	TCAGCCTAGA	AATTGACCCC	TTTTTAGAAG	ACGATGCGAT	TAAAAGCATT	360
GATGAAGCCA	AGCGGTTATT	CAAAACATTA	AACCGCCCCA	ATGTGATGAT	TAAAGTCCCG	420
GCGAGTGAAA	GCGCTTTTGA	AGTCATTAGC	GCTCTGGCTC	AAGCCTCTAT	CCCCATTAAAT	480
GTAACCTTAG	TCTTTTCGCC	TAAAATTGCC	GGTGAAATCG	CTCAAATCTT	AGCCAAAGAA	540
GCACGAAAAA	GAGCGGTCAT	TAGCGTGTTT	GTCTCACGAT	TTGACAAAAG	AATAGACCCA	600
CTAGTGCCAC	AAAATTTGCA	AGCTCAAAGT	GGGATCATGA	ACGCTACCGA	GTGTTATTAT	660
CAATCAACC	AGCATGCTAA	TAAGCTAATA	AGCACCCTTT	TTGCATCCAC	CGGCGTTAAA	720
TCTAATCTT	TAGCTAAAGA	TTACTACATT	AAAGCGCTGT	GTTTTAAAAA	CTCTATCAAC	780
ACAGCCCCC	TAGACGCCCT	AAACGCTTAT	TTGCTTGACC	CAAAACACCGA	GTGTCAAACC	840
CCTTTTAAAA	TACAGAAAAT	TGAAGCGTTC	AAAAAAGAAT	TAAAAACGCA	CAATATTGAT	900
TTAGAAAAA	CCGCCCAAAA	ACTCCTTAAA	GAAGGCTTGA	TAGCGTTCAA	ACAATCCTTT	960
GAAAAGCTTT	TAAGCAGTTT	T				981

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148

GGGTTTAAAG	TGCGTTTGTT	TAGATTTGTG	GGGTGGTATT	ATTTCAAATA	CTTTTTAATC	60
GTGCTTTTAG	CTTTGGAATT	GTTTTTTGTA	GGCATTGACA	GCCTGAAATA	CGCCGATAAA	120
ATGCTGATT	CTGCGAACAT	GATCATTTTA	TTTTTCACCT	ATGATATTTT	ATTCGCTCTC	180
AATTACACCT	TGCCCATTTT	CTTGCTTTTA	GCGATGGTTT	TATTTTATAT	CACCTTCATT	240
AAATCCAACC	AATACACCGC	CCTGCTCTCT	ATTGGATTTT	CCAAATGCCA	GATTTTAAGC	300
CCTATTTTTT	TGATTAGCCT	GTTTTTCACG	GCTGTTTATG	TGGGGTTGAA	CGCGACTCCT	360
TTTGTTGATA	TGGAAGAAAA	AACGCAAAAT	TTAATTTATA	AAGACAATTC	TTTGAGCGTT	420
TCAGAGCATT	TGTTAGTGAA	ATACAACGAT	GATTACGTGT	ATTTTGATAA	GATTAATCCC	480
TTATTGCAAA	AAGCCCCAAA	TATCAAGGTT	TTTCGCCTAA	AAGATAAAAC	TTTAGAATCT	540
TATGCTGAAG	CTAAAGAAGC	TTTTTTTGAA	GACAAATATT	GGATTTTACA	TGACACTACT	600
ATCTATGAGA	TGCCCTTGAG	TTTTGAACTG	GGCGCGAACC	CTTTAAACAC	CACGCATTFA	660
GAAACCTTTA	AAACGCTCAA	AAATTTCCGC	CCTAAAGTTT	TAGACACCAT	TTATCAAAAC	720
AAGCTGCGG	TTTCTATCAC	AGACGCTCTT	TTATCCTTGC	ATGCTTTAGT	GCGCCAAAAC	780
GCGGACACGA	AAAAAGTGCG	CTCGTTTTTG	TATGTGTTTG	CGATTTTGCC	CTTTTTTGTTG	840
CCGTTTTTAA	GCGTTTTAAT	CGCTTATTTT	TCGCCCAGTC	TCGCCCGCTA	TGAAAACCTG	900
GCTCTTTTGA	GGCTAAAGTT	TATCATTATC	ACGCTCGTTG	TTTGGGGGCT	ATTCTTTGCT	960
TTAGGGAAGT	TCAGCATTTT	AGGGATACTC	ATTCTTGAAA	TAGGCGTTCT	ATCGCCCTTT	1020
TTGCTATTTT	TAGCTCTCAG	TCTTTGGTAT	TTTAAAAAAC	TTAATAAGAG	ATTG	1074

(2) INFORMATION FOR SEQ ID NO:1149:

SUBSTITUTE SHEET (RULE 26)

831

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149

AAGAGAAGAG	TGGTGAAATT	CTATACTTAT	AGTGGGGAAA	CGGCCGCTGA	AGCTTTAAAG	60
ATCGCTCAAA	GCCACCATGG	GGTGGATACG	CTGGTGTTTA	AAACCCAAGA	AATCCGTAAA	120
AAAACGCTCA	CTTCTTCTGG	GCTTTATGAA	ATCGTTGTGG	CGGTTGAAGA	AGAAGAAAAC	180
AAAAAAGCCC	CCCTCATTC	AGAGAGTTTG	TATGATGAAG	AATTGAATGA	AGAAGACGTG	240
GTCATGCAGC	TTTCAAGCAC	CGTAGAAGAA	ATGCGCAAAC	TCGCCGGGGT	TTCATCTAAC	300
CAGCGCAACT	ATACTTTTTT	AAAAAATAAG	ACTCTTTTAG	AAAAAGACGC	TCCATTAGAG	360
GATACGCCCT	TAGAGGCTAA	TAAGCAAGAC	GCCTTGTTGC	AAGCCTTAAA	AGATGAAGCC	420
AACCATAAAA	AAGAAAGAGA	AAAAAGAGAA	GTCAAACAAG	AAGAAGAAAT	TAAAGATATT	480
AATGCGCAAC	TAAGTAAAAT	CAGAGACAGC	TTAAAACTCA	TTCAAAACAT	GTTTITGGGAT	540
GAGAAAAACC	CTAATTCTGT	CAATATCCCT	CAAGAATTG	CCGAAATTTA	CAAACTAGCC	600
AAACAAAGCG	GCATGAAATC	CAGTCATTTA	GATGAAATCA	TGCAATTAAG	CCTGGAATTG	660
ATGCCTTTAC	GCATGCGGGA	AAATTCCGTA	ACGATCAAGC	GCTATTTTAG	AGAAGTGTTG	720
CGTAAAAATA	TCCTGTGTCT	CCCTGAAGAT	TTGAATTTGA	GGCAAAAACG	CATTTTAATG	780
CTTGTAAGGC	CAACAGGCGT	GGGGAACG	ACGACTTTGG	CTAAATTAGC	CGCAGCTAT	840
TCTAGAATGC	TGGCTAAAAA	ATACAAGGTG	GGCATTATCA	CTTTAGACAA	TTATCGCATT	900
GGGGCTTTGG	AGCAATTGAG	TTGGTATGCT	AATAAAATGA	AAATGAGTAT	AGAAGCGGTG	960
ATTGACGCTA	AGGATTTTGC	TAAAGAAATT	GAAGCTTTGG	AATACTGCGA	TTTTATTTTA	1020
GTGGATACGA	CAGGCGATT	GCAATACGAT	AAGGAAAAAA	TTGCCGTTT	GAAAGAGTTT	1080
ATAGATGGGG	GTTATAATAT	TGATGTATCC	TTAGTGCTTT	CGGTTACCAC	TAAGTATGAA	1140
GACATGAAAG	ATATTTATGA	TTCTTTTGGG	GTGTTAGGGA	TTGACACTTT	AATCTTTACG	1200
AAATTAGATG	AGAGTAGGGG	GTTAGGGAAT	TGTGTTTCTT	TAGTGATGAA	AAGCCAAAAG	1260
CCTATCAGTT	ATCTTTCTGT	CGGCCAAGAA	GTGCCTATGG	ATTTGAAAGT	GGCTACTAAT	1320
GAGTATTTAG	TGGATTGCAT	GCTAGATGGC	TTAGTAAC	CTAATAAGGA	ACAAGCA	1377

(2) INFORMATION FOR SEQ ID NO:1150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1065 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature

832

(B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150

ATCATGGCTG	ATATTTTAAG	CCAAGAAGAA	ATTGATGCGC	TTTTAGAAGT	CGTTGATGAG	60
AATGTGGATA	TTCAAAATGT	CCAAAAAATA	GATATTATCC	CCCAACGCAG	CGTAACCCTC	120
TATGATTTCA	AGCGCCCTAA	TCGTGTGAGT	AAGGAGCAAT	TGCGCTCTTT	TAGGAGCATC	180
CATGATAAAA	TGGCTAGGAA	TCCTTCCAGT	CAAGTCTCTT	CTATCATGCG	TTCTATTGTA	240
GAAATCCAGC	TTCATAGCGT	GGATCAAATG	ACTTATGGCG	AATTTTGTAT	GAGTTTGCCT	300
AGCCCTACGA	GTTTTAATGT	CTTTTCCATG	AAGCCTATGG	GGGGAACGGG	GGTTTTAGAG	360
ATTAATCCTA	GCATCGCTTT	CCCTATGATT	GACAGACTAT	TAGGGGGTAA	GGGGAGCGCG	420
TATGATCAAA	ACAGGGAGTT	TAGCGATATT	GAATTGAATT	TATTGGATAC	GATTTTACGC	480
CAGGTGATGC	AAATTTTAAA	AGAAGTGTGG	TCGCCTGTGG	TGGAGATGTA	TCCTACCATT	540
GACGCTAAAG	AATCCAGCGC	GAATGTGGTC	CAAATCGTCG	CTCAAAATGA	AATTTCTATC	600
ATGGTGGTTT	TAGAGATTAT	CATTGGGCAT	AGCCGTGGGA	TGATGAATAT	TTGTTACCCG	660
GTGATTTCCA	TTGAGAGCAT	TCCTTCTAAA	ATGGGGAGTA	GGGATTTCAT	GCTTTCAGAA	720
ACGAACTCCA	AAAAGAGCCG	TAATAAGGAA	TTGCAAGCAC	TATTGAGCGG	GGTGAGCGTG	780
GATATGATGC	TGTTTTTGGG	CGCGGTGGAA	TTGAGTTTGA	AAGAAATGTT	GGATTTAGAT	840
GTGGGGGATA	CTATCCGGTT	GAATAAAGTC	GCTAACGATG	AAGTGAGCGT	GTATGTACAT	900
AAGAAAAAAG	GTTATTTAGC	GAGCGTGGGG	TTTCAAGGGT	ATAGGAAAAC	CATTCAAATT	960
AAAGAAGTGG	TTTATAGCGA	AAAAGAACGC	ACTAAAGAAA	TTTTAGAAAT	GCTAGAAGAA	1020
CAGCGCAGAG	GCAAGTGGG	CGATATTATG	AAGATAGAAG	AAGAG		1065

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151

GGAACAAGCA	TGAGTAATCA	AGCGAGCCAT	TTGGATAATT	TTATGAACGC	TAAAAATCCC	60
AAAAGTTTTT	TTGATAATAA	GGGGAATACC	AAATTCATCG	CTATCACAAG	CGGTAAGGGG	120
GGCGTGGGGA	AATCCAACAT	TAGCGCTAAT	TTAGCTTACT	CTTTATACAA	GAAAGGTTAT	180
AAGGTAGGGG	TATTGATGCG	GGATATTGGT	TTAGCGAATT	TAGATGTCAT	TTTTGGGGTG	240
AAAACCCATA	AAAATATCTT	GCATGCCTTA	AAAGGCGAAG	CCAAATTGCA	AGAAATCATT	300
TGCGAGATTG	AACCCGGGCT	TTGCTTAATC	CCTGGGGATA	GCGGCGAAGA	AATTTTAAAA	360
TACATCAGCG	GCGCGGAAGC	TTTGGATCGA	TTCTGATATG	AAGAGGGGGT	TTTAAGCTCT	420
TTAGATTATA	TTGTGATTGA	TACGGGTGCT	GGGATTGGGG	CCACTACGCA	AGCGTTTTTG	480
AATGCGAGCG	ATTGCGTGGT	GATTGTTACC	ACACCCGATC	CTTCAGCGAT	TACCGATGCG	540
TATGCATGCA	TTAAATCAA	CTCCAAGAAT	AAAGATGAAT	TGTTCCCTTAT	CGCTAACATG	600
GTAGCCCAAC	CTAAGAAGG	CAGGGCGACT	TATGAAAGGC	TATTCAAGGT	GGCTAAAAAC	660
AATATCGCTT	CCTTGAATTT	GCACTATTTA	GGGGCGATTG	AAAACAGCTC	CTTATTGAAA	720
CGCTATGTGA	GGGAGCGAAA	GATTTTGAAG	AAAATAGCCC	CTAACGATTT	GTTTTCGCAA	780
TCCATTGACC	AGATAGCGAG	CCTTTTAGTT	TCTAAACTAG	AAACCGGCAC	TTTAGAAATA	840
CCAAAGAAG	GTTTAAAAAG	CTTTTTTAAA	AGGCTTTTGA	AGTATTTGGG	G	891

(2) INFORMATION FOR SEQ ID NO:1152:

SUBSTITUTE SHEET (RULE 26)

833

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1593 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1593
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152

ATTTCCGGAGT	TTAACCACCG	CAGTGGCGCT	TTAATCATT	ATTATGTGAA	TACCATTTTT	60
AAAAAAGCTT	ATCAAAATTC	ACCCACCGCT	TACTTGGAGC	AAAAATACCC	TAAAACCTCC	120
AACAATAAAC	ATGTTACAGA	GGGCTATGTT	AAAGTCTCTT	TAGTGGCTGA	TGAAAAAGAA	180
TTGTTATTAG	AACAAATCTT	ACAAGAAGCT	CAAAACCTTT	TAGAACATCG	TATTGATCCT	240
AAAGACATTA	CCATTTTGTT	CGCCACCAAT	AAGGACGCTT	TAGAAATCAA	AAATTATTTG	300
CAAGAGTATT	TGAGCGCAAT	TCGCCCAAGC	ACGGAATCTA	GCGCGAAATT	GTCTCAATTG	360
GTAGAGTCTA	AAATCATTAA	GAACGCTTTA	GAATACGCTT	TAGCGGAAGA	ACCTTACAAG	420
CCCTTTTATA	AACACAGTGT	TTTAAAACTC	GCTGGATACT	TGCATGATGA	TGTGATCGCT	480
TTACCTGGTT	TTAACCTTAA	AAAAGAGAGC	GTGGCAAGCT	TTGTGTGGAA	AATTATGGAG	540
CAGTTTAAAC	TTTATGAAGA	GCCTGCGCAA	AGCTGTTTGG	AATTAGCGGT	TGGGTGCGAA	600
GACGCCGATG	GATTTTGTGA	AAAATTAGAG	GCTAAAGAGA	TCGCTTCTTT	CAATCCAAA	660
GGCGCGCAGA	TCATGACCAT	TCATAAATCT	AAAGGCATGC	AATTCCCTTA	TGTGATTGTG	720
TGCGAACGCT	TGGGCAATCC	TAATTCAAGC	CATGCCAATC	AACTCCTTGA	AGAATATGAC	780
GGCACAGAGC	TTGCGCGCCT	TTATTACAGA	ATGAAAAATC	GTGAGGTGGT	GGATAAAGAT	840
TACGCCAGGG	CTTTAGACAA	AGAAGAAGCG	GCTAAAGATC	ACGAAGAAAT	TAATGTGTAT	900
TATGTCGCAT	TCACTAGGGC	TGAGTTAGGG	CTGATTGTGC	TGGCCAAAGA	CAAGAAAGAA	960
AGCAAAAAAG	AAAGCAAAAA	CAAAAAAATG	CACGAACAAT	TGGAACCTCGC	ACCTTTAGAA	1020
GAGGGAGAAA	TCGCGCCGGT	TATTTCTCCT	CAAAAAGAGC	CTTTAATGAC	AAGCGTTGTC	1080
ATCAAGCCCC	ATGCCTATGG	CGAGCAAGTC	CAAGAAATAG	AAGAAGAGTC	AGATAGCGAT	1140
TATGAAAGA	ATAACGACCA	GGAAAGCGATC	AATTTTGGTA	TCGCCCTTGA	TAAGGGATTG	1200
GAATACCAAT	ACGCTTACAA	CATTCCCTAAA	CAAAGCGTTT	TAGAATATTT	AACTACCAC	1260
TATGGTTT	ATGGTTTGA	TTACCAAGCG	TTAGAAGAAA	GTTTAGAGCT	TTTGAAGAAC	1320
GATGCAGGGA	TACAAGCCCT	TTTTAAAAAT	CATGCCTTAA	AGGGTGAAGC	GGCTTTTTTA	1380
TTCCAAGGGG	TTGTGTCTAG	GATIGATGTT	TTATTGTGGG	ATAGAGGGCA	AAATTTGTAT	1440
GTTTTAGATT	ATAAAGCTC	TCAAATATAC	CAGCAAAGCC	ATAAAGCGCA	AGTGTCTCAT	1500
TACGCTGAGT	TTTTGCGAAC	TCAAGCCCCC	CATTTTAAAG	TACAAGCGGG	CATTATTTAC	1560
GCTCATAAAA	GACTGCTTGA	AAAATTATGG	GTT			1593

(2) INFORMATION FOR SEQ ID NO:1153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 759 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

834

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153.

TTATCAACCG	CTTATCAGGC	GGTAGAACTC	CATTGGTTCC	TGAAAGCTGT	TCTAGTCCTG	60
GAGCGATCAC	CATCTTCACC	AGAAATAAAA	GGTATTTGGG	ATAGGGATTA	CCACACGCCT	120
ATCACCAGTT	CTTTCACCC	TGATGTGAGC	TATGACAACA	CCGATGATTA	TTATTTCCCT	180
AGAAATGGGG	TTATCTTTAG	TTCTATGCG	ACAATGTCTG	GTTTGCCAAG	CTCTGGCAGC	240
CTCAATTCTT	GGAACGGGTT	AGGCGGGAAT	GTCCGTAACA	CCAAAGTTTA	TGGTAAATTC	300
GCCGCTTACC	ACCATTTGCA	AAAATATTTA	TTGATAGATT	TGATCGCTCG	TTTTAAAACG	360
CAAGGGGGCT	ATATCTTTAG	GTATAACACC	GATGATTACT	TGCCCTTAAA	CTCCACTTTC	420
TACATGGGGG	GCGTAACCAC	GGTGAGAGGC	TTTAGGAACG	GCTCAATCAC	ACCTAAAGAT	480
GAGTTTGGCT	TGTGGCTTGG	AGGCGATGGG	ATTTTACC	CTTCTACTGA	ATTGAGCTAT	540
GGGGTGTTAA	AAGCGGCTAA	AATGCGTTTA	GCGTGGTTTT	TTGACTTTGG	TTTCTTAACC	600
TTTAAAACCC	CAACTAGGGG	GAGTTTCTTC	TATAACGCTC	CCACCACGAC	GGCGAATTTT	660
AAAGATTATG	GCGTTGTAGG	GGCTGGGTTT	GAAAGGGCGA	CTTGAGGGC	TTCTACAGGC	720
TTACAGATTG	AATGGATTTC	GCCCATGGGG	CCTTGGTGT			759

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154

GCGAGGATCA	TGCTTGATAA	ACGCATTAAA	ACGCTTTTAC	TTTTTTTGG	TCTTAATATG	60
GTGTGTTTGA	GCGTGAGTTT	TACCAATAAG	CCTCATTTGT	GTTTTTGGTT	TTTAGTGTTA	120
GGTTGTTTAT	TAGTTTATGA	GTGGCAAAAG	AAACAAAAAA	AAGATTTTCA	AAGCGCTAAA	180
AGTTTGAAAT	TTGACAGCGT	TAGCGAATTA	GAAAAGGATT	TGAACATGGA	AGTAACTAAT	240
GATGAATGGG	ATACCCAT					258

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 816 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

835

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155

TCACGGAGTG	TTGAAATGAA	CTACCCTAAT	CTACCTAACA	GCGCTTTAGA	GATAAGCGAA	60
CAGCCAGAAG	TGAAAGAAAT	CACTAACGAG	CTTTTAAAGC	AATTACAAAA	CGCTTTAAGG	120
AGCAACGCGC	ATTTTAGCGA	GCAAGTGGAA	TTAAGCCTTA	AATGCATCGT	TAGGATTTTA	180
GAAGTGCTTT	TGAGTTTGGA	TTTTTTTAA	AATGCGAATG	AGATTGATAG	CAGTTTAAGA	240
AATTCATTG	AGTGGCTGAC	TAACGCCGGC	GAGAGCTTGA	AATTAATAAT	GAAAGAATAC	300
GAGCGCTTTT	TTAGCGAGTT	TAATACGAGC	ATGCATGCCA	ACGAGCAGGA	AGTAACCAAT	360
ACCTTAAACG	CTAACGCCGA	GAACATTAAA	AGCGAAATTA	AAAAGCTAGA	AAATCAATTG	420
ATAGAAACCA	CGACAAGACT	TTTAACGAGC	TATCAAATCT	TTTTAAACCA	AGCCAGAGAT	480
AACGCTAACA	ACCAAATCAC	AAAAAACAAA	ACCCAAAGCC	TTGAAGCGAT	TACACAAGCT	540
AAAAACAACG	CTAATAATGA	AATAAGCAAC	ACTCAAACGC	AAGCGATAAC	TAATATCACC	600
GAAGCGAAAG	CGAAGCTTAA	TAATGAAATA	AGCAACAATC	AAACGCAAGC	GATAACTAAC	660
ATTAACGAAG	CCAAAGAAAG	CGCTACAACG	CAAATAAACG	CCAATAAGCA	AGAAGCAATA	720
AATAACATCA	CGCAAGAAAA	AACCCAAGCC	ACAAGCGAGA	TCACCGAAGC	GAAAAAGACC	780
GATCATTATC	AAAACATTGA	TTTTTTTGAG	TTTGAA			816

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156

GGATTGTCGG	TGTTAGAACG	CTATGCGAAT	GAAGAAATGA	AAGCCCTATG	GAATGAGCAA	60
ACCAAATTTG	AAACTTATTT	GGAAGTGGAA	AAAGCTGTCG	TTAGGGCGTG	GAATAAGCTT	120
GGGCAAATTC	AAGATAGCGA	TTGTGAAAAA	ATCTGCTTAA	AAGCGGCATT	CAATCTTGAA	180
CGCATCAAAG	AAATTGAAAA	AACCACTAAG	CATGATTTAA	TCGCTTTCAC	TACTTGCGTG	240
GCTGAAAGCT	TGGGCGAAGA	ATCCCGCTTC	TTTCATTATG	GGATCACTTC	TAGCGATTGC	300
ATTGATACGG	CTATGGCGTT	ATTGATGACC	AAAAGCTTAA	AACTCATTCA	AAAAGGCGTT	360
AAAAACCTCT	ATGAAACCCCT	TAAAAATAGG	GCTTTAGAGC	ATCAAGACAC	GCTAATGGTG	420
GGCAGAAGCC	ATGGGGTGTT	TGGCGAACCC	ATCACCTTTG	GTCTAGTTTT	AGCTCTTTTT	480
GCTGTAGAAA	TCAAACGGCA	TTTAAAAGCC	CTGGATTTAA	CGATGGAATT	TATCAGCGTA	540
TGGGCGATCA	GTGGGGGTCT	CGGGAATTTT	GCGCACGCC	CTTTAGAATT	AGAAGAATTA	600
GCGTGCGGAT	TTTTAGGCTT	AAAAACCGCT	AATATCAGCA	ATCAAGTCAT	TCAAAGAGAC	660
CGCTACGCTA	GGCTTGCTAT	CGATCTGGCT	CTTTTAGCGA	GCAATTGTGA	AAAAATCGCT	720
GTCAATATCC	GCCATTTGCA	ACGCAGTGAA	GTCTATGAAG	TGGAAGAAGC	TTTTTCAGCA	780
GGGCAAAAGG	GAGCTCTG	GATGCCTCAT	AAAAGAAACC	CCATCTTGAG	CGAGAATATC	840

SUBSTITUTE SHEET (RULE 26)

836

ACCGGGCTTT	GCAGGGTGAT	TCGCTCTTTT	ACTACCCCCA	TGCTAGAAAA	TGTCGCCTTA	900
TGGCATGAAA	GGGACATGAG	CCATAGCTCT	GTGGAGCGTT	TTGCGCTGCC	TGATCTGTTT	960
ATCACCAGCG	ATTTTCATGCT	CAGCCGTTTG	AATAGCGTGA	TTGAAAATCT	GGTGGTTTAT	1020
CCTAAAAACA	TGCTTAAAAA	TTTAGCTTTG	AGTGGGGGGC	TAGTCTTTTC	GCAACGGGTG	1080
TTATTGGAAT	TGCCTAAAAA	AGGTTTGAGC	AGAGAAGAAA	GCTATTCTAT	CGTGCAAGAA	1140
AATGCGATGA	AAATATGGGA	GGTTTTGCAA	CAAGGCGCTT	TTAAAAACGC	TGATGAAAAT	1200
TTATTTTAA	ACGCCCTACT	TAACGATGAA	CGCTTGAAAA	AATATTGAA	TGAGAGCGAA	1260
ATCAGAGCAT	GTTTTGATTA	CAGCTATTAC	ACTAAAAATG	TGGGGGCGAT	TTTAAAAGG	1320
GTGTTTGA						1329

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157

AATGATAGTG	GCTCAAAACA	TTTCATCTTG	CCTTTTTTAA	CGCTCCTTTT	GCAAATGTAT	60
TTGAGCCGCA	CACGAGAATA	CATGGCCGAT	AGCGGGGCGG	CGTTTTTAAT	GCATGACAAT	120
AAGCCCATGA	TCAGAGCCTT	ACAAAAGATT	TCTAACGATT	ACACCAACAA	CGATTATAAA	180
GAAATAGATA	AAAATAGCAC	CCGATCAGCG	GCCTATCTTT	TTAACGCTGA	AATGTTTAGC	240
ACCCACCCTA	GTATTAAAAA	TCGTATCCAA	TCCTTAAGAA	AGCGTGTGAT	C	291

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158

ATGGAAAAAT	TTTTCAACCA	ATTTTTTGAA	AACATCGGCG	AAGACAAGAA	TCGAGAAGGT	60
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TTGAAAGAGA	CGCCTAAAAG	GGTTCAAGAA	TTATGGAAAT	TCTTGTATAA	A-----	120
GAAGATCCTA	GAGTGGCTTT	AAAAAGCGCG	TATTTTCAAG	GCGTTTGCGA	TGAAATGATA	180
GTGGCTCAAA	ACATTGAATT	TTACTCCACT	TGCGAGCACC	ATTTGCTCCC	TTTTTTGGG	240
AATATTAGCG	TGGGATATAT	CCCTAAGGAA	AAGATTGTAG	GCATTAGCGC	GATCGCTAAA	300
CTCATTGAAA	TTTATAGCAA	ACGCCTGCAA	ATCCAAGAAA	GGCTGACCAC	TCAAATTGCA	360
GAAACTTTTG	ATGAAATCAT	AGAGCCAAGG	GGCGTGATCG	TGGTTTGTGA	AGCCAAGCAC	420
TTGTGCATGA	GCATGCAAGG	GGTGCAAAAG	CAAAATGCCA	TCATTAAAAC	AAGTGTGTTA	480
AGAGGCCTCT	TCAAAAAGA	CCCTAAAACC	AGAGCTGAAT	TTATGCAACT	CTTAAATCT	540

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159

GTTATAATTC	TAGGCATGAG	TAACCCTAAT	TTATCCTTTT	ATTGTAATGA	GTGCGAGCGT	60
TTTGAAAGCT	TTTTAAAAAA	CCATTATTTA	CACCTTGAAG	GCTTCCACCC	TTATTTGGAA	120
AAAGCCTTTT	TTGAAATGGT	GCTTAATGGG	GGCAAAAGGT	TCCGCCCAA	GCTTTTTTTA	180
GCCGTGCTTT	GCTCTTTAGT	GGGTAAAAAA	GATTATTCTA	ACCAACAAAC	AGAATATTTT	240
AAAATCGCTT	TAAGCATTGA	ATGCTTGCAC	ACTTATTCGC	TCATCCATGA	CGATTTGCCT	300
TGCATGGATA	ACGCTATTTT	AAGAAGAAAC	CACCCCACTT	TACACGCCAA	ATACGATGAA	360
ACCACAGCCG	TTTAAATCGG	CGATGCGCTC	AACACCTATT	CTTTTGAATT	GCTCTCAAAT	420
TCCTTACTAG	AAAGCCGTAT	CATTGTGGAA	TTAGTCAAAA	TCCTAAGCGC	TAATGGGGGG	480
ATTAAAGGCA	TGATTTTAGG	GCAGGCTTTG	GATTGCTATT	TTGAAAACAC	CCCCTTAAAT	540
TTAGAGCAGC	TCACTTTCTT	ACACGAGCAT	AAAACCGCTA	AATTGATTAG	CGCAAGCCTG	600
ATTATGGGGC	TTGTTGCGAG	CGGCATTAAC	GATGAAGAGC	TTTTAAAATG	GCTTCAGGCT	660
TTTGGGTAA	AAATGGGTCT	TTGTTTTCAA	GTGCTAGATG	ATATTATAGA	CGTTACACAA	720
GATGAAAAAG	AAAGCGGTAA	AACCACGCAT	TTAGACAGCG	CTAAAAACAG	CTTTGTGAAT	780
TTATTGGGGC	TAAAAAAGGC	AAGCGGTAC	GCCCAAACCT	TAAAAACAGA	GATTTTAAAC	840
GATTTGAATG	CATTAGAACC	TACTTATCTT	TCATTGCAAG	AAAATTTAAA	CGCATTATTG	900
AACACTCTAT	TTAAAGGCAA	GACA				924

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

838

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160

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CTTCTCAATA CATCAAAGAA AAAGCGCAAT TTGAATTGGA ATTTTACTTG CCTAAAGGGA      60
GTTATGCGAG CGCGCTGCTC AAAGAAATCA AGCATGAGAA AGGAGAAAAT AATGACGAAT      120
TTTGAAAAGA TTATCGCGCA AAACAGGCTC AAAACGAACG CGGTTTTAAC CACTTACTGC      180
GCGATTTTGG CTTTATTGGG GTTGTGGTGG GATGCTATTA GAATCAACGC TAATGATTTA      240
GGTATAGCCC TTTTAAACT CATGACTTTT CAAATTTTTC CTACGATTAC TATTGTTCATG      300
TTTGTGGTGG CTTTGTTCAT TATTCTTGTT TGTATCCAAA ATTTTAGCTC TATCATGTTA      360
AGCGGCGATG AATACAAGCT TATTGACCCA AGCAAGGTTT TAAGCTCTAA AGAAAATCAA      420
ATCCATCGCC TTTTGTTAGA GCTTTTAGAA GAGGCTAAGC TTCATTTTGA GCCTAAGCTT      480
TATATCATT ACGCCCCTTA CATGAACGCT TTTGCGAGCG GGTGGGATGA ATCTAATTCC      540
CTTATCGCTC TTACAAGCGC TTTAATAGAG AGGTTAGATA GAGACGAATT AAAAGCCGTG      600
ATCGCTCATG AGCTCAGCCA CATA CGGCAC AACGACATCC GCTTGACCAT GTGCGTGGGG      660
ATTTTGAACA ATATCATGCT ATTGGTGGCT AATTTTAGCG TGTATTTTTT CATGGGGAAT      720
CGCAAGAATA GCGGGGCGAA TTTAGCCCCG ATGATTTTAT GGGTTTTACA GATCATCTTG      780
CCTTTTTTAA CGCTCCTTTT GCAAATGTAT TTGAGCCGCA CACGAGAATA CATGGCCGAT      840
AGCGGGGCGG CGTTTTTAAT GCATGACAAT AAGCCCATGA TCAGAGCCTT ACAAAGATT      900
TCTAACGATT ACACCAACAA CGATTATAAA GAAATAGATA AAAATAGCAC CCGATCAGCG      960
GCCTATCTTT TTAACGCTGA AATGTTTAGC ACCCACCTA GTATTAAAAA TCGTATCCAA     1020
TCCTTAAGAA AGCGTGTGAT C                                     1041

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(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161

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ACACAGCCAC ACAAACAA GAGATTAAAC AAGAGATTAA ACAAGAGATT AAACAAGAGA      60
TTAAACAAGA GATTAAACAA GAGATTAAAC AAGAGATTAA ACAAGAACT AAACAAGAGC      120
AAGAAAAAGA AAATAAGCCT AAACAAACA GTGTCTCGCC CGTTCAAAC GATCAAAAAA      180
CCCCACAAC CCCCT                                     195

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(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

839

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162

GGGGTAAACA	TGCTTATTTT	AGGACACCCT	TTAATCCCTA	GCGCTCGTTT	TGTTTTTCATT	60
AAAAACACCG	ATGCTATTCA	TTCCAGCGCC	AATAACGATA	TAGTGTGTTT	TGAAGCAAAC	120
CCAAAAAATT	TGGAATTAGC	CCAATATTGC	TGTGAAAATG	GCGTCCATTT	TAGCGTGATC	180
TTTTTATCGC	ACAAGATAGA	GACGGACACC	TTTTTTTAT	TCAACGCTTT	CAAACCGCTC	240
TATTGTATTT	TTAAGGATAT	TAAGCAAGCC	ATACTCGCCC	AACAACACGC	CACTAATTAC	300
TTGTTAGATA	GCAAAATCTT	GTTTTCTATG	GATTTTAAAG	ATACAGAGTC	ATGGGAGATT	360
TGCGCTAAAA	ATCAAATAGA	TGGTGTCAAT	TCTAAAGATT	CACTCCTTTT	GAAA	414

(2) INFORMATION FOR SEQ ID NO:1163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163

TTTAAATGCA	ATCTTAAAG	GAGAAGTGCT	TTGAACTAC	TGGTAGTAGA	TGATAGCTCA	60
ACTATGAGAA	GAATTATTAA	AAACACACTT	TCACGCTTAG	GCTATGAAGA	TGTTTTAGAA	120
GCTGAGCATG	GGGTGGAAGC	TTGGGAAAAA	CTAGACGCTA	ATGCCGACAC	TAAGGTGCTT	180
ATTACGGATT	GGAACATGCC	TGAAATGAAC	GGTTGGATC	TCGTTAAAAA	GGTGCGTGCG	240
GATAACCGAT	TTAAGGAAAT	CCCTATCATT	ATGATCACCA	CAGAGGGCGG	TAAAGCTGAG	300
GTCATTACGA	CTTTAAAGC	GGGCGTGAAT	AACTACATTG	TGAAACCTTT	TACCCCCCAA	360
GTTTTGAAAG	AAAAATTAGA	GTTTGTTTTA	GGGACAAACG	AT		402

(2) INFORMATION FOR SEQ ID NO:1164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

840

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164

CGGGTTATGG	CGGTGCGAAT	CATGGCGACG	GTATGGACAA	ACTCATGCAA	GGAATTGGA	60
CTCGTATCGC	TCTTTTTAAG	CTTGTTGGTG	CTAGTGGTGG	TGGGGCGTTT	TTTCATTAAG	120
GGGGCGTTTT	ATGGGCTAAA	AAATGGCGTT	TTGGGCATGG	ATTTGAGCGT	GTCTTTTGGG	180
GCGTTGTCCG	CCTTTGTTTA	TTCCCTTTAT	GCGATGTTGG	TGTCTCAAGA	GACCTATTTT	240
GAAGCGAGCA	GCACGATTTT	AACGCTTGTT	TTTGCTCTTA	AGTTTTTTGA	ATTAAAGGCT	300
AGGCTGTTTT	CGAATGAAAA	ATGCTGGGCC	CTAGAATCGC	ATGAAATCCA	TAGCGTGATC	360
GTTGTAGAAA	ACGGCAAGCA	GATAGAAAAA	CACCCTAAAG	ATGTGGCGAT	AGGCTCGGTT	420
GTTTGGGTGC	CAAGCGGGGC	TAAAATCGCT	TTAGATGGCG	TGCTTTTAAA	TAGCGCGAGC	480
GTGGATGCGT	CTTTGATCAG	CGGGGAGTTT	AAGCCTTTGG	AATTGGGGGT	TAATGATCCA	540
ATTTTAGGGG	GTTATGTGAA	CGTGGGCGTG	CCTTTTAGCT	ATCAAGTGAG	CGCGACCTTT	600
CAAACTCAC	GCCTTTCTAG	TTTGCTAGAA	ACTTTAAAAA	AGAGTTTTTT	AGAAAAAGCC	660
TTAATTGAGA	GCAGCGCGAA	TAAAATCGCG	GATATTTTTT	CTAAAGCGGT	GTTGTTTTTA	720
GCTTTGTGA	GCTTTTTATT	GTGGCAATTT	GTTTGGGGG	GTAATTTTGA	AAAAGCTTTA	780
ATGCTGTGTA	TTAGCGTGCT	AGTCATAAGC	TGCCCTTGCG	CGTTCGCTCG	GCTACGCCCA	840

(2) INFORMATION FOR SEQ ID NO:1165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165

CGTGCTAGTC	ATAAGCTGCC	CTTGCGCGTT	CGCTCGGCTA	CGCCCATAGC	GTTAGTGATA	60
GGGGTGTTTA	AAAACCCCTT	GATCGTGTTC	AAAGAAGCGT	TGTTTTTAGA	AACTCTGGCT	120
AAAGTGAAAA	AAATCTTTAT	AGACAAAACC	GGCACCCTCA	CGCAAAAAGA	AGTCCTTTTA	180
AAAGAAAAAA	TCATTTCATGA	AGAATTTGAT	GAAAGGCTTT	TAAAGAGCCT	TTTAAAAACT	240
AGGGAGCATT	TAGCCCATAA	TGCGATTCTT	AAAACATTAG	ATGGCGATGA	GGTTGATTGG	300
GAAAAGATAG	AGTTTTTCGC	TCATGGCCTG	AAAGCGAGCT	ATCAAAACGA	AACCTTGCTA	360
GTGGGGAGTT	TGAAATTTTT	AAACGCTATG	GGGGTTGATT	TAAAGGTTAA	AGAGAGCGCT	420
AATATCATGG	TAGGCTTTGC	GAAAAATAAG	ACCTTATGCG	CGTTATTTCAT	TTTAGAAGAG	480
CGTTTGAAAG	CTAACGCTAA	AGAAGTCATT	CAGGCTTTAC	AAAATCAAGG	CTTGGAATTA	540
GAAATTTTAA	GCGGGGATAA	TGAAAGCTCG	GTTAAGGAGT	GCGCGAAA		588

(2) INFORMATION FOR SEQ ID NO:1166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2001 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2001
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166

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ACCCCAACCA AAGCCCCTAA AATCGTGCAA GAGCAGGTTA CTTACCCGTT GGTTCCTACT      60
TTCATGAGTA TCGCTAACAT TGACACGGTT AGAGGGATTT CTAGCTATGA AAGCGGCTTG      120
ATTATACATCA TTTTAAAGA CGGCGTCAAT TTGTATTGGG CTAGAGATAG GGTTTTAGAG      180
CAATTAAACA GAGTAAGCAA TCTGCCTAAG GACGCTAAAG TGGAAATAGG GAGCGATTCC      240
ACTTCTATTG GCTGGGCGTA TCAATACGCT TTATCTAGCG ATAGCAAGAA TTTAAGCGAT      300
TTGAAAGTCT TGCAAGATTT CTATTACCGC TATGCGCTTT TGGGGGTTGA TGGGGTGAGT      360
GAGGTGCGGA GCGTGGGGGG CTTTGTGAAG GATTATGAAG TAACGCTTCA AAACGATTCT      420
TTGATCCGTT ATAACCTGAG TTTAGAACAA GTCGCTAACG CGATTAAAAA TTCCAATAAC      480
GATACCGGTG GGGGCGTTAT TTTAGAAAAC GGGTTTGAAA AAATTATAAG ATCGCATGGC      540
TATATCCCAAT CTTTAAACGA TTTAGAAAGAA ATTGTGTTTA AAAAAAGAAG GGCTATCCCT      600
TTAAAAATCA AAGATATAGC GAGCGTTAGG CTAGCGCCCA AACCGCGCAG AGGGGCGGCT      660
AATCTCAACG GCGATAAGGA AGTGGTGGGC GGGATTGTTA TGGTGCCTA TCACGCTGAC      720
ACTTATAAGG TGCTTAAAGC CATTAAAGAA AAAATCGCCA CCTTACAAGC GAGTAACCCCT      780
GATGTGAAAA TCACCAGCGT GTATGACAGG AGCGAATTGA TTGAAAAGG CATTGACAA      840
TTGATTACACA CGCTCATAGA AGAAAGCGTC ATTGTGCTAG TCATTATTGC GATTTTCTTA      900
CTGCATTTCA GGAGCGCTTT AGTGGTGATT ATCACTCTGC CTTTAAGCGT GTGCATCAGT      960
TTCTTGCTCA TCGGTTATTT CAATATTGAA GCGAGCATCA TGAGTTTGGG GGGCATTGCG      1020
ATCGCTATAC GGGCGATGGT GGATGCGGCG ATAGTGATGG TGGAGAACGC TCACAAGCAT      1080
TTGCAACACA TTGACACGAG AGACAACACT CAAAGGGTTA ATGCCATCAT GCAAGGGGTT      1140
AAGCATGTGG GGGGCGCGAT ATTTTTCGCC TTAATGATCA TCGTGGTTTC TTTCTTGCCT      1200
ATTTTCGCGC TCACCGGTCA AGAAGAAAAG CTTTTCGCC CTTTAGCTTA CACCAAAACC      1260
TTTGCCATGC TAGTGGGAGC GCTGCTTTCT ATTACGATAG TCCTGTGTTT AATGGTATGG      1320
CTCATTAAAG GCGCGATTTT AGAAGAGTCC GAAAGCCCCG TTAACGCTTT TTTATGAAA      1380
ATTTATGGCG TGAGTTTGAG GGTGTGCTT AAGTTTCTAGT ACGCTTTTTT AATAGCGAGC      1440
GTCTTAGGTT TAGGGGGTTT AGTTGTAGCG TATAAAAAAC TCAACTGGGA ATTTATCCCC      1500
CAAATCAATG AAGGGGTAAT CATGTATATG CCTGTAACCTA TTAATGGCGT GGGTATTGAT      1560
ACCGCTTTAG AATATTGAA AAAAAGTAAC GCTGCTATCA AGCAACTGGA TTTTGTCAAA      1620
CAGGTTTTTG GTAAAGTGGG GCGCGCTAAC ACCAGCACCG ATGCCGCCGG TTTAGGAATG      1680
ATAGAAACCT ACATTGAATT AAAGCCGCAA AACGAATGGA AAGAAAAGCT CAGCTATAAA      1740
GAAGTTAGGG ACAAATTGGA AAAAACCCCTG CAATTAAAGG GCTTGACTAA TTCATGGACT      1800
TACCCCATTC GTGGCAGAAC GGACATGCTC TTAACCGGCA TTAGAACGCC CCTAGGCATC      1860
AAGCTCTATG GTAACGACAC GGACAAATTA CAAGAAATGG CGATCCTTAT GGAGCAACAG      1920
CTCAAAACCC TCAAAGAGAG TTTGTCCGGC TTTGCCGAGC GATCCAATAA CGGCTACTAC      1980
ATCACGCTGG ATTTGGAACG A

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(2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid

842

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167

CGCAACGTGG AAGCGCGTTA TTATTATGGG GACACTTCAT ACTTTTATTT GCATGCGGGA	60
GTTTACAAG AGTTCGCTCA CTTTGGATCG AATGATGTGG CGTCTTTAAA CACCTTTAAA	120
ATCAATGCCG CTCGCAGTCC TTTAAGCACC TATGCAAGAG CGATGATGGG TGGGGAATTG	180
CAATTGGCTA AAGAAGTGT TTTGAATTGG GCGGTGGTTT ATTTGCACAA TTTGATTTCC	240
AACGCAAGCC ATTTGCTTC CAATTTAGGA ATGAGGTATA GTTTC	285

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168

AAACCTACCA ATGTTTGGGC TAACGCTATT GGGGAGCGA GCTTGAATAG CCGCTCTAAC	60
GCTTCATTGT ATGGCACAAG CGCCGCGCTA GACGCTTCC TTAACGGGAA TGTGAAGCC	120
ATTGTGGGCG GTTTTGGGAG CTATGTTAT AGTCCTTTA GCAATCAAGC GAACTCTCTT	180
AACTCTGGGG CCAATAACGC TAATTTTGGC GTGTATAGCC GTTTTTTTGC CAACCACCCT	240
GAATTTGACT TTGAAGCTCA AGGGGCGCTA GGGAGCGATC AATCAAGCTT GAATTTCAAA	300
AGCACTCTAT TACAAGATTT GAATCAAAGC TATAATTACT TAGCCTATAG CGCCACAGCA	360
AGAGCGAGTT ATGGTTATGA CTTGCGGTTT TTTAGGAACG CTTTAGTGT AAAACCAAGC	420
GTGGGCGTGA GCTATAACCA TTTAGGTTCA ACCAACTTTA AAAGCAATAG CCAATCACAA	480
GTGGCTTTAA AAAATGGCGC GAGCAGTCAG CATTTATTCA ACGCTAACGC AACGTGGAAG	540
CGCGTTATTA TTATGGGGAC ACTTCATACT TTTATTTGCA TCGGGGAGTT TTACAAGAGT	600
TCGCTCACTT TGGATCGAAT GATGTGGCGT CTT	633

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs

843

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169

AATAAAATCC TAGCCAGTGA GCTAGAAATTT AAATTTTAA TCAAAGGAGT CATCATGGCA	60
CACCATGAAG AACAAACACGG CGGGCACCAC CACCATCACC ACCACACACA CCACCACCAT	120
TATCATGGCG GCGAACACCA CCATCACCAC CACAGCTCTC ATCATGAAGA AGGTTGTGTC	180
AGCACTAGCG ATAGTCATCA TCAAGAAGAA GGTGTGTGCC ACGGGCATCA CGAG	234

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170

GGGGTTTTGA TTAGAACCCC CAAGCATTTA ACCAAGCAAG AGAGCGTGAA TTTAGGGGCT	60
TACTACACGC CCCCTTATTT AGTGGATTGC GCTTACAAGC TTTTAAAAA GCATGTTGGT	120
ATTGAAACT ACACGCTTTT AGACACCGCA TGTGGTAATA AAGAGTTTTT AAAGCTCCAC	180
CACCTAAAA AAATAGGAGC GGATATTGAC CCTAAGTGTG ATGCTTTAAT AATAAACGCT	240
CTAGCCAATC CTAAAAGAGA AAATTATGGC ATTAGCCAAG ATGAACCTTT AATCATCGTG	300
GGCAATCCCC CCTATAACGA TAGAATCTCC TTTATCAAAC AAGATATTAA AAATAAAGAT	360
TTCAATTTTG AGATAGACAA CGATTTGAAA TCCCGAGATT TAGGGATAAG TTTTTTAAA	420
TCTTTTGCAA TTTTAAAGCC GCGGTTTATT TCGTGCTAC ACCCTTTATC TTATCTCATC	480
AAAGAAGCTA ATTTTAAGCA ATTAAAGCTA TTTAAGGATC ATTACAGGCT TTTAGACGCT	540
TTTGTGTTT CTCTAAATC TTTCACTAAA AGTAACGAAT TTCCTATTGT GATAGCTTTA	600
TATGAGCGAG GGCGAATGGA CTATGCAGGT ATTAGGCGTT TTGTTTTTCC AACTGATTGC	660
GATACGACGC TATGCTTAAA CGATTTTGAC TACATAGCCA ATTATGTGGA TAAATACCTT	720
AACGCTAAA AGGTTGGGGC ATGCGTGGGC TATTTTTTC CTATGCGAGA CATTACGCT	780
CTCAACGCA ACAAACTTT TTTAAACGCG CCAAGCGAAA ATGCGGTGCG AATCAGTCAA	840
GATAAATGA TTTATTACCA ATATATCCAT TATTTTAAGG AAATTGCTCC TAAATCCCT	900
TATTATTTG GTAATTGGA TATTATCATT GATCATTTTG CTTTTTTAGA AATTAAAGAC	960
GCTTTTTTAA AAGATAAAG AGCGCGTTTA GAATATTTTA AAAAATTGTT TCAAGGACAC	1020

SUBSTITUTE SHEET (RULE 26)

844

CCTTGTGAGT TTGAT

1035

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171

AATATTTTAA	AAAATTGTTT	CAAGGACACC	CTTGTGAGTT	TGATTAAAGT	TAGTGGTGAT	60
AAAAAAGTGA	TTGAGGTTTC	TATTCCTTTA	ACTTCCATTT	CAGGCAAAGC	GCGTGTGAAA	120
ATCAGACATG	CCTTTAGCGA	TTATGGTATT	TCAACAGCGA	CTAGAAAAAT	CCCTTTTAGT	180
TTAAAGCATT	ATGTAGAGTG	GCAGATCGGT	TATGATGTCC	CCATTAAAGA	TAAAGAAAAA	240
TTTGAAGTCA	CTACTTTTAA	AGATGAAAAA	TATCATTTTT	TAGGGGCTAA	TAATAAAGTA	300
AAAACCTCTT	ATGAATTGAG	CGAAATGATT	TATTACGCTA	AGCGATTGGG	TTTAATCAGT	360
TTAGAAAATT	TAGAAAATAC	TTTAAAATTT	TTAGAAAAAC	AAAAACAATT	TATAGAAGAT	420
AAATTTATGA	TTACAAGAGA	AAGATTTAGA	TCGCATCAAT	TTGGTGCCAT	GGATTTTGAA	480
CTCTTACGCA	TTTCTTATCC	TTTGCTCATT	CATTCTTTTG	ATGATAATGA	GTTGAGCGAA	540
ATAGTTATTA	AGGAACAACA	ATATGGCTCT	AAAACCCAAG	CCATGCTGTA	TTTTTGCTTT	600
TCTATTTTGG	AGTTAAAAAC	CGCTACCCCC	TTATTAAACA	GAACCGCTAT	GCCCAAAGAA	660
CATGCCCTTT	TGATTATCCA	TGAAACCAAC	GCTCTTGTGT	TTTTAGAAAT	GCTTAAATTT	720
TTTGGACTTT	TAAGCCAAGT	GCACCATAAC	GATGTGTTAA	AGATTTTAGA	AAAAATACTT	780
CAAAAT						786

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172

SUBSTITUTE SHEET (RULE 26)

845

TTGAAGGCAT	TAAACGACTG	CATGGTATTT	TTTCATAAGA	AAATTATTTT	AAATTTTATC	60
TATTCCTTAA	TGGTTGCTTT	TTTATCCCAT	TTATCCTATG	GGGTTCTTTT	AAAAGCCGAT	120
GGAATGGCTA	AAAAGCAAAC	TCTTTTAGTG	GGTGAAAGGC	TTGTGTGGGA	TAAGCTCACG	180
CTGTTAGGGT	TTTTAGAAAA	AAACCATATC	CCCCAAAAAC	TCTACTACAA	TTTGAGCTCT	240
CAAGATAAAG	AATTGAGTGC	TGAAATCCAA	AGCAATGTTA	CCTACTACAC	TTTAAGAGAT	300
GCAAATAACA	CGCTCATTCA	AGCCCTTATC	CCTATTAGCC	AGGATTTGCA	AATCCATATT	360
TACAAAAAAG	GAGAGGATTA	TTTTTTAGAC	TTTATCCCCA	TTGTTTTTCAC	TCGTAAAGAA	420
AGAACCCTCC	TTCTTTCTTT	ACAAACTTCG	CCCTATCAAG	ATATTGTCAA	AGCCACCAAT	480
GACCCCTTTT	TAGCCAACCA	ATTGATGAAC	GCCTATAAAA	AAAGCGTGCC	TTTTAAACGC	540
CTAGTGAAAA	ACGATAAAAT	CGCTATCGTT	TATACAAGGG	ATTATCGTGT	GGGGCAAGCG	600
TTTGCCAGC	CGACCATCAA	AATGGCGATG	GTTAGCTCTC	GTTTGCACCA	ATACTATCTT	660
TTTTCCCAT	CAAACGGGCG	TTATTACGAT	TCAAAAGCGC	AAGAAGTGGC	AGGGTTTTTA	720
CTAGAAACCC	CGGTGAAATA	CACCCGCATT	TCTTCGCCTT	TTTCGTATGG	GAGGTTCCAT	780
CCTGTTTTAA	AAGTTAAACG	GCCTCATTAC	GGCGTGGATT	ATGCGGCTAA	ACATGGCAGT	840
TTGATCCATT	CTGCTTCAGA	CGGCCGTGTG	GGTTTTATAG	GGGTAAAGGC	GGGTTATGGG	900
AAGGTGGTTG	AAATCCATTT	GAATGAATTG	CGCTTGGTGT	ATGCTCACAT	GAGCGCGTTC	960
GCTAACGGAT	TAAAAAAGG	CTCGTTCGTT	AAAAAAGGGC	AAATCATAGG	AAGAGTGGGA	1020
AGCACGGGTT	TAAGCACCGG	GCCGCATTTG	CATTTTGGCG	TGTATAAAAA	CTCCCGCCCC	1080
ATTAACTCTT	TAGGCTATAT	CCGCACCGCT	AAAAGCAAGC	TGCATGGCAA	ACAAAGAGAG	1140
GTTTTTTTAG	AAAAAGCTCA	GTATTCTAAG	CAAAATTAG	AAGAACTTTT	TAAAACCCAT	1200
TCTTTTGAAA	AAAATTCATT	TTATCTTTTA	GAGGGTTTT			1239

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173

GGATGCTTGA	TGAAAGCAT	TTTGCTCTTT	ATGATTTTTG	TAGTTTGTCA	GTTAGAAGGC	60
AAAAAATTTT	CACAAGATA	TTTTAAGGTG	GATTATAACT	ACTATTTGCG	CAAACAGGAT	120
TTGCACATCA	TTAAACGCA	AAACGATTTG	TCCAATGCCT	GGTATCTCCC	TCCACAAAAA	180
GCCCCCAAAG	AACATTCTTG	GGTGGATTTT	GCTAAAAAAT	ATTTAAACAT	GATGGATTAT	240
CTAGGCACCT	ATTTTTTGCC	TTTTTATCAT	AGTTTCACCC	CCATTTTTCA	ATGGTACCAC	300
CCTAATATCA	ACCCCTACCA	ACGCAATGAG	TTTAAGTTCC	AAATCAGTTT	TAGAGTGCCT	360
GTATTTAGGC	ATATTCTTTG	GACTAAAGGC	ACGCTTTATC	TGGCTTATAC	CCAAACTAAC	420
TGGTTTCAAA	TTTATAATGA	CCCTCAATCC	GCCCCCATGC	GAATGATCAA	TTTCATGCCT	480
GAATCATCT	ATGTTTATCC	TATTAATTTT	AAACCTTTTG	GGGGTAAAAAT	AGGGAATTTT	540
TCTGAAATTT	GGATAGGTTG	GCAGCACATT	TCTAATGGTG	TGGGGGGTGC	GCAATGTTAC	600
CAGCCTTTTA	ATAAAGAAGG	TAATCCTGAA	AACCACTTTC	CAGGACAACC	TGTAATCGTT	660
AAAGATTATA	ACGGGCAAAA	AGATGTGCGC	TGGGGGGGGT	GTCGTTCCGT	GAGCGCGGGC	720
AACGCCCTGT	GTTTCGTTTG	GTGTGGGAAA	AGGGAGGCC			759

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

SUBSTITUTE SHEET (RULE 26)

846

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...272
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174

ATGTGAAATT AAAGGGCATG GATAAAGAAG AAAATGAAGA AAATAAAATT AACCAAGCGA	60
ATGATAGCTA CGGCCAAAAA AGCCCTTTCC AAAAGCTATG GATATTGTTT GGTGGGGCGT	120
TTTTTAATTT TCTTTTTCG GTTTTAGTGT ATTTTTTCT GGCATTGAGC GGGGAAAAAG	180
TCTTACTGCC CGTCATTGGC GGTTTAGAAA AAAACGCGCT AGAAGCCGGG CTGTAAAGG	240
GGGATAGAAT CCTTCTATCA ACCATCAAAA AA	272

(2) INFORMATION FOR SEQ ID NO:1175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175

AGAATTGAGT GGGGTAATAG GCATTGTGGG GCGTTAAGCC ATGCCAATAG CGTGAGCATG	60
CTTTTGTGT TTGGGGCGTT TTTATCTATC AATCTAGGGA TTTTAAATTT ATTACCCATT	120
CCAGCCTTAG ATGGGGCGCA AATGCTAGGG GTCGTTTTTA AAAATATTTT TCATATCGCT	180
TTGCCAACGC CCATACAAAA TGCGTTGTGG CTAGTGGGGG TGGGGTTTTT GGTTTTGTGTC	240
ATGTTTTTAG GGCTTTTTAA TGACATTACT CGTTTGCTA	279

(2) INFORMATION FOR SEQ ID NO:1176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

847

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176

AATTTAGGCG	GAGCGGCCAA	TGTGGCTAAT	AACCTTACCT	CTTTAAAAGC	TAAAGTCTTT	60
TTATGTGGGG	TAGTGGGAGA	TGATTTAAAA	GGCAAGCATT	TCATTAGCAC	TTTAAATTCT	120
ATAAGGATTG	ACAC TTCAGG	TGTTTTAATA	GATAAAACCC	GTTGCACCAC	GCTTAAACG	180
CGCATCATCG	CGCAAAACCA	GCAAATCGTG	CGCGTGGATA	AGGAAATCAA	AGACCCCTTA	240
AACGCTGATT	TAAGAAAGAA	TC TTTTAGAT	TTTATCGCAG	AAAAAATTCA	AGAAATAGAT	300
GGCGTGATCC	TTTCAGATTA	CAATAAGGGT	GTGTTGGATT	TTGAACTCAC	TCAAACCATC	360
ATCACGCTAG	CTAATAAGCA	TCATAAGCTC	ATTTTATGCG	ACCCTAAAGG	AAAGGATTAT	420
AGCAAATATT	CCCATGCGAG	TTTGATCAGC	CCTAATCGCG	CTGAATTAGA	GCAAGCGCTC	480
CATTTGAAAT	TAGACAGCCA	TGCGAATTTA	TCAAAAAGCGC	TCCAAATTTT	ACAAGAAACT	540
TATCATATCG	CTATGCCTTT	AGTAACCTTG	AGCGAACAAG	GCATCGCTTT	TTTAGAAAAA	600
GGCGAGTTAG	TCAATTGCCC	CAC TATCGCT	AAAGAAGTTT	ATGATGTAAC	GGGGGCAGGC	660
GATACGGTGA	TAGCGTCTTT	AACGCTCTCT	TTATTGGAAT	CAAAAAGCTT	GAAAGAAGCT	720
TGCGAGTTTG	CTAATGCGGC	TGCGGCGGTG	GTGGTGGGTA	AAATGGGGAG	CGCGTTAGCG	780
AGTTTAGAAG	AAATCGCTTT	GATTTTGAAC	CAAACGCACC	CTAAAATCCT	CCCTTTAGAA	840
AAGCTGTTAG	AAACTTTAGA	ACGCAACCAG	CAAAAAATCG	TTTTCACCAA	TGGCTGTTTT	900
GATATTCTCC	ATAAAGGGCA	TGCGAGCTAT	TTGCAAAAGG	CTAAAGCTTT	AGGGGATATT	960
CTTGTTGTGG	GGTTAAATAG	CGATAATTCC	ATTAAAAGGC	TTAAGGGGGA	TAAACGCCCC	1020
ATAGTGAGCG	AAAAAGACAG	GGCGTTTCTT	TTAGCGAGCT	TGTCTTGCGT	GGATTATGTT	1080
GTGGTGTGTTG	GAGAAGACAC	GCCCATAAAA	TTGATTCAAG	CCCTAAAGCC	TGATATTTTA	1140
GTCAAGGGAG	CGGACTACCT	CAATAAGAA	GTCATAGGGA	GCGAGTTGGC	TAAAGAAACC	1200
CGTTTGATAG	AATTTGAAGA	AGGTTATTCC	ACAAGCGCTA	TCATAGAAAA	AATTTAAAGG	1260
ACACATAATG	AT					1272

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 963 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177

GGATCGCTTA	TGTTGAATGT	GT TTTTCAAG	CAGCAAAAAT	TCGTCATTAA	AAAACGCTTT	60
AATGACTTTA	ATGGTTTTGA	TATAGAAGAA	AATGAAGTGT	TGTGGTTTGA	ATTAATCAAC	120
CCTACGCCCA	ATGAATTAGC	CACTCTAAGC	CAAGAAATACG	CTATCCACTA	CAACACGGAT	180
CATTCCTCAAC	GAGTCTCATC	AGTTACCAAA	TACTGGGAAG	ACAGCTCCAG	CGTTACGATC	240

SUBSTITUTE SHEET (RULE 26)

848

AACGCTTTTT	TCACCAACCA	GGATGAAAAT	GAGACTTTCC	ACATGGAAAT	GGCGACCTTT	300
ATTTTGTCTA	ATAACATTCT	TTTCACGATT	TATTACGGGA	CTTTAGAAAT	CTTTGATTCT	360
ATCCAAAAAA	AGGTTTGGC	TAGCCCTAAA	AAATTTGAAG	ACGGGTTTGA	TATTCTAACT	420
AAAATCTTTG	AAGTGTATTT	TGAAAAAGGG	GTGGAATGTT	TGGAATGGAT	CAACAAACAA	480
ACGAGCCTGT	TGCGCAAAAA	CATCATTTTC	AAAGAACTT	CTACGCATGA	TGATATTTTA	540
GTGCGCTTGT	CCAATTGCA	AGAATTTAAT	GTGGCTTTAA	GGGATTCCTT	TTTTGACAAA	600
CGGCGCATTA	TCACCGCTTT	ATTAAGGAGC	AATAAAGTGG	ATAGCGATAC	TAAAAATAAT	660
TTAAATATCA	TTTTAACCGA	TTTAGCTCT	TTGGTGGAGT	CTACAACGGT	CAATCTCAAC	720
TCGCTTGATA	ACATTCAAAA	CCTGTTTCGCT	TCTCAAGTCA	ATGTGGAGCA	AAATAAAATC	780
ATTAACTCT	TCACTGTGGC	GACTATGGCG	ATGATGCCCC	CCACATTGAT	TGGCACGATT	840
TATGGCATGA	ATTTTAAATT	CATGCCGGAG	TTAGAATGGC	AATACGGGTA	TCTTTTTGCG	900
CTGATTGTCA	TGGCGATTTC	TACGATTTTG	CCGGTGATT	ATTTCAAAA	GAAGGGTTGG	960
TTG						963

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178

CCTTTCATGG	AATTTTTATC	CTCACTCTTA	GACGCTCTTT	CTACACCGCA	TGGCATAGTC	60
TCCTTGGCTA	CGCTCACGCT	TTTAGAGATC	GTTCTAGGGA	TTGATAATAT	CATTTTTATC	120
ACGGTGATGG	TTTATAAACT	CCCCAAACAC	CAGCAAAATA	AGGTCATGAT	TTTAGGCTTG	180
GGCTTAGCGA	TGATCACTCG	TATAGGGCTT	TTAGGGAGCT	TGTTTTTCAT	CAGCCATTG	240
CAAAAGCCTT	TATTTCGCTAT	AGCGGGCATG	AGCTTTTCAT	GGCGTGATGT	GGTGCTGCTT	300
TTAGGGGGGG	CGTTTTTGGC	TTTTAAGGCG	TTAGTGGAAT	TAAAAGAGCA	GATCTATCCT	360
AAAGAAAAAC	GCCAAGAAAA	AGCGTTTGGC	TTTTTCATCA	CTTTAATAGA	AATCATGTTT	420
TTAGACATTG	TTTTTCTTT	GGACTCCGTG	ATCACGGCTA	TTGGGATCGC	TAAACACTTA	480
GAAGTCATGG	CGCTTGCTAT	TATTTTATCT	GTAATCGTGA	TGATGTTTTT	TTCCAAAATC	540
GTTGGCGATT	TTATTGAAAA	GCATTATCGC	GTCAAAACTT	TAGCCTTTGT	GTTTTTGCTC	600
GTTGTGGGCG	TGTTTTTGT	TTTAGAAGGC	TTGCATTTAC	ACATCAATAA	AAACTATTTG	660
TATGCGGGTA	TTGGTTTTGC	CTTGCTCATA	GAATGCTTGA	ATATTTTCAT	AGAAAAGAAA	720
ATGAAAAAAA	GT					732

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

849

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179

GTATATGGCT	TTTGGGCTTG	TGTTTGTGC	TAGGGATTTA	AGTTTGGTTT	TGTTTATTTT	60
GCGCAAACAA	GGGCGTTTCA	ATTAGACAA	AACCATTCTT	TCCATTAGCG	CTATCAATGA	120
AATGAGCATG	ATTTTAGGCC	TGTTTCATGCT	CACAGCCGGG	AATTTCTTAG	GTGGGGTGTG	180
GGCGAATGAA	TCTTGGGGGC	GCTATTGGGG	GTGGGACCCT	AAAGAACTT	GGGCGTTGAT	240
TTCTATTTGC	GTCTATGCCT	TGATCTTGCA	TTTGCCTTTT	TTAGGCTCTC	AAAAATGGCC	300
CTTTATTTTA	GCGAGCAGCA	GCGTGCTAGG	GTTTTATTCC	GTTTTAATGA	CTTATTTTGG	360
CGTGAATTAC	TACCTTTCTG	GCTTGCACAG	CTATGCCGCA	GGTGATCCTT	TGCCGATCCC	420
TACTTTTTTA	TACTTTTGG	TAGCGATACC	TTTCGCTCTC	GTATCTTGGC	GTATTTCAAA	480
CGCCATT						487

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180

CGATATTCCG	ATCAGACGAA	TCTATTAGCC	CTAAATGCTG	CTATTGAAGC	CGCAAGGGCC	60
GGCGAGCATG	GTAGAGGCTT	TGCGGTGGTG	GCTGATGAAG	TTAGGAATTT	AGCTGGGCGC	120
ACTCAAAAGT	CTTTAGCCGA	AATCAATTCC	ACTATCATGG	TGATTGTCCA	AGAAATCAAT	180
GATGTGAGTT	CGCAAATGAA	TCTCAATTCC	CAAAAAATGG	AGCGCTTGAG	CGATATGAGT	240
AAAAGCGTGC	AAGAACTTA	CGAAAAAATG	AGTTCTAATT	TAAGCTCAGT	CGTTTATGAC	300
AGCAATCAAA	GCATGGACGA	TTACGCTAAA	TCCGGACACC	AAATTGAAGC	TATGGTAAGC	360
GATTTTGCAG	AAGTGAAAA	AGTGGCTTCT	AAGACTTTGG	CTGATTCTTC	AGATATTTTA	420
AACATCGCTA	CGCATGTGAG	TGGAACGACC	ATGAATTTAG	ACAAACAAGT	GAATTTGTTT	480
AAAACT						486

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

850

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181

ATTTGTTTAA AACTTAATCA GGGGGGAGTT TATCAAAAAA GGGTTGGATT GTTAAAGGTT	60
TCTGTGATCA CGGCGTGTTT TAATAGCGAA AAAACCATTG AAGACACCAT TCTTTCCGTG	120
CTTAATCAAA CTTATAAAAA CATTGAATAC ATCATTATAG ATGGGGCTAG CGCGATAGCA	180
CTT	183

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1992 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182

AATCATATTG TGCCTGGCGT TGATTCTGAT CGTGGCGTGA GCATTTTAGG GGTGTCCTTA	60
AACAGCAGGG TGAAAGAGAT TTTAAAAGAA AGCGCTCTGC ATTCAATGCA AGATAGTTTG	120
CATTTCAAGG TTAAGGAAGT GCAAAGTGTT TTGGAAAACA CTTATACGAG CATGGGCATT	180
GTCAAAGAAA TGCTCCCTGA AGACACCAAA AGAGAAATCA AAATCCAGTT GTTAAAAAAC	240
TTCAATTTAG CCAATTCGCA TGTCGCTGGG GTGAGCATGT TTTTAAAGA CAGAGAGGAT	300
TTGAGATTGA CGCTTTTACG AGATAACGAT ACGATCAAGT TGATGGAAAA CCCGTCATTA	360
GGGAGTAACC CTTTAGTGCA AAAAGCGATG AAAAATAAAG AAATTTCTAA AAGCTTGCCT	420
TATTACAGGA AAATGCCTAA CGGGGCGGAA GTTTATGGCG TGGATATTCT TTTACCACTA	480
TTCAAGGAAA ACACGCAAGA AGTGGTGGGG GTTCTGATGA TTTTCTTTTC CATTGACAGC	540
TTCAAGTAATG AAATCACTAA AAACAGGAGC GATTATTTT TAATTGGCGT TAAAGGTAAA	600
GTGCTTTTGA GCGCGAATAA AAGCTTGCAA GACAAATCCA TCACCGAAAT TTATAAAAGC	660
GTGCCTAAAG CCACTAATGA AGTGATGGCT ATTTTAGAAA ATGGCTCTAA AGCGACTTTA	720
GAATACTTGG ATCCCTTTAG CCATAAGGAG AATTTTITAG CCGTTGAAC CTTTAAATG	780
CTAGGCAAAA CAGAAAGTAA AGACAATCTT AATTGGATGA TCGCTTTGAT CATTGAAAAA	840
GACAAGGTCT ATGAGCAAGT GGGATCGGTG CGTTTTGTGG TGGTTGCAGC GAGTGCTATC	900
ATGGTGTTAG CCTTAATCAT AGCGATCACT CTTTAAATGC GAGCGATCGT GAGCAATCGT	960
TTGGAAGTCG TTTCTAGCAC CTTGTCTCAT TTTTAAAT TATTGAACAA TCAAGCCCAT	1020
TCTAGCGACA TTAATTTGGT TGAAGCGCGA TCTAATGACG AATTAGGGCG CATGCAAAACA	1080
GCGATCAATA AAAATATCTT GCAAACCCAA AAAACCATGC AAGAAGACTG GCAAGCCGTC	1140
CAAGACACCA TTAAAGTGGT TTCAGATGTG AAAGCGGGGA ATTTTGCGGT GCGCATCAGC	1200
GCTGAACCCG CAAGCCCTGA TTTGAAAGAA TTGAGAGACG CGCTAATGGA TCATGCACTA	1260
TTTGCAAGAA AGCGTGGGAC TCACATGCCA AGCATTTTCA AAATCTTTGA AAGCTATTCT	1320

SUBSTITUTE SHEET (RULE 26)

851

GGCTTGGATT	TTAGAGGGCG	GATCCAAAAC	GCTTCGGGTA	GGGTGGAATT	GGTTACTAAC	1380
GCTTTAGGGC	AAGAAATCCA	AAAAATGCTA	GAAACTTCGT	CTAATTTTGC	CAAAGATCTA	1440
GCGAACGATA	GCGCGAATT	AAAAGAATGC	GTGCAAAATT	TAGAAAAGGC	TTCAAACCTC	1500
CAACACAAAA	GCCTGATGGA	AACTTCCAAA	ACGATAGAAA	ATATCACCAC	TTCCATTCAA	1560
GGCGTGAGCT	CTCAAAGTGA	AGCCATGATT	GAACAAGGGA	AAGACATTAA	AAGCATTGTA	1620
GAAATCATT	GAGATATTGC	CGATCAAACG	AATCTATTAG	CCCTAAACGC	TGCTATTGAA	1680
GCCGCACGAG	CCGGCGAGCA	TGGCAGAGGC	TTTGCGGTGG	TGGCTGATGA	GGTGAGGAAG	1740
CTCGCTGAAA	GACGCAAAA	ATCCCTCAGT	GAGATTGAAG	CCAATATTAA	TATTCTCGTT	1800
CAAAGCATT	CAGACACGAG	CGAAAGCATT	AAAAACCAGG	TTAAAGAAGT	AGAAGAGATC	1860
AACGCTTCTA	TTGAAGCCTT	AAGATCGGTT	ACTGAGGGCA	ATCTAAAAAT	CGCTAGCGAT	1920
TCTTTAGAAA	TCAGTCAAGA	AATTGACAAA	GTCTCTAAG	ATATTTTAGA	AGATGTGAAT	1980
AAAAAGCAGT	TT					1992

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183

CGTGGTGAAT	GCTATTTTGA	AAGAGAAATT	GGATTGATGA	GGAAAATTTT	TTCTTATATT	60
TCTAAGGTTT	TATTATTTAT	TGGGGTGGTT	TATGCAGAGC	CTGATTCTAA	AGTGAAGGCC	120
TTAGAAGGGA	GGAAGCAAGA	GTCTTCTTTG	GATAAAAAAA	TCCGCCAAGA	ATTGAAGAGT	180
AAGGAATTGA	AGAATAAGGA	ATTAAAGAAT	AAGGATTTGA	AAAATAAAGA	AGAAAAGAAA	240
GAAACAAAAG	CCAAGAGAAA	ACCCAGAGCA	GAAGTCCATC	ATGGGGACGC	CAAAAATCCC	300
ACTCCAAAGA	TCACGCCTCC	TAAATCAAA	GGGAGTAGTA	AGGGCGTTCA	AAATCAAGGC	360
GTTCAAAACA	ACGCGCCAAA	ACCTGAAGAA	AAAGATACAA	CCCCTCAAGC	TACTGAAAAA	420
AATAAGGAAA	CAAGCCCTAG	CTCTCAATTC	AATTCCATT	TTGGTAATCC	TAATAACGCT	480
ACCAACAACA	CCCTTGAAGA	TAAGGTCGTA	GGGGGCATTT	CATTGCTTGT	TAATGGTTTC	540
CCTATCACGC	TGTATCAAAT	CCAAGAAGAG	CAAGAAAAAT	CTAAAGTGAG	TAAGGCTCAA	600
GCTAGGGATC	GTTTGATCGC	TGAACGCATT	AAAAACCAAG	AAATTGAGCG	CTTAAAAATC	660
CATGTAGATG	ATGACAAGCT	AAACCAAGAA	ATGGCGATGA	TGGCGCAACA	ACAAGGCATG	720
GATTTAGACC	ATTTCAAACA	GATGCTTATG	GCTGAGGGGC	ATTATAAACT	CTATAGAGAT	780
CAACTTAAAG	AGCATTTAGA	AATGCAAGAA	TTGTTGCGTA	ATATTTTGCT	CACGAATGTG	840
GATACCAGCT	CTGAAACCAA	AATGCGCGAA	TATTACAACA	AACACAAGGA	GCAATTCAGT	900
ATCCCCACAG	AAATAGAAAC	CGTGCGCTAC	ACTTCCACCA	ATCAAGAGGA	TTTAGAAAGG	960
GCTATGGCAG	ACCCTAATTT	GGAAGTCCCA	GGGGTGAGTA	AGGCCAATGA	AAAAATAGAG	1020
ATGAAAACCC	TAAACCTCA	AATCGCCCAA	GTCTTTATTT	CGCATGAGCA	AGGCTCTTTC	1080
ACGCCCCGTA	TGAATGGGGG	TGGGGGCGAG	TTTATATCAA	GGAAAAAAGG		1140
GGTAAAAATG	AAGTGAGCTT	CAGTCAGGCC	AGCAATTCA	TCGCCCAAAA	ATTAGTGGA	1200
GAACTTAAGG	ATAAGATTTT	AGAAGAGCAT	TTTGAAAAAT	TGCGCGTTAA	GTCTAGGATT	1260
GTGATGATCA	GAGAG					1275

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs

SUBSTITUTE SHEET (RULE 26)

852

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184

ATTGTGCAAC	ACTTCAATTT	CCTCTATAAA	GATTCTTTAT	TTTCTATCGC	TTTATTTCACT	60
TTTCTATCGC	CTCTTGTGAT	TTTATTAGAA	CAGGCTAGAG	CGTATTTTCAC	CCGAAAGAGA	120
AACAAAAAAT	TTTGTCAAAA	ATTCGCCCAA	AATCAAAACG	CCTATGCGAG	CAGCGAGAAT	180
TTAGACGAGC	TTTTAAAGCA	TGCTAAAATT	TCCAGTTTGA	TGTTTTTAGC	TAGGGCGTAT	240
TCTAAAGCGG	ATGTGGAAAT	GAGCATTGAA	ATCTTAAAAG	GGCTTTTGAA	TCGCCCTTAA	300
AAAGATGAAG	AAAAAATCGC	TGTTTTAGAT	TTATTGGCTA	AAAATTATTT	TAGCGTGGGG	360
TATTTCGAGA	AAACAAAAGA	CACCGTGAAA	GAAATTTTGC	GCTTTTCCCC	AAGGAATGTG	420
GAAGCGTTGT	TGAAGCTTTT	GCATGCGTAT	GAATTAGAAA	AAGATTATTC	AAAGGCTTTA	480
GAACTTTTGG	AATGTTTGGG	AGAATTAGAG	GTGCCTAAAA	TTGAAACGAT	TAAAAATTAC	540
CTCTATTTAA	TGCATTTAAT	AGAGAATAAG	GAAGATGCGG	CTAAAATCTT	GCATGTTTCA	600
AAAGCGTCGT	TAGATTTGAA	AAAAATCGCT	CTGAATCACT	TAAAATCGCA	TGATGAAAAT	660
CTTTTTTTGGC	AAGAAATTGA	TACAACCGAA	CGGCTAGAAA	ATGTGATCGA	TCTTTTATGG	720
GATATGAATA	TCCCTGCTTT	TATTTTAGAA	AAACATGCCC	TTTTGCAGGA	CATCGCGCGA	780
TCTCAAGGGT	TGCTTTTGGG	TCACAAACCT	TGCCAAATTT	TTGAATTAGA	GGTTTTACGC	840
GCTCTATTGC	ATAGCCCTAT	AAAAGCGAGT	CTGACTTTTG	AATACCGCTG	CAAGCATTGC	900
AAACAAATCT	TTCTTTTGA	AAGCCATAGG	TGCTCTGTGT	GTTACCAGTT	AGCGTTTATG	960
GATATGGTGC	TTAAAATCTC	TAAAAAACG	CATGCTATGG	GAGTGGAT		1008

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185

ATTAGAGGCG	CAAAAACGGG	TCAAAACGAC	CACTTAAAGG	GAAAAATGAT	GAAAAACAAA	60
CGCTCTCAAA	ATAGCCCTTA	TGTAACGCCT	GACAACCCTT	ATCTAACGCT	AGAAAAAGCT	120
TTAGGGTATT	CTTTTAAAGA	CAAGCGTTTA	TTGGAGCAAG	CCTTAACGCA	TAAATCATGT	180
AAGCTCGCTT	TAAACAATGA	CGCCTTGGA	TTTTTGGGCG	ATGCGGTGTT	GGGCTTGGTG	240

SUBSTITUTE SHEET (RULE 26)

853

ATAGGGGAGC	TGCTATACCA	TAAATTCAT	CAATACGATG	AGGGCAAAC	CTCTAAATTA	300
AGGGCTTCTA	TTGTAGCGC	GCATGGTTTC	ACTAAATTAG	CGAAAGCGAT	TGCTTTACAA	360
GATTATTTGC	GCGTTTCTTC	TTCTGAAGAA	ATTTCTAAGG	GGAGGGAAAA	ACCCTCTATT	420
CTGTCAAGCG	CTTTTGAGGC	TTTAATGGCT	GGGGTGTATT	TAGAAGCAGG	GTTAGCTAAG	480
GTGCGTAAAA	TCATACAAAA	TTTACTCAAT	CGTGCTTACA	AGCGTTTGGG	TTTGGAGCAT	540
TTGTTTATGG	ATTATAAAAC	CGCTTTGCAG	GAATTGACCC	AAGCGCAGTT	TTGCGTGCATC	600
CCCACCTACC	AATTACTCCA	AGAAAAAGGC	CCCGATCACC	ATAAAGAATT	TGAAATGGCT	660
CTATACATT	AAGATAAAAT	GTATGCGACC	GCTAAAGGCA	AGAGTAAAAA	AGAAGCCGAA	720
CAGCAATGCG	CTTATCAAGC	GCTTCAAAAA	CTTAAGGAAG	TCAA		765

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186

GCGCATCAAT	CATCTCGTGG	TGTTAGCATG	ATTTTAGCAT	GCGATGTGGG	GTTAAAACGC	60
ATTGGAATCG	CTGCGCTTTT	AAACGGCGTT	ATCTTGCCCT	TGGAAGCGAT	TTTACGCCAC	120
AACAGGAATC	AAGCCTCTAG	GGATTGAGC	GATTTATTGA	GAAAAAAGA	CATTCAAGTG	180
CTGGTGGTGG	GCAAACCCAA	CGAAAGCTAT	GCAGATACCC	ACGCCCCGAT	TGAGCATTTT	240
ATCAAGCTTG	TAGATTTTAA	GGGCGAAATC	GTTTTTATCA	ATGAAGATAA	TTCTAGCGTA	300
GAAGCTTATG	AAAATTAGA	GCATTGCGGT	AAGAAAAATA	AGCGGATCGC	TACCAAAGAT	360
GGCCGGTTAG	ACTCTTTGAG	CGCTTGTAGG	ATTTTAGAGC	GCTATTGCCA	GCAGGTTTTA	420
AAAAAGGGC						429

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1731

SUBSTITUTE SHEET (RULE 26)

854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187

AAGAATGAAA	ATTTTATCAA	GGTTTTAATA	TTGGATTTAA	AGGTATTATT	GCAACGGATT	60
GTTGATTTTT	TCATCAAGCT	CAATAAAAAG	CAAAAAATCG	CCCTGATCGC	AGCGGGGGTT	120
TTGATCACCG	CTTTACTCGT	GTTTTTATTG	CTCTATCCTT	TTAAAGAAAA	AGACTACGCG	180
CAAGGGGGTT	ATGGGGTTTT	ATTTGAAAGA	TTGGATTCTA	GCGATAACGC	CTTAATCTTA	240
CAACACCTCC	AGCAAAACCA	AATCCCTTAT	AAAGTCTTAA	AAGACGACAC	CATTCTTGTC	300
CCTAAAGATA	AAGTGTATGA	AGAAAGGATC	ACTCTGGCTT	CTCAAGGGAT	CCCTAAAACG	360
AGTAAAGTGG	GCTTTGAAAT	CTTTGACACT	AAAGACTTTG	GGGCGACTGA	TTTTGATCAA	420
AACATCAAAC	TCATTGCGCG	CATTGAGGGG	GAATTGTCGC	GCACGATTGA	AAGTTTAAAC	480
CCCATTCTTA	AAGCCAATGT	GCATATTGCA	ATCCCTAAAG	ACAGCGTGTT	TGTGGCTAAA	540
GAAGTCCCTC	CTAGCGCTTC	AGTGATGCTC	AAGCTTAAAG	CTGACATGAA	GCTTTCACCC	600
ACTCAAATTT	TAGGGATTAA	AAATTTAATC	GCTGCAGCTG	TGCCTAAACT	CACGATAGAA	660
AACGTGAAAA	TCGTGAATGA	AAATGGCGAA	TCAATAGGCG	AGGGCGATAT	ACTAGAAAAC	720
TCCAAAGAAT	TAGCCTTAGA	GCAATTGCGC	TACAAACAAA	ATTTTGAAAA	CATTTTAGAA	780
AATAAGATCG	TCAATATCTT	AGCCCTTATT	GTGGGGGGTA	AAAACAAGGT	GGTCGCAAGG	840
GTCAATGCGG	ACTTTGATTT	CAGCCAAAAG	AAAAGCACCA	AAGAGACTTT	TGATCCCAAT	900
AATGTCGTAA	GGAGCGAGCA	AAATTTAGAA	GAAAAAAAAG	AAGGCGCTCC	TAAAAAACAA	960
GTTGGCGGTG	TGCCGGGAGT	TGTGAGCAAT	ATTGGGCCTG	TGCAAGGATT	GAAGGACAAT	1020
AAAGAGCCAG	AAAAATACGA	AAAGTCTCAA	AACACGACCA	ATTATGAAGT	GGGTAAAACC	1080
ATTATCGAGA	TCAAGGGCGA	GTTTGGCACC	TTAATGCGTT	TGAATGCGGC	GGTTGTGGTG	1140
GATGGCAAGT	ATAAAATCGC	GCTCGAAGAC	GGGGCAAACG	CTTTAGAATA	CGAGCCTTTA	1200
AGCGATGAAT	CGCTTAAAAA	AATCAACGCC	CTAGTCAAAC	AAGCCATTGG	TGATAATCAA	1260
AATAGAGGCG	ATGATGTGGC	GGTGAGTAAT	TTTGAGTTTA	ACCCATATGC	GCCTATGATT	1320
GACAACGCCA	CTTTGAGCGA	AAAAATCATG	CATAAAACTC	AAAAAATCTT	AGGCTCATTT	1380
ACGCCTTTAA	TCAAGTATAT	TTTGGTGTTT	ATAGTGTTAT	TCATTTTCTA	TAAAAAAGTG	1440
ATCGTGCTTT	TCAGCGAACG	CATGCTGGAA	GTGGTGCTTG	ATGAAGATAA	GGAAGTGAAA	1500
TCCATGTTTT	AAGAAATGGA	CGAAGAAGAA	GATGAGTTGA	ACAAACTCGG	CGATTTGAGG	1560
AAAAAAGTAG	AAGATCAATT	AGGGCTTAAT	GCAAGCTTTA	GCGAAGAAGA	AGTAAGATAT	1620
GAAATTATTT	TAGAAAAGAT	TAGAGGAACC	CTTAAAGAGC	GTCTTGATGA	AATCGCCACG	1680
CTCTTTAAAC	TCTTAATCAA	AGATGAAATC	TCTTCAGACA	GCGCGAAAGG	T	1731

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188

AAATGGTGCG	GTTATTGTGA	GCGGAGGAGC	GTTAGGCGTG	GATATTATCG	CTCAAGAAAA	60
CGCCTTACCA	AAAACCATCA	TGCTTTTCGCT	TGCAGTTTGG	ATTTTATCTA	TCCCACGAAC	120
AACCATAAAG	TGATCCAAGA	AATCGCGCAA	AACGGTTTGA	TTTTAAGCGA	ACATGAAAAG	180
GATTTTCATG	TTATTAAAGG	TTTTTTTMTA	GTTAGAAATT	GTCTGGTGAT	CGCTTTAACC	240
GACGCGGTGA	TTATCCCCCA	AGCGGATTTA	AAAAGCGGCT	CTATGAGTAG	TGTGAGATTA	300
GCCCAGAAAT	ACCAAAAACC	CTTGTTTGTT	TTACCCCAAC	GCCTGAATGA	GAGCGACGGC	360
ACTAATGAGC	TTTTAGAAAA	AGGGCAGGCT	CAAGGGATAT	TTAATATTCA	AAATTTTATA	420
AACACCCTTT	TAAAAGATTA	CCATTTAAAA	GAAATGCCTG	AAATGAAAGA	TGAATTTTAA	480
GAATATTGCG	CGAAAAACCC	TAGCTATGAA	GAAGCGTATC	TCAAATTTGG	GGATAAGCTT	540

855

TTAGAATACG AGCTGTTGGG TAAGATTAAG CGCATCAATC ATCTCGTGGT GTTAGCA

597

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189

AGGTTAAAAA	TGGCAACCAA	GCTTACCCCC	AAACAAAAGG	CTCAATTAGA	CGAACTTTCC	60
ATGAGTGAAA	AAATCGCCAT	TTTACTCATT	CAAGTGGGCG	AAGACACCAC	AGGCGAGATT	120
TTAAGGCATT	TAGACATTGA	CTCTATTACA	GAGATTTCCTA	AGCAAATCGT	GCAATTAAAC	180
GGCACGGACA	AGCAAATCGG	CGCGGCGGTT	TTAGAGGAAT	TTTTTGCGAT	CTTTCAGTCT	240
AACCAATACA	TCAATACCGG	CGGTTTAGAA	TACGCTAGGG	AGCTTTTAAC	CAGGACTTTA	300
GGGAGCGAAG	AAGCCAGGAA	AGTGATGGAC	AAACTCACTA	AAAGCTTGCA	AACGCAAAAA	360
AACTTCGCTT	ATTTAGGCAA	AATCAAGCCC	CAACAACCTCG	CTGATTTTCAT	CATTAACGAA	420
CACCCCTAAA	CCATCGCCTT	GATTTTGGCC	CACATGGAAG	CCCCTAATGC	GGCTGAAACT	480
TTGAGCTATT	TCCCTGATGA	AATGAAAGCC	GAGATTTCCTA	TTAGAATGGC	GAATTTAGGC	540
GAAATATCGC	CCCAAGTGGT	TAAAAGGGTT	TCCACGGTGT	TAGAAAACAA	ACTAGAATCG	600
CTCTAGTACT	ATAAAATTGA	AGTGGGCGGC	TTGAGAGCGG	TGGCTGAAAT	CTTTAACC GC	660
TTGGGCCAAA	AGAGTGCCAA	AACCACGCTC	GCTCGCATTG	AAAGCGTGGA	TAACAAACTC	720
GCCGCGCGCA	TTAAAGAAAT	GATGTTCACT	TTTGAAGATA	TAGCCAAACT	AGACAATTTT	780
GCTATCATGA	GAGATTTTAA	AAGTGGGGGA	TTAAAAAAGA	CTGGTCTT		828

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190

856

AGAAGTTTGG	GAAAAGGGCG	ACCAATGAAC	AAGAAAAATA	GCGTAATTC	TGGTTTGATG	60
AATTTTTTTA	GCGAAAAGAA	TGAGCGCTGG	CTGTTAGCCC	ACAGGCACAC	GAGGGGGTTT	120
GTGATAGTGG	CGTGGCTTTT	TAGGTTTAAA	AGCATTGCGT	TTTCTATTTT	AATCACTCTG	180
TTGGTTATTT	TAGTGGATAT	TTGGGTGTAT	AGCGATGTGC	GCCAGTTTMT	ATTGGACACT	240
TCTAGCTCTT	TTATTTGGCT	TTTAATCGCT	TTACTAATCA	AGTGGGGCGT	GATTGTTATA	300
AGTGGCGCGA	AATGCTACCA	ATTGAGCCAA	AAAATGTTTG	CGTTAATCCA	AAGAAAAAGG	360
CAAAATCAGAG	AGAATTTAAA	AAACCGCTCC	AATCGCAAAG	ATGCTAAAAA	TTTTGAAAAA	420
CTCTCTAACA	TCGCTGAAGA	AATCATTTCA	AAAAACAAG	AAGAGTCCCA	CCACAAAGAA	480
GATTCTAATG	ATGAAAACCA	CAAAGACAAG	CTTTCTAACA	TTACCGAAGA	AATGATTCTC	540
AAAAACAAG	AGGAACGAA	AGCTAGAAAG	GATAAGGGGG	AT		582

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191

CTTATGGATA	GAGCCAAATT	TATATTCGTT	ACAGGGGGCG	TGTTAAGCTC	TCTAGGGAAA	60
GGGATTTTCAT	CTTCTTCAAT	CGCTACGCTT	TGCGAGCAIT	GCAATTACCA	GGTTTCTATT	120
TTGAAGATTG	ATCCTTATAT	CAATATTGAT	CCAGGCACCA	TGAGCCCTTT	AGAGCATGGG	180
GAAGTGTITT	TACTAGCGA	TGGCGCTGAA	ACGGATTTAG	ACATCGGGCA	TTATGAACGC	240
TTTTTGAACA	GGAATTTAAC	GAGGTTGAAT	AATTTCACTA	CCGGGCAGAT	TTTTTCAAGC	300
GTGATAGAAA	ATGAAAGGAA	AGGGGAATAT	TTAGGCCAAA	CCATTCAAAT	CGTCCCCCAT	360
GTAACCGATG	AAATCAAAG	GCGCATTAAT	AGTGCGGCTA	AGGGGTTGGA	TTTTTTAATC	420
GTGGAAGTGG	TGGAACCGT	GCGGATATG	GAGGGCATGT	TTTATGTGGA	ACCGATCCGC	480
CAGCTGAAAC	TGGAATTACG	GAATAAAGCA	CTCATCAATA	TGCATGTAAC	CTTGATGCCC	540
TATATCCGTG	CCACTAGCGA	ACTAAGAAGC	AGACCCACGC	AACACTCCGT	CCAGGAATTA	600
CGGCGTCTTG	GCGTAACCCC	TCAAATCATT	TTGGCGCGAT	CGCCTAAGCC	TTTGATAAAA	660
GAATTGAAAA	AGAAAATCGC	TTTGAGTTGC	GATGTGGAAC	AAGACAGCGT	GATTGTAGCC	720
ACAGACACTA	AAAGCATTTA	CGCATGCCCT	ATTCTTTTCT	TGCAAGAAGG	CATTTTAACC	780
CCCATTTGCCA	GACGCTTTAA	TTTGAATAAG	TGCAACCCTA	AAATGCGCGC	TTGGAACACT	840
TTAGTAGAAA	AAATCATCGC	TCCTAAACAC	AAGGTCAAAA	TTGGTTTTGT	GGGCAAGTAT	900
TTAAGCTTAA	AAGAATCTTA	TAAATCCTTG	ATTGAAGCCC	TAATCCATGC	GGGGGCGCAT	960
CTGGATACGC	AAGTCAATAT	TGAATGGCTG	GATAGCGAGA	ATTTTAATGA	AAAGACTGAT	1020
TTAGAGGGCG	TTGATGCGAT	TTTAGTGCCG	GGGGGCTTTG	GAGAAAGGGG	GATTGAGGGC	1080
AAAAATTGCG	CCATTCAAAG	GGCTAGGTTA	GAAAAACTCC	CCTTTTITAGG	GATTGTGTTG	1140
GGCATGCAAT	TAGCGATCGT	TGAATTTTGT	CGCAATGTTT	TAGGCTTGAA	AGGGGCTAAC	1200
TCTACGGAAAT	TTAACCAACG	CTGCGAATAC	CCTGTGGTGT	ATTTGATTGA	AGATTTTATG	1260
GATCAAAACC	ACCAAAAACA	GGTGCGCACC	TATAATTCCG	CTTTAGGAGG	CACCATGCGA	1320
TTAGGCGAAT	ACGAATGCGA	AATCATGCTT	AATAGCTTGC	TAGAAAAAGC	CTATAAAAAG	1380
CCTAACATCA	AAGAAAAGCA	CCGCCATCGT	TATGAAATCA	ACCCCAAATA	CCGCCAAGAG	1440
TGGGAAAATA	AAGGCTTGAA	AGTGGTGGGC	TTTGGGGCGA	ATCATTTGAT	TGAAGCGATT	1500
GAATTAGAAG	ATCACCCGTT	CTTTGTGGGG	GTGCAATTCC	ACCCGGAATT	CACCTCCAGG	1560
TTGCAAAGCC	CTAACCTTAT	TATTTTGGAT	TTCATTAAGA	GCGCTCTTCA	TAAATCC	1617

(2) INFORMATION FOR SEQ ID NO:1192:

SUBSTITUTE SHEET (RULE 26)

857

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192

ATATGGCGTG	GATGTGGAAG	CCATGACAGG	GTGCATGATG	AGTTTGTTTT	TGCTCGTTAC	60
ACGAAGGCTA	ATTACGAAAA	CACTTATTAC	GATACAGAGT	TTTCGCATTT	AAAAGAAGCG	120
AGCGCGTATT	TTCCGGACAT	TGATGAAGCG	AGCCTTTTTA	CGGATTTGCA	AGATTATTTT	180
AACTCATGGA	AAGAAATGTC	TAAAAACGCC	AAAGACTCCG	CTCAAAAACA	GGCTCTCGCT	240
CAAAAAACAG	AAGCTTTAAC	GCACAACATT	AAAGACACCA	GAGAGAGGTT	AACGACCTTA	300
CAGCATAAAG	CGAGCGAAGA	ATTAAAAAGC	GTCATTAAAG	AAGTCAATAG	CCTGGGTTCT	360
CAAATCGCTG	AGATCAACAA	ACGCATTAAA	GAAGTGGAAA	ACAACAAGAG	TTTAAAGCAT	420
GCGAATGAGT	TAAGGGATAA	GCGAGATGAA	TTAGAGTTTC	ATTTGCGAGA	GCTTTTAGGG	480
GGGAATGTTT	TTAAAGCAG	CATTAAAACC	CATTTCGCTCA	CAGATAAAGA	CTCAGCGGAC	540
TTTGATGAGA	GCTATAACCT	TAATATCGGG	CATGGGTTCA	ATATCATTGA	TGGCTCTATT	600
TTCCATCCCT	TAGTGGTTAA	AGAATCCGAA	AATAAAGGGG	GTTTGAACCA	GGTTTATTTT	660
CAAAGCGATG	ATTTTAAGCT	CACTAATATT	ACCGACAAGC	TCAATCAAGG	GAAAGTGGGG	720
GCGTTATTGA	ATGTGTATAA	TGACGGCTCT	AACGGGACTT	TAAAGGGCAA	GTTGCAAGAT	780
TATATTGATT	TGTTGGATTG	TTTIGCTAGG	GGCTTGATAG	AATCCACGAA	TGCGATTTAC	840
GCTCAAAGCG	CGAGCCATCA	TATTGAGGGC	GAGCCTGTGG	AGTTTAATAG	CGATGAAGCC	900
TTTAAAGACA	CGAATTACAA	TATCAAAAAC	GGCTCGTTTG	ATTTAATCGC	TTACAACACC	960
GATGGTAAAG	AAATCGCCAG	GAAAACCATT	GCTATCACGC	CCATTACAAC	CATGAACGAC	1020
ATTATCCAAG	TCATTAACGC	TAACACCGAT	GACAATCAAG	ACAACAACAC	CGAAAACGAT	1080
TTTGATGAAT	TATTTACAG	CGAGCTT				1107

(2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...813
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193

858

AAAACAAAGC TCGTTTTAT GATAAAGCG CGGTTTAAAA AACGCCTTTT AGGATCTAGG	60
GGCGCGTTTG ATTTGAATAT AGACTTAGAA ATTAAAGAAG CAGAAGTTGT CGCTTTATTA	120
GGAGAATCGG GAGCGGGTAA AAGCACGATC TTACGCATTT TAGCAGGGCT TGAAGCGGTG	180
AGTAGCGGCT ATATTGAAGC CAATCATTCA GTATGGTTAG ACACTCAAAA AAAGATTTTT	240
TTAAAACAC AACAGCGAAA AATCGGCTTT GTGTTTCAAG ATTACGCCCT ATTCCCTCAT	300
TTAAACGTGT ATCAAAACAT CGCCTTTGCT CACCCTAAAG ATAAAAATAA AATCCACGAA	360
GTGTTACGCT TAATGCGTTT AGAAAACCTA AGCCAGCAAA AAATTCCCAA ACTCTCTGGC	420
GGGCAAGCCC AACGAGTCGC TTTAGCAAGA GCTTTAATCG CAGCCAAAAA TCTATTGCTT	480
TTAGATGAGC CTTTAAACGC CCTAGATAAC GCCTTAAAAA ACGAGGTGCA ACAAGGTTTG	540
CTTGATTTTA TCAAGCGTGA AAATTTAAGC GTGTTATTGG TAAGTCATGA TCCAAACGAA	600
ATAACCAAAC TCGCGCGAAC TTTCCTCTTT TTAACAATG GCGTTATTGA TCCTAATCAA	660
GAAAATCGGC TTTTTCAAA CCGCTTATTG GTAAAACCTC TCTTTGAAGA TGAAAATTAT	720
TGCCATTATG AGGTCATTCC TCAAACGATC AGTTTGCCCA AAGATTGTCT GAACCCAACT	780
TTTAAGCTTG ATTTCAATTCA AAACAAAAA TTT	813

(2) INFORMATION FOR SEQ ID NO:1194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194

GGCTTATCCG CTACTATCTT TGGTATGTGG ATTATGTCTT CACTTTCTAG TTCATTCTTT	60
CATTCGCTCT TCTTCATCAA ATCAAACCTT GGCCAACCTT TAAAAGGTTG GGGTTCAAAA	120
ATCTTTTTC TAAATAGAAA GTTTGTTTTA GCACAGTATA ATCCTAGCGT TTCAATTTTT	180
ATTTTACTCA ATAGGGTGTG TGGTGTGGC GTT	213

(2) INFORMATION FOR SEQ ID NO:1195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

859

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195

ATTGAGCGCT CGCACCAGCT CTTTAATTTG CAAGAAAAAA AAGGGATTCT TGGTTTTTTA	60
CACCAAAAAA ATATCTTAAA TATTGCTCAA AATGACATCC ACCAGCTCCT TATTCTCATG	120
GTGGTCTTTT CTATGTTAGC AACCCCTTTT ATTTTAAAT ACCTAGAATC TATCGCTCAA	180
TTTATTTTGC ACCAAAAGAG CCAAGAAAC GAGCCGGCTA AAAAA	225

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196

GGCTTGATGC GCATTATCAT AAGTTACTT TCATTAAAA TGAACGCTTT TTTAAACTC	60
GCGCTCGCTT CTTTGATGGG GGGGCTTTGG TATGCTTTCA ATGGCGAAGG CTCTGAGATT	120
GTCGCTATAG GGATTTTGT GTTGATCTTG TTTGTTTTTT TTATCCGCCC TGTGAGTTTC	180
CAAGACCCAG AAAAACGAGA AGAATACATA GAACGGCTTA AAAAAACCA TGAGAGGAAA	240
ATGATCTTAC AAGACAAGCA AAAAGAAGAG CAAATGCGCC TCTATCAAGC CAAAAAGAG	300
CGAGAGAGCA GGCAAAACA AGACCTTAA GAACAAATGA AAAAATACTC A	351

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197

AGGAAAAAAA TGGAATCAT TTTATTAATT GTTGGGCGG TTGTGTTGTT TTATTTTTAC	60
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860

AACACCCTCA	AAGAATATTT	GAAAAACCCC	CTAAACCCTA	AAACCAAAAC	CGAAGAATAC	120
GACTTGAAAA	ATGACCCCTA	TTTGCTGGTG	CAATCTAGCC	CCCTAGACAA	ATTCAAGCAA	180
ACCCAAATAG	GCGCGTATAT	GCGTCTTTTA	AAATTTTTAG	ACATTCAAAA	AAACGCCCTG	240
GATAACGCTT	TAAGAACGCT	TTTTATCCAT	GAATTGGAGC	AGCCCTTAAA	CAGCGAACAG	300
CAAAATTTAG	GCCAAAGAGC	TTCTCAA				327

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198

ATGCCTAATA	ACGCTTTATT	GCAAATCAAA	CAAGACACCC	TAAGTCTCAT	TGACGATTTA	60
AAAGTCATTT	GCAAGGATGC	TGGTTTAGCG	GGCGACGGCA	ACGGATACAA	GATCATCACC	120
CAATGCTTTT	TGTATAAATT	CTTATGCGAT	AAGTTTGAAT	TCTTTTTTGA	ACAAAAATTC	180
CCCAACAAAA	CGATACGAGA	CTACAAAGAC	TTTAACGAGG	AAGAAAAAGA	ATATTTTTTC	240
CTTACCTTAA	GCGATAAAAA	ACTCCCCAAA	CTCGCTTATG	ATGAGCTTTT	AAACTATCTT	300
TTTGAAAAAC	ATTTTTACGA	TAACGATTTA	CACCTAAAGC	TAGATGCTAT	TTTCAATCGC	360
ATTTCTAGCA	ATAATGCCGA	GCTTTTAAAC	ACCAAAAGCA	CGGATGAAAC	CACTATCGCC	420
TTATTTGAAA	GCGTCTCACA	ATACATTAAT	GAAGGGTCTA	AAAGGGCTAA	TTTTACAAGA	480
TCTTTATTAG	ACAAACTCAA	AAATTTTAAT	TTCAAACAAG	CTTTTTTAAA	TTTACAAAAAC	540
CAACAAGGCT	ATGACTTTTT	CGCCCCCATT	TTTGAATACT	TACTCAAAGA	TTACAATAAT	600
AACAGCGGAG	GGACATACGC	CGAATACTAC	ACCCCTTTAA	GCATCGCTAG	CATCATTGCC	660
AAGCTTTTAG	TGAATAAACC	CACTCAAAGC	GTCAAAATCT	ATGATCCAAG	CGCTGGCACA	720
GGAAACGCTT	TAATGGCATT	AGCCCACCAA	ATAGGCACCG	ATTCTTGAC	CCTTTATGCC	780
CAAGACATTT	CGCAAAATC	CTTAAGAATG	CTCAAACTCA	ACCTGATTTT	AAACGACTTG	840
ACCCACTCTT	TAAGACACGC	CATTGAGGGA	AACACTTTGA	CTAACCCTTA	CCACTCCAAA	900
GACCACAAAG	GGAAATGGA	TTTCATCGTG	AGTAACCCCC	CTTTCAAATT	GGATTTTTTC	960
AACGAGCATG	CCGAGATTTT	GCAAAACAAA	AACGATTTTT	TCTTAGGCGT	GCCTAATATC	1020
CCTAAAAACG	ATAAAAGCAA	AATGCCCAT	TACACGCTCT	TTTTCCAGCA	TTGCCTGAAC	1080
ATGCTCAGTC	CAAAAGGTAA	GGGAGCTATA	ATCGTGCCAA	CCGGATTCAT	TAGTGCTAAA	1140
AGCGGGGTAA	ATAATAAGAA	TGTCCGGCAT	TTAGTGGATG	AAAGGCTCGT	TTATGGGGTG	1200
ATTGTCATGC	CCAGTCAGGT	TTTTGCCAAC	ACCGGCACCTA	ACGTGAGCAT	CATCTTTTTT	1260
CAAAAAACGC	CAAGCGCAAA	GGAAGTGATC	TTGATTGACG	CTTCCAAACT	CGGCGAAGAA	1320
TACACCGAAA	ACAAAAACAA	AAAAACGCGC	TTAAGACCAA	GCGATATGGA	TTTGATTTTA	1380
GAAACTTTCC	AAAATAAAGC	CCCAAAATCG	GATTTTTGCG	CTCTGGTTTC	TTTTGATGAA	1440
ATTACAGAAA	AAAATTATTC	TCTAAACCCC	GGGCAGTATT	TCACTATAGA	AGACACGAGC	1500
GAGACAATCA	GCCAAGCGGA	GTTTGAAAAC	TGATGCAAC	AATATTCAAG	CGAACTAGCG	1560
AGCCTTTTTG	ATGAAAGCCA	AAATTTGCAA	CAAGAGATTT	TAGAAACTTT	AAAAGGGGTT	1620
AGGTTTGAG						1629

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid

861

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199

AAAGGGGATT TCATGAAAGA ACAAGAATGG GATTTAAGCG CTTTATTTGA AAATAAAGAA	60
AGCGCAGAAG AATTTTAA AACCTTACAA ACAGAAGTGC AAGAATTTGA GAACGCTTAT	120
CAAAATAACC TTAAGAATTT AGACGCTGCA AAATTTGCCA ACACTCTTAA ACATTACGAA	180
AATTTGTCAG AAAAGATCTC TAGAGCGATG GCTTACGCTC AATTACTTTT TGCCAAGAAC	240
ACTAAGAAG CGAAGTTTTC TTCGCAATGC GAAATGGCTT GTGCAAATAT CCAACAACAC	300
CTTTTATTCT TTGAAATTGA ATTTAAGAAT TTGGACGCCA AAAACAGCT CGCTTTCATT	360
AAAAAATGCA AAGATCATGC TTTTATTTTA AACAATCTCA TAGAAAAGAA AAAGCACACC	420
CTAAATTTAG ATGAAGAAAA GATCGCTCTA GCCCTTTTCG CTTGTGGAGT GGGTGCCTTT	480
AGCTTTGTTA TGGATGAACA TTTGTTTTCT TTGAACATCT CTTTACATAG AATAAATTT	540
AAGCGAAGAA TAAATTTTAG CCCTCTTGCA CAACCC	576

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200

GCCAAAGAGC TTCTCAATGA GCCTGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA	60
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT	120
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTTAGAT	180
GTGGGGGCGT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA	240
CACCTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAATCT TTTTGAAATC	300
CAAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT	360
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA	420
ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTAAAAAG ACTCA	465

(2) INFORMATION FOR SEQ ID NO:1201:

862

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1215
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201

ATGCCCTTTT	TAAAAGCCCT	AGCATCTTTT	GATGCGCCCT	TTTGTAGAAA	AGAAATTTCA	60
AAGCGTTTTA	GGGATAATTT	AGTPTTTTTT	AAATCTTATC	ACCCTAATCT	GTTTAACGCC	120
CTCAATACGC	CTTTTAAAAA	TTACCAATTG	CTTTTGTAAA	CAAACCATCT	TAATCTCTTA	180
CACACGCCCA	CGAACGCTTT	AAGCTACCCT	AAACATCAAA	TGATAGAAAC	CGCTTTTAAC	240
ATGGCTAAAA	ACCCCTTGAA	TAATCCCAGA	TGGTCATTAG	ACAATAACCA	CCTCTCTTTA	300
CATTATTTAA	AATCTCAAAA	CAACCACAAA	CTCCCCCTAA	CCCTTAAAGC	CACGCATGCG	360
ATCTCAAAC	TTTTAGATAA	TCATCAAACG	CCTTGCTCTT	TAAAGAAATT	CCTACCCCTT	420
ACCATGATT	ATGGCGTTTT	AGACGGCTTG	TTTTTGGCTA	TTTTACAGGC	TCAAAATTAC	480
CGCTTCCATT	CGCTTTATTT	GTTTGAAGAA	AATTTAGACT	TGTTTTAAAT	CAGTTGCTAT	540
TTTGC GCGTT	ATGAAGATT	GATTAAAAAA	GGGGCTAAAC	TTTTTTATTCA	AGGGTTTTTTT	600
AACCCTAATG	AATTGAAAAT	GGATTTTTTG	AAACGCCCTA	TCACGCATTC	TTTTTTAAAG	660
CTAGAAATCA	TGCCCTATAA	AAGCGCTTTT	AATTTGCGCA	TGCGAGAAAA	CATTCAAAGC	720
TATTACAAAC	AAGCCTTAAG	GGTTGGGGGG	AGTTTTGAAG	ACGAATTGCT	AGGGGTAAAG	780
AACACGCTTA	AAAACCTACC	CCTATGCCAA	ACCCTAAAAA	CCAAACCCAA	AAAAATTAAAC	840
GCCCCCATT	GCGTGGTGGG	TAATGGGCCA	AGCCTGGATT	TATTGTTAGA	TTTTTTAAAA	900
GAAAATGAAG	AAAAATTCAT	CATTTTTTCA	TGCGGAACCG	CTTTAAAGCC	TTTAAAAGCG	960
CATGGCGTTA	AAGTGGATT	TCAAATAGAA	GTGGAGCGCA	TAGACTATCT	TAAGGAGGTT	1020
TTAGAAAGAG	CCCCCCTAGA	AGACACCCCC	TTAATGGGCG	CTAACATGCT	CAATCCTAAC	1080
GCTTTTGATT	TAGCCAAAGA	AGCGTTGATG	TTTATGCGTG	GGGGGAGCGC	TTGCGCATAT	1140
AAGCCCTTTG	AGTATAGAAT	ACGCAGCGCC	TTTTGTGGGC	AATGCCGGGG	TGGCTTTAGC	1200
GGGTTTGATG	AGCGA					1215

(2) INFORMATION FOR SEQ ID NO:1202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1239

863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202

AAGGGGTTAG	GTTTGAGTGA	GTGGCAAACA	TTTTGTTTAA	AAGATTTAGG	GAAAATAGTC	60
GGCGGCGCTA	CCCCACCTAC	CAATAACCCC	AAAAATTATG	GCAATAAAAT	TGCTTGGATT	120
ACCCCTAAAG	ATTTATCCAC	TTTACAAGGG	CGCTACATTA	AAAAAGGCAG	CCGCAGCATT	180
TCACGATTAG	GGTTTAAATC	ATGCTCTTGT	GTGTTGCTCC	CAAAGCATGC	CATTTTATTT	240
TCTTCAAGAG	CTCCCATAGG	TTATGTGGCA	ATTGCTGAAA	AAAGGCTATG	CACCAATCAA	300
GGTTTAAAAA	GTATTATCCC	TAACAAAAAA	ATTATTTTGT	AATTTTTTATA	TTACTTATTA	360
AAATACTATA	AGGATAACAT	TTCCAACATA	GGGGGCGGAA	CTACTTTTAA	AGAAGTTTCA	420
GGGGCTACTT	TAGGTCTATT	CCAAGTTAAG	ATACCCCCCA	CTTATTACGA	ACAACAAAAA	480
ATCGCCCA	CACCTTCTAT	TTTAGATCAA	AAAATAGAGA	ACAACCATAA	AATCAATGAG	540
CTTTTACACA	AAATCTTAGA	GCTTCTTTAT	GAGCAATACT	TCGTCCGTTT	TGATTTTTTA	600
GATGAAAACA	ACAAACCCTA	TCAAACCTAGC	GGCGGGAAAA	TGAAATTTTC	TAAAGAATTA	660
AACCGCCTTA	TCCCTAACGA	TTTTAAAGTC	AAAACGCTAG	GGGAACCTAAT	AACTTGGATT	720
TCCGGAAGTC	AGCCACCCAA	AAGTTGTCAC	ATATACGAGT	ATAAAGAGGG	TTACATTCGT	780
TTCATACAAA	ACAGAGATTA	TAGCTCTAAT	AATTATGTTA	CATATATTCC	TATATCAAAA	840
AATAACAAGA	TTTGTTATCA	ATATGATATT	ATGATGGACA	AATACGGAGA	AGCTGGATCC	900
GTGCGTTTTG	GACTTCAAGG	GGCTTATAAT	GTGCGCTTAA	GTAATAATTAG	CGTATTAAAT	960
CAATCCATGC	AGGAATATAT	ACGCAGTTAT	CTAAATTCAA	AACCTATAAA	AAAATATCTT	1020
TCTAATGCTT	GCATGGCATC	TACGAGAGCA	TCACTAAATG	AAAATCATAT	TTATTCTTTA	1080
ATGCTCCCCA	TACCACCTAT	TAATCTATTA	CAAAAATACG	AAAAAATCGC	AAAAAATATC	1140
ATAACAGCCA	TTATTAAAAA	CAATCAATCA	ACCCAAACCC	TAACCGCGCT	CAGAGACTTT	1200
CTACTCCCCC	TACTCTTAAA	ACAACAAGTC	AAACCACAA			1239

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203

GGTGTAACCT	TAATTCAACA	AGAAGGATTT	ATTATGATTA	AAAGAATTGC	TTGTATTTTA	60
AGCTTGAGCG	CGAGTTTAGC	GTTAGCTGGC	GAAGTGAATG	GGTTTTTCAT	GGGTGCGGGT	120
TATCAACAAG	GTCGTTATGG	CCCTTATAAC	AGCAATTACT	CTGATTGGCG	TCATGGCAAT	180
GACCTTTATG	GTTTGAATTT	CAAAATAGGT	TTTGTAGGCT	TTGCCAATAA	ATGGTTTGGG	240
GCTAGGGTGT	ATGGCTTTTT	AGATTGGTTT	AACACTTCAG	GGAAGTGAAC	CACCAAAACC	300
AAATTTGCTCA	CCTATGGCGG	CGGTGGCGAT	TTGATTGTCA	ATCTCATTCC	TTGGGATAAA	360
TTGCTCTAG	GCTCTCATGG	TGGCGTTCAA	TAGCCGGGAA	ACACTTGGAT	GTTCCCTTAT	420
GATGTCAATC	AAACCAGATT	CCAGTTCCTA	TGGAATTTAG	GCGGAAGAAT	GCGTGTGGGG	480
GATCGCAGTG	CGTTTGAAGC	GGGCGTGAAA	TCCCTATGG	TTAATCAGGG	TAGCAAAGAT	540
GTAGGGCTTA	TCCGCTACTA	TTCTTGGTAT	GTGGATTATG	TCTTCACTTT	C	591

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid

864

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204

TTTCGCTTTT	ATTTCTTTAA	AGCAAATCGA	TCCTACTGGG	GAAAGGTTTT	TATGGTAAAC	60
AGCACACTTT	ATATTGTTAT	TGCCGGCTTA	TGGCTTGCTG	TAGGCTTTGG	AATCTTTTAA	120
AAGAAATTAG	ACATGCCCCG	TATCATTGGC	TACATTGCA	CAGGAACGGT	CTTAGCGGCT	180
TTTTTTAAAA	TAAATGATTT	TAATTTGTTG	TCTGATATTG	GTGAATTTGG	TATCGTCTTT	240
TTAATGTTTA	TGATAGGCAT	TGAGTTTAAT	TTTGACAAGC	TCAAGTCCAT	CAAACAAGAA	300
GTGCTCGTTT	TTGGGCTTTT	ACAGGTTGTT	TTATGCGCTT	TAATCGCTTT	TTTATTGGGG	360
TATTTTGTTT	TGGGTCTTTC	GCCCATTTTT	TCCCTTGTTT	TAGGCATGGG	GCTTTCACCT	420
TCTTCAACCG	CCATGTGTG	GAAATTCTTT	GAAGATTCCA	AACAGCTTAG	CACGCCTATG	480
GGAAAGAGCG	CGGTGGGGAT	TTTGATTTTC	CAAGATATTG	CAGCCATTCC	CATGCTTTTA	540
ATTTTGACGA	TTCTAGGCAG	TAAGGATTCT	CATGTCAATT	TGCTCATTCT	TAAAACCCCT	600
ATTTCAGCGG	GGATTATTTT	AATTCTTTTA	TTATTGCCTG	AAAAAAAAGG	GGCTAATCTC	660
ATCTTAGAGC	AAGCGAAAAG	CACGCGCTTG	CCTGAAATCT	TTATAGGCAC	GGTTTTAGTG	720
ATTGTTTGCA	GCGCGGCGGG	GTTGAGCCAT	TTTTTTGGGT	TTTCTATGTC	TTGGGGGGCG	780
TTCAATTGTG	GCAATGCGAT	TTCTAAATCG	CGCTATAAAA	TCAATGTCCA	AGAAGAATTC	840
GCGCAATTAA	AAAACCTCTT	TTTGGCCCTT	TTTTTCATTA	CGATAGGGAT	GCAGATTAA	900
GTGAGTTTCT	TCATGGAGAA	ATTCTTTGTC	GTCATCTTTT	TACTCATTTT	AGTGATGAGT	960
TTTAAGACTT	TTATCATTTA	TGCGCTATTG	CGTTTTTTTA	GAGACGCTAA	AACCGCCATC	1020
AAAACCGCTC	TTTCTTTGGC	GCAAATTGGG	GAGTTTCTTT	TCGTGATCTT	TTTAAATTCA	1080
GCGCTCGCAC	CAGCTCTT					1098

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205

TGTTTATGCG	TGGGGGGAGC	GCTTGCGCAT	ATAAGCCCTT	TGAGTATAGA	ATACGCAGCG	60
CCTTTTGTGG	GCAATGCCCG	GGTGGCTTTA	GCGGGTTTGA	TGAGCGATGA	AATTTATTTG	120
TGCGCTTTAG	ATTGCGCTTA	TATCAAAGGG	TTTAAAAAGC	ACGCTCAAAA	TTCCTATTAT	180

865

GGAGATGAAA	AAGAGATTGA	CACCTCATCT	TTAATCAGCG	TAGAGGGTAA	TGTTGAAGGT	240
TATGAAACTT	TTAGCGACTC	GCTTTTTTTG	CTCTCTAAAG	AAAGGATTGA	AGAAGCCCTT	300
CATTATTACC	AGCCTAAAAA	AGTCTATAAT	TTAAGCTATG	GGGCGAAAAT	CAAGCACGCC	360
GTTAGCCTCA	ATCACTCTCA	AGTGAAATTG	AAACAAATCA	ACAAACAAGA	CGCTATCGTT	420
CGCATTAAAA	GCATGTTTAG	CCCTAGAAGT	AATCATGCTA	AGGATTTAAA	AAATTTACAA	480
AAAAATCTGA	TTCGTTTTAA	AGAGGATTTT	TTCACGCATT	TAAACACGCC	TTGTAAAACC	540
AAGCAAGAAG	CATTGAATG	GGTGGATAGC	TTGAGTGGAT	TTTGCCAAAC	AGCCAGCGCT	600
AAAACCCCCA	CTATAGGCAT	TTTATTTGAA	GGGAGTGTG	CCCATATCTT	ACAAAGCGTT	660
CTAATCGTTT	CATTGCATCT	TAAAGAAAAT	GAGCTGACGC	TTTTATCAAA	TTCTCTCAAA	720
ACGCCT						726

(2) INFORMATION FOR SEQ ID NO:1206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206

ATCCTTCTTG	TTGAATTAAA	GTTACACCCT	AAGATCGGTT	ATTTTCTTAA	AAGATTTAAT	60
TTTTTATCAA	AGATGAGGGT	TTTAGAGTGG	AAATATTGGT	TAAATACTGA	TAAGTGGGAT	120
ACGCCCACCA	ACAAACCGCC	TCAAACCTTT	AAAATACAAA	TTTTTAAGAT	ACAAATAGGT	180
ATAATCAATA	ACTTCAATCA	TTAATCAAAA	GGGAGTTCTA	TGAAAAACGC	TTTCAAAGCG	240
TTTGCCTTGT	TAATCGTATT	TTTCTCAAAC	GCTCTATTAG	CGCAGGATTT	AAAAATCGCT	300
GCTGCTGCTA	ATCTCACGCG	CGCTTTAAAA	GCCCTTGTTA	AAGAATTTCA	AAAAGAACAC	360
CCAAAAGACG	CTATTAACAT	TAGCTTTAAT	TCTTCAGGCA	AACTCTACGC	TCAAATCGCT	420
CAAAACGCCC	CTTTTGATTT	ATTCATTTCA	GCGGATATTG	CTAGACCCAA	AAAACTTTAT	480
GATGAAAAAA	TAACCCCTTT	TAAAGAAGAA	GTCTATGCTA	AAGGCGTGTT	GGTTTTATGG	540
AGTGAAATC	TAAAAATGGA	TTCTTTAGAA	ATTCTTAAAG	ACCCTAAAAT	TAAACGTATC	600
GCTATGGCTA	ATCCTAAACT	AGCCCCCTTAT	GGAAAAGCCA	GCATGGAAGT	CTTGGATCGT	660
TTAAACTCA	CTCCTAGTCT	TAAATCTAAA	ATCATTATG	GCGCTTCTAT	TTCTCAAGCC	720
CATCAATTCA	TCGCCACCAA	AAACGCTCAA	ATAGGCTTTG	GAGCGTTATC	TTTGATCGAT	780
AAAAAAGACA	AAAACCTCTC	TTATTTTCATC	ATTGATAAAA	CCCTTTATAA	CCCTATTGAA	840
CAAGCCTTAA	TCATCACTAA	AAATGGGGCT	AATAACCCTT	TAGCCAAAGT	TTTTAAAGAT	900
TTTTTATCA	GCCCTAAAGC	TAGAGCTATC	TTTAAAGAAT	ACGGCTATAT	TGTGGAT	957

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

866

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207

AAAAGGCGAA	CAATGGATCA	TGAGTTTTTG	ATTACCATGC	GTTTGAGCTT	TTCTTTAGCT	60
TTGATTACCA	CCCTTATTTT	ACTCCCTATA	GGGATTTTTT	TAGGCTATTT	TTTAAGCCTT	120
AAACGCAATC	TTTTAACGAG	CTTAACAGAA	ACGCTTGTGT	ATATGCCTTT	AGTTTTACCC	180
CCAAGCGTGC	TAGGGTTTTA	TCTTCTTTTA	ATCTTTTCGC	CTTCTTCTTT	TTTGGGAGCG	240
TTTTTACAAG	ATGTGTTAAA	TGTGAACTC	GTTTTTAGTT	TCCAAGGGCT	TATCTTAGGG	300
AGCGTGATTT	TTTCCTTGCC	CTTTATGGTA	AGCCCTATTA	AAAGCGCGTT	AATTCCTTG	360
CCCACCTCTT	TAAAAGAAGC	CAGTTATAGC	TTGGGTAAAG	GGGAATACTA	CACCCTTTTT	420
TTTGTCCCTAC	TCCCTAACAT	CAAACCCAGT	GTGTTGATGG	CTATCATTAC	AACTTTTATG	480
CACACTATAG	GTGAATTTGG	CGTGGTGATG	ATGCTTGGGG	GTGATATATT	AGGGGAAACA	540
AGAGTGGCTA	GCATTACGAT	CTTTAACGAA	GCTGAAGCAC	TCAATTATTC	TAAAGCCCAT	600
CAATACGCCT	TAACGCTCAC	GCTTATTAGT	TTTAGCCTCT	TGTTTGTTAC	CCTATTTTTTA	660
AATAAAAAAC	AAAGCTCGTT	TTTA				684

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 561 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208

AATTTTATTT	TTGGAGAATT	TATAATGAAG	AGATCTTCTG	TATTTAGTTT	CTTGGTAGCT	60
TTTTTATTGG	TAGTTGGCTG	TAGTCATAAA	ATGGATAATA	AGACTGTGGC	TGGCGATGTG	120
AGCACTAAAG	CGGTTTCAGAC	TGCGCCTGTT	ACTACAGAAC	CAGCTCCAGA	GAAAGAAGAG	180
CCTAAACAAG	AGCCAGCTCC	AGTGGTTGAA	GAAAAGCCGG	CTATTGAAAG	CGGGACTATC	240
ATCGCTTCTA	TTTATTTTGA	TTTTTGACAAG	TATGAGATCA	AAGAATCCGA	TCAAGAGACT	300
TTAGATGAGA	TCGTGCAAAA	AGCTAAAGAA	AACCACATGC	AAGTGCTTTT	GGAAGGCAAT	360
ACCGATGAAT	TTGGCTCTAG	CGAATACAAC	CAAGCGCTTG	GCGTTAAAAG	GACTTTGAGC	420
GTGAAAAACG	CTTTAGTCAT	TAAAGGGGTA	GAAAAAGATA	TGATCAAAAC	CATCAGTTTT	480
GGCGAAAGCA	AACCCAAATG	CGTCCAAAAA	ACTAGAGAAT	GTTACAGAGA	AAACAGAAGA	540
GTGGATGTCA	AATTAGTGAA	G				561

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 603 base pairs

(B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

867

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209

AAACGAATCA	AAAGAGGGTT	TTTTATGCAA	GAAGCGTTGT	TGCGTTTTCA	AGAGGGCTTT	60
AAGGAGTGGG	GTATATCTTAT	TTTATTTTTG	TATTCCTTGG	GGGGTGGGTA	TGTAGGGATT	120
GTCATCGCTT	CCATTTTGAG	CGCTACCACG	CACGCTTTGG	ATATAAAAAT	AACCATTCTT	180
GTCGCTTTTT	TAGGGAATTT	AATAGGGAGT	GGGGCTCTTG	TAATCTTTGC	CCGCTATCAA	240
AAAAGAGAGT	TTTTAAAGTA	TTTCCAAAAG	CATAGAAGAA	AGCTTGCTTT	GGCGAGTTTG	300
TGGGTGAAAC	GCTACGCCCT	GCTCATGATT	TTTGTCAATA	AATATCTCTA	TGGGATTAAA	360
AGCGTGTGTC	CTTTGGCAAT	TGGTTTTAGC	AAATACCCCT	TAAAAAAGTT	TTTATGGCTT	420
AATGTTTTTT	CCAGTTTTTT	GTGGGCGTTA	ATCGTGGGGA	GCGTTTCTTT	TCAAGCGAGC	480
GATTGGGTGA	AAACGCTGTA	TGAAAGGCTT	TCTCATTACA	CTTCGTTTTT	TGTCATAAGT	540
TTTGTTCCTA	TAGCGCTTTT	AATATGGTTT	TTATTGAAAC	GATATTCGCG	CAAAATGGGT	600
TTT						603

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1182 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210

GCTAGTTTTA	ATTACAATTT	TCAAATGTTA	AGGAAAAACA	TTTTAGCTTA	CTATGGGGCG	60
AAATTTCTCT	TAATCATCGC	TCAAAGCTTG	CCCCATGCGA	TTTTAACCCC	CTTGTTCCTT	120
TCTAAAGGGC	TTAGTTTGAG	TGAAATCTTG	CTCGTGCAAA	CCTTTTTTAG	TTTTTGCGTG	180
CTGGTGGCTG	AATACCCAAG	CGGCGTTTTA	GCGGATTGTA	TGAGCCGGAA	GAATTTATTC	240
CTGGTTTCTA	ATGTGTTTTT	AATCGCTAGT	TTTTCGTTTG	TGCTGTTTTT	TGATAGTTTT	300
ATCCTCATGC	TTTTAGCGTG	GGGGTTGTAT	GGTTTGTATA	GCGCATGCTC	TAGCGGCACG	360
ATTGAAGCTT	CACTCATCAC	AGACATTAAG	GAAAACAAAA	AAGATTTATC	CAAGTTTTTA	420
GCCAAAAACA	ATCAAATTAC	TTATTTGGGC	ATGATTATAG	GGAGTTCTTT	GGGATCGTTT	480
TTGTATCTCA	AAGTCCATGC	GATGCTGTAT	GTCGTGGGGA	TTTTTTTAAT	CATGCTCTGT	540
GCGCTAACAA	TCATCATTTA	TTTTAAAGAA	AAAGAAGGGG	ATTTTAAAAG	CCAAAAAAT	600
TTGAAACTCC	TAAAGAGCA	AGTCAAAGGC	AGTCTTAAAG	AGCTTAAAGA	TAACCCCAAG	660

SUBSTITUTE SHEET (RULE 26)

868

CTTAAAAATTT	TGTTAGTGGG	GCATTTGATT	ACGCCTGTCT	TTTTATGAG	CCATTTCCAA	720
ATGTGGCAAG	CGTATTTTTT	AAAACAAGGC	GTAAAGAGC	AATACCTTTT	TGTGTTCTAT	780
ATCGCTTTTC	AAGTGATTTT	CATCCTCATT	CATTTTTTAA	AAGCCAAAAA	TTACAGCCAA	840
AAAATCGCCC	TGAGTTCGCT	TTTGGTGTG	CTAGGCGTTA	GCCCCTTGTT	GCTTAGCAAT	900
ATCCCTTATT	GTTTCATAGG	GGTGTATGCG	CTCATGGTGG	CGTTTTTTGC	TTACATGAGT	960
TATTGCTTGG	GGTATCAATT	CTCCAAATTC	GTTTCTAAAA	ACAACATTTC	ATCGCTCTCA	1020
TCGCCTTTAT	CAAGCTGTGT	GCGCGTGGTC	TCTGTGCTAA	TCTTGTGCGT	CAGTAGCCTA	1080
GAGTTGCGTT	ACTTCTCACC	CCTAACTATC	ATAACCATGC	ATTTTGCCCT	AACGCTTATC	1140
ATCCTCTTTT	TCTTTTGTGA	TAAGGCTAAG	CCGTTTGATG	AG		1182

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211

CGCAGAAATC	TTACTAGACA	ACATGGAAGT	GTAAAAAGC	GTGAGAAGCG	TTTTAAAACG	60
CATGCGAGCC	TTTGGGATAG	CGTGAGGAGC	GGTAAAAGAT	TAGGCTATAC	CAATCAAGTG	120
ATCACCATA	TTGTCAATAT	CGGTATTGGG	GGGTCAGATT	TAGGCGCTTT	AATGGTTTGC	180
ACCGCCCTAA	AACGCTACGG	CCACCAAGA	TTAGAAATGC	ATTTTGTGTC	TAATGTGGAT	240
GGCACGCAGA	TTTTAGACGT	T				261

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212

CAGCATTATC	CTAATAACCT	AAAAGATATA	GAGATGAATA	CAGAAATTTT	AACCATCATG	60
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869

TTAGTTGTCT	CCGTGCTTAT	GGGATTGGTA	GGCTTAATAG	CGTTTTTATG	GGGGGTAA	120
AGCGGTCAGT	TTGACGATGA	AAAACGCATG	CTTGAAAGCG	TGTTGTATGA	CAGCGCGAGC	180
GACTTGAACG	AAGCGATTTT	ACAAGAAAAA	CGCCAAAAGA	AT		222

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213

GAAATGCAGT	TTTTACATGC	GCATCTTTTA	AGCGTGGTGA	TCTTTTTCCC	CATGCTGAGC	60
GCTCTATTAG	CGTTCCTTAT	GAGCGATCAA	CGGAGCAGGG	CGTATGCGAT	CGTCATCGCC	120
TTGATTGAAT	TGTTATTGGT	CTTGTTGTTA	TGGCATGGGT	TTGATATTCA	AACCGCAGGC	180
ATGCAGTTTG	AAGAAATGAA	AGAATTAGCC	TATCAAATTG	GCGTGAATTA	CCATGTTGGC	240
GTTGATGGCA	TCGCGCTCTT	TTTGTGCTC	TTAAACGCTA	TCGTGGTGT	ATTGTCCGTG	300
ATTTATGTCA	AAGAGCGTCG	TAAAGACTTT	GTGATTTGTC	TTTTATTGTT	AGAAGGGATC	360
TTAATGGGCG	TGTTTTCTTC	TCTTAATGTG	ATCTMTTCT	ACGCTTTTTC	GGAAATCTCG	420
CTCTTGCCGG	TTTTATACCT	CATCGGTCGT	TTTGCCCGTA	ATAACAAAAT	CTATTCTGGC	480
ATGAAGTTTT	TCCTCTACAC	CTTTTATAGC	TCGTTGTGCA	TGCTTTTAGG	CATTTTATAC	540
ATCGGGTATG	ACTACGCCAA	TAATTACGGC	ATGATGAGTT	TTGATATTTT	AGACTGGTAT	600
CAGTTGAATT	TTTCTAGCGG	GATTAACACC	TGGCTCTTTG	TAGCTTTCTT	AATAGGGATT	660
GCGGTTAAAA	TCCCGCTCTT	TCCCTTCACA	CATGGCTGCC	TTATGCGTAT	TCTACGCCC	720
CCACTC						726

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214

AAGAGGTCTC	TTATGTTAAT	AGATATTCTC	CACATCTCTT	TGATAGCTT	TAGTTTTGAG	60
AGCAITTTTAC	CCATGCTGGT	GTTGGTGTGT	GGGGGGATTT	TCACGCTCTT	AATCAACGCT	120
TTCACTTTCCA	GGTTTTTCGG	CAATTTGAAT	GTGTTTTTAT	GCATGCTCTT	TTTGGTTTTG	180
GATTTTTTATG	TGGTTTCAGG	GTTAGAAGAG	CAAGAAAACG	CCTTTTTTGG	GTTTTTTAAGC	240
CTAGATACTC	TCTCGCTCAT	CTCTCAAAGC	ATTGTCTTGA	TTTCAGCTTT	TTTTCTCATT	300
TTCTTAGCCC	TTTCAAAAGA	ACGCTTCAAC	GAATTTCAAA	CCGCTGAATT	TTATTCCCTA	360
TACTTGTTTT	TTGTCGCTGG	CTTTACGTTT	ATGTTTTCAA	GCAACCAGTT	TGTTGTAATC	420
CTTATTGGGT	TAGAAACAGC	GCCTTTGCCC	CTTTGTGTGT	TAATGGCGTT	GAGCGATAAA	480
CGCTACGGCT	TAGAAGCAGG	GATCAAGTAT	TTCAACCATG	GGGCGATGGC	GAGCGCGTTT	540
TTTGCTATGG	GCGCGATGGC	TTTTTACCTG	CTTACAGGGA	GCTTGAATCT	TGAAGTCATT	600
ACCTTATACT	TACACACTGA	GGGCATCACA	AACCCCATGC	TCTTTGCGAT	GGGCACTATT	660
TTTTTGATTG	GAGCGATTGG	CTTTAAGGTT	TCCTTAGTGC	CTTTCCATAC	CTGGATGCCCT	720
GATGTGTATG	AGGCAATAA	CCAGTCTTTT	GCGAGCTATA	TTTCCATTGT	GCCTAAAATC	780
GCTGGCTTTG	TGGTAGCGAC	TCGCCTTTTT	GGGGCGTTTA	TAGACACTCA	TACCGCTTGG	840
GTAGAAGACA	TTTTTTATGT	TTTGATCCTT	ATGACTATCA	CCATCCCTAA	TTTCATTGCT	900
TTATGGCAAG	AAGATGTCAA	AAGGATGCTC	GCTTATAGTT	CTATTTTCGA	TTCTGGGTTT	960
GCTTTAGCGT	GCGTGTATTAT	CCACACTGAA	GATAGCCAAC	AAGCGATGTT	TGTTTATTGG	1020
TTTATGTTTG	CCTTCACTTA	CATTGGGGCT	TTTGGCCTTT	TATGGCTCTT	AAAAAGCCGG	1080
GAAAAACAT	GGGATGAACG	CTACGATCAC	CCCTATTCTA	AATTCAACGG	CCTTATCAAA	1140
ACCCACCCCT	TAGTGGCGAT	CTTGGGCGCT	ATTTTTGTTT	TTGGGCTTGC	AGGGATCCCG	1200
CCTTTTAGCG	TGTTTTGGGG	GAAATTTTTA	GCCGTTGAAA	GCGCGTTAGA	GAGCAATCAC	1260
ATTCTTTTAG	CGGTGGTGAT	GTTAGTTAAT	AGCGCGGTGG	CTGCGTTTTA	TTATTCCCGT	1320
TGGCTCGTGG	CGATGTTTTT	CAATAAGCCC	TTACAAACCC	AAAGCTACGC	TCAAAACGAT	1380
ATTTACACCC	AAAACGCCAC	CATGCCCAT	TATGCGGTCA	TTATTGCCAT	GGCGTTAGCG	1440
TGCTTGTTCT	CTGTGTTTAT	GATGCGAGGG	CTTTTAGAGT	TTGTGGCT		1488

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215

AATCCCGCTC	TTTCCCTTCA	CACATGGCTG	CCTTATGCGT	ATTCTAACGC	CCCCACTCTA	60
GGCTCTGTCA	TGCTTTCAGC	CTTGCTTTCT	AAAATGGGGA	CTTACGCCTT	ATTACGCTTC	120
TTGCTCCCGC	TTTTTCCTGA	ACTTTCAGAA	ATTTATTTAA	CCCCCATAGC	CATTGTGGCG	180
CTGTGCATGA	TCATTTATGG	AGGTTTTCTA	GCCTACGCTC	AAAAAGATTT	AAAAACCCCTC	240
ATCGCTTATA	GCTCTTCTC	GCACATGGGA	GTCGTGGTGC	TTGGGGTTTT	TTCTTTCAAT	300
GTTGAAGGGG	TTTCAGGGGC	GGTGTATTAT	ATGTTTGCCTC	ATGGCGTTAT	CGTCATGGGA	360
TTATTTTATC	TCGCTGGTAT	CTTGGAAGAA	CGCGCCAGCA	GTTTAGAAAT	CGCTCGCTTT	420
GGATCGATCG	CTAAAAGCGC	TCCTGTTTTT	GCAGCTTTTT	TTATGATCGT	TTAATGGCGC	480
AATGTGGGCA	TGCCTTTAAG	CATTGGTTTT	GTGGGAGAGT	TTTTGAGCTT	GTTAGGGTTT	540
TTTGCCACTT	ACCCTCTTTT	GGCTATCATT	GCCGGGACAA	GCATCATTCT	ATCAGCGGTT	600
TACATGCTCA	CTTCATATAA	AGATGTGTTT	TTTGCAAACT	TAAAAACCGG	GAACAACCAA	660
ATCAGCGTGT	TTGAAGATTT	AAACGCTCGT	GAGGTAGGGG	TTTTAAGCGT	GATTTTAGCT	720
TTGATCTTAA	TTTTAGGGAT	TTATCCTAAA	GCGCTTTTAA	AACCGATTGA	GCAAGGCTTT	780
AAGCAGCTTT	TAGAGGTGAT	AGAAATCCGC	TCGCTCCTTT	TTTTAGGTTT	ATTGGACACT	840

871

AAGATAAAAG AGGTCTCTTA TGTTAATAGA TATTCTCCAC ATCTCTTT

888

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216

ATTTATTCAA	AAACAAGGAG	TCATGACATG	GACATTAGCA	TTTTTAGAGA	ATACGATATT	60
AGAGGCATTT	ACCCACCAC	TTTAGATGAA	AATACGGCTT	TTAGTATCGG	CGTGGAGTTG	120
GGAAAAATCA	TGCGAGAATA	CGATAAAAGC	GTGTTTGTAG	GGCATGACGC	AAGGGTGCAT	180
GGGCGTTTTT	TGTTTGAAGT	TTTGAGCGCG	GGGCTGCAAT	CAAGCGGCTT	GAAAGTGTAT	240
GATTTAGGGC	TAATCCCCAC	ACCGGTAGCG	TATTTTGC	CGGCTTTAATGA	AATAGACAAT	300
ATCCAATGCC	CTAATCCAT	CATGATCACT	GGCTCTCACA	ACCCCAAAGA	ATACAACGGC	360
TTTAAAATCA	CGCTCAATCA	AAACCCGTTT	TATGGCAAGG	ACATTCAGGC	TTTAAAAAAC	420
ACGCTTTTTTAA	ACGCAAAGCA	TGAAATAAAG	CCCCTAAAAG	AAACGCCAGA	GAAAGTCAAT	480
GCCCTAGAAG	CGTATCATCG	CTATTTGATC	AAGGATTTTA	AGCATTTAAA	AAATCTTAAA	540
TACAAAATCG	CCCTGGATTT	TGGTAATGGC	GTGGGGGCGT	TAGGATTAGA	GCCGATTTTA	600
AAGGCTTTTAA	ACATTGATTT	TAGCAGCCTT	TATAGCGATC	CTGATGGGGA	TTTTCTTAAC	660
CACCACCCAG	ACCCTAGCGA	AGCGAAAAAC	TTAAAAGACT	TAGAAAAACA	CATGCGAGAA	720
AACGCTATTT	TAATAGGCTT	TGCTTTTGAT	GGCGATGCGG	ATAGGATTGC	GATGCTAAGC	780
TCTCATCATA	TCTATGCGGG	CGATGAATTA	GCGATTTTAT	TCGCTAAACG	CTTGCATGCT	840
CAAGGCATCA	CCCCTTTTGT	GATCGGCGAA	GTCAAATGCT	CTCAAGTGAT	GTATAACGCA	900
ATCAATACTT	TTGGTAAAGC	GCTCATGTAT	AAAACCGGCG	ATAGCAATTT	AAAAATCAAG	960
CTCAAAGAAA	CTAATGCGCA	TTTTGCGGCT	GAAATGAGCG	GGCATATCTT	TTTTAAAGAA	1020
CGCTATTTTG	GCTATGATGA	CGCTCTTTAC	GCATGTTTAA	GGGCTTTGGA	GTTATTGCTT	1080
GAACAAAGTC	CAAGCGACTT	GGAAAACACC	ATTAAAAACC	TCCCCTATTC	CTACACCACG	1140
CCTGAAGAAA	AAATCGCCGT	GAGCGAAGAA	GAAAAATTG	AAATCATTCG	CAACTTACAA	1200
GAAGCGCTTA	AAAACCCGCC	AAGCCATTTC	CCTACAATCA	AAGAAATCAT	CAGCATTGAT	1260
GGCGTGAGAG	TGGTTTTTGA	ACATGGCTTT	GGGCTTATTC	GCGCAAGCAA	CACCACCCCC	1320
TATTTAGTCA	GCCGCTTTGA	AGGCAAGGAT	GAAACAACAG	CGTTAGAATA	TAAAAGGGCG	1380
TTGCTTGGGC	TATTAGAAAA	ACTT				1404

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

872

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217

GGAATTTT	TGAATGAGAT	CATTTTAATC	ACCGGCGCTT	ATGGCATGGT	GGGGCAGAAC	60
ACGGCGTTGT	ATTTTAAAAA	AAACAAGCCT	GATGTTACCT	TACTCACCCC	TAAAAAGAGC	120
GAATTGTATT	TGTTGGATAA	AGACAACGTT	CAAGCCTATT	TGAAGAATA	CAAGCCTACA	180
GGCATTATCC	ATTGTGCCGG	GAGAGTGGGG	GGCATTGTGG	CAAACATGAA	CGATCTTTCA	240
ACTTACATGG	TTGAGAATTT	ACTCATGGGT	TTGTATCTTT	TTTCTAGCGC	TTTAGATTTG	300
GGCGTGAAAA	AAGCCATTAA	TCTAGCGAGC	TCTTGCGCTT	ATCCTAAATA	CGCCCCCTAAC	360
CCTTTAAAG	AGAGCGATTT	ATGAACGGC	TCTTTAGAAC	CAACGAATGA	AGGCTACGCT	420
TTAGCCAAAC	TCTCTGTGAT	GAAGTATTGC	GAATACGTGA	GCGCTGAAAA	AGGCGTTTTT	480
TATAAAACTC	TAGTGCCTTG	TAACCTTTAT	GGCGAGTTTG	ACAAGTTTGA	AGAAAAGATA	540
GCGCACATGA	TACCAGGGCT	TATTGCTAGG	ATGCACACCG	CTAAATTAAA	AAATGAAAAA	600
AATTTTGC	TGTGGGGCGA	TGGCACGGCC	GAAGAGAGTA	TC		642

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218

GCTCAGCCA	ACCGCACCAT	CATCCACAGG	ATTGATGATA	GCATCGCGCA	GCGCGTGGAT	60
AATGCCATT	GCCCCATGCG	TTTGTTAGA	GGGTTTGCCC	CCCTTTACCT	CACTTTACCC	120
AAACGCTCTT	TTAATGCGCC	CAAAAAGATT	TTAGCCCTTG	GAGCGGAGCA	AAAAGGGCAT	180
TTTAGCTTAC	TAGATAGCGA	AACTTCTGTT	CTTTTACTCT	CGCCTTTTTG	TGGGGATTG	240
AGCGTTTTAG	AAAATGAAAA	ACACTTTAAA	GAAACTTTGA	ATTTTTTCTT	AAAAACCTAT	300
GATTTCAAAC	CCACGCTCTT	AGCTTGCGAT	GAGCATCAAA	ACTACACCAC	CACCAAAATG	360
GCTTTTGATT	TTAATACGCC	CTTGTTGCAA	GTCCAGCACC	ACCATGCCCA	CTTTTTAGCG	420
AGCGTCTTAG	ACGCATTATT	ACAAGATCCG	CATTTAAATC	ACCCCTTTAT	AGGTATTGTT	480
TGGGACGGGA	GTGGGGCTTA	TGAAAATAAG	ATTTATGGGG	CGGAGTGTTT	TGTGGGGGAT	540
TTGGAACGCA	TTGAAGAAGT	GGCTAGATTT	GAAGAATTTT	GGCTTTTAGG	GGGGCAAAAA	600
GCGATCAAAG	AGCCTAGAAG	ATTGGTTTTA	GAAATCGCTT	TAAACACCCA	GCTCAACAAG	660
CTTTTAAAC	GCGTTCAAAA	GCATTTCAA	GAAGACGAAT	TAGGAATTTT	TAAACAAATG	720
CATGACAAAA	AAATTCAAAG	CGTCGCCACC	AATTCCATAG	GGCGTTTGTT	TGATATAGTG	780
GCGTTTAGTT	TGGGCGTGGT	GGGAACGATT	AGTTTTGAAG	CCGAGAGCGG	GCAGGTTTTA	840
GAAAATCTAG	CCCTACAAAG	CGATGAGATC	GCTTTTACC	CTTTTGAAAT	CAAAAACAGC	900
GTGGTGCGTT	TGAAGGAATT	TTATCAAGCG	TTTGAAAAGG	ATTTGGGCGT	TTTAGAACCC	960
AAACGCATCG	CTAAGAAATT	TTTAAACAGC	TTAGTAGAAA	TCATTACCGC	TTTGATTGCG	1020
CCTTTTAAAG	GGCATGTCGT	GGTGTGCAGT	GGGGCGGTGT	TTTGCAACCA	ATTGTTGTGC	1080
GAACAATTAG	CCAAGCGATT	GAAAAAGCTT	CAAAGGGAGT	ATTTTTTCCA	CAAGCATTTT	1140

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873

CCCCCTAATG ACAGCAGTAT CCCTGTCGGT CAAGCCTTAA TGGCGTATTT CAACCCTACA 1200
ATCATCAAAA AAGGA 1215

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219

CGCTTTGAGT	CGCGAGCGAG	CGACATGAGC	GGGTGGCTTT	TAATGGGATT	ACCGGGAGCT	60
TTATATGTGG	GGGGGCTTAT	CAATTCACAC	ATCGCCATAG	GCTTGAGTTT	GGGCGCACTC	120
ATTAACCTGG	TTTTTGTTGG	TAAGCGCTTA	CGCATTATATA	CGAGCGTGAT	CGCTAATTCT	180
ATTACCATTT	CAGATTATTT	TGAAACGCGC	TTTAGCGATG	ATAAACACAT	CTTGCGCTTG	240
ATTTTCAGCTT	TGTGATTTT	AATCTTAAAG	ATTTTITATT	TTCTTCAGG	GCTAGTGAGT	300
GGGGCTAAAC	TCTTTGAACC	GACCTTTGGC	ATTCAATACA	CCTACGCTTT	AAGCATTGGC	360
ACGCTGATTA	TGTCTTCTTA	CACCTTTTTA	GGAAGGTATA	AGCGGGTGTG	CTGGACGGAT	420
TTGATTCAAG	GGCTTTTGAT	GATGAGCGCT	TTAATCGTGG	TGCCGATCGT	TATGATAATC	480
CATCTTGGAG	GGATTGGAGA	GGGGATTAAA	ATCATTAAAG	AGATCAAGCC	TGAAAACCTT	540
TCTTTCTTGC	AAGGCTCTAG	CGTAGTCGCT	ATTATTTCAA	GCCTTGCTTG	GGGGTTAGGC	600
TATTTTGGGC	AACCCCATAT	TTTAGTGCGC	TTCAATGTCTA	TCCGCTCCAT	TAGAGATGTG	660
CCTAAAGCGA	CCACTATTGG	GATTTCTTGG	ATGGTTATTT	CTTAAATTGG	GGCATGCGTT	720
ATGGGGCTTT	TAGGCGTTGC	TTATGTACAT	AAATTTGACT	TGAGTTTAGA	AGACCCTGAA	780
AAGATTTTCA	TTGTAATGAG	TCAATTGCTC	TTTAACCCCT	GGATCACAGG	CATTTTATTG	840
AGCGCGATTT	TAGCGGCGGT	GATGAGCACG	GCCAGTTGCG	AACTGCTTGT	AAGCTCTTCT	900
ACCATTGCTG	AAGATTCTTA	TGCGACGATT	TTCAATAAAA	ACGCCCCCCA	AAAATTAGTG	960
ATGACGATTT	CTAGGCTTTC	GGTTTTAGGG	GTGGCTTGCA	TGCCTTTTTT	CATTTCAACG	1020
GATAAAAACG	CTAGCATCCT	CAGCATCGTG	AGTTACGCAT	GGGCTGGCTT	TGGCGCGAGT	1080
TTTGGCTCTG	TGATTTTGT	TTCACTTTT	TGGTCAAGAA	TGACGCGCAT	TGGCGCGATT	1140
GCTGGCATGC	TCTCTGGGCG	TAGCACGGTG	ATTTTATACG	ATAAATTGG	CAAAAGCTTT	1200
TTGGATATTT	ATGAAATCGT	TCCGGGCTTT	ATTGTAGCGA	GCGTAGCTAT	TGTTGCGTTT	1260
AGTTTGTTTT	CTAGCGTGCG	ATCAGGCACT	AAAGAGGCCT	TTGAAACCAT	GCTTAAAGAA	1320
ATTGAGAGCT	TAAAGCAT					1338

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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874

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220

AATAAGTGGG	TTAAAGGGGC	GGTTGTTTTT	G TAGGGGGTT	TTGCAACGAT	TACAACCTTT	60
TCTTTAATCT	ACCACCAAAA	GCCAAAAGCC	CCCCTAAATA	ACCAGCCTAG	CCTTTTGAAT	120
GACGATGAGG	TGAAATACCC	CTTACAAGAC	TACACTTTCA	CTCAAAACCC	ACAGCCAACT	180
AACACGGAAA	GCTCCAAAGA	CGCTACCATC	AAAGCCTTAC	AAGAACAGCT	CAAAGCCGCT	240
TTAAAAGCCC	TAAACTCCAA	AGAAATGAAT	TATTCCAAAG	AAGAGACTTT	TACTAGCCCT	300
CCCATGGATC	CAAAAACAAC	CCCCCTAAA	AAAGACTTTT	CTCCAAAACA	ATTAGATTTA	360
CTGGCCTCTC	GCATCACCCC	TTTCAAGCAA	AGCCCTAAAA	ATTACGAAGA	AAACCTGATT	420
TTCCCTGTGG	ATAACCCTAA	TGGCATTGAT	AGTTTCACTA	ACCTTAAAGA	AAAAGACATC	480
GCCACTAATG	AAAACAAGCT	TTTACGCACC	ATTACAGCTG	ACAAAATGAT	ACCCGCTTTT	540
TTGATTACGC	CCATTTCTAG	CCAGATCGCT	GGTAAAGTGA	TTGCGCAAGT	GGAGAGCGAT	600
ATTTTTGCAA	GCATGGGCAA	AGCCGTCTTA	ATCCCCAAAG	GCTCTAAAGT	CATAGGCTAT	660
TACAGCAACA	ATAACAAAAT	GGGCGAATAC	CGCTTGGATA	TTGTATGGAG	TCGAATCATC	720
ACTCCCCATG	GCATTAATAT	CATGCTCACT	AACGCTAAAG	GGGCGGACAT	TAAAGGCTAT	780
AACGGCTTAG	TGGGGGAATT	GATTGAAAGG	AATTTCCAAC	GCTATGGCGT	GCCGTTACTG	840
CTTTCTACGC	TCACTAACGG	CCTATTGATT	GGGATCACTT	CGGCTTTAAA	CAACAGAGGC	900
AATAAAGAAG	AGGTGACTAA	TTTCTTTGGG	GATTATCTTT	TATTGCAATT	GATGAGGCAA	960
AGCGGCATGG	GGATCAATCA	AGTGGTCAAT	CAAATTTTAA	GAGACAAGAG	CAAGATCGCC	1020
CCCATTGTGG	TGATTAGAGA	GGGGAGTAGG	GTCTTCATTT	CGCCCAATAC	TGACATCTTC	1080
TTCCCTATAC	CCAGAGAGAA	TGAAGTCATC	GCTGAGTTTT	TGAAG		1125

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221

AAAGCGGCGT	TTTGATAGG	GATTTTTTTC	TATGGCGCTT	ATTATTTCTT	AGATGAATTT	60
TTAATCAAGC	TTTATTGCA	GCCAAGCGAG	CAAGACGCGC	TCTTTATGCA	AGAGACTAAA	120
AGAGCGATGA	ATATTTATTA	TGTGGGCTAT	GTTTTTTTAG	GCATGACTTT	GTTGTGCGCG	180
GTGTTTTTCC	AATCTATTCA	ACGCACTAAA	AGTTTCGTTA	TCATCACGAT	TTCCGACACG	240
CTAGGGTTTA	TCGTTATCCT	ATTGCCGATT	TTAAGTCATT	TTTATGGGGT	TAATGGCATT	300
TGGGTAACCT	ACCCTATTGC	GCAATTTTTA	GCCGTTTTTG	GTAGCGTTAG	GGGTAACTTA	360
TTA						363

(2) INFORMATION FOR SEQ ID NO:1222:

875

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222

ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTATTAC	60
TTCATCCCTT TAGTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG	120
TTTGTGGGCA AAAAAGCTGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT	180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATTGTGGGG	240
TATTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT	300
TTTGTGCGTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAATATC	360
GCGCGTTTTT TGGGAGCAAT GACGCTTTAT	390

(2) INFORMATION FOR SEQ ID NO:1223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...483
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223

AATCATTTTA ATGGTTGTGT TTTTAGGGTT CAGCACCTTT TAGCGGATGT CTTTGTGGTG	60
AATGACAAAC GGCCCGTTTT AGCGATGGTA GCGATGTTGA TTGGCTCGTT AGCGAATATC	120
TTTTTCAATT ACTTGTATTAT TTTTGTGTTG GAAGTGGGGG TTCAAGGCAG CGCGATAGCC	180
ACCGTGATAG GGCATGCGAT AGGGGTTTTA GTCTTAATGC AGCATTTTTG GCGCAAAAAA	240
GGGCAGTTGT ATTTTATCAA ACGATTTTCT TTATCTTCAG TCATTTCTTC AGCTAAAAGC	300
GGTGTGCCTC AAAGCACGGC GGAATTTAGC GCTTCTATTA TGATTTTATT GTTTAATACC	360
GCTATCATGC ACACGCGCGG GGAAGGTTT GTGAGCATGT ATGGGATCGT TATGTATAAT	420
GCGATTATCT TTTTACGAC TTTGTTTGCG ATTTCTCAAG GCATCCAACC GATTGCAGAG	480
CTT	483

(2) INFORMATION FOR SEQ ID NO:1224:

876

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224

TTTCTTAACA	TTAGGGATTT	GACGATGATT	TTTAGCTCTC	TTTTTAGTGT	TGTAGGGATG	60
GCGGTGCTTT	TTCTTATTGC	TTGGGTGTTT	TCTGGCAATA	AAAGGGCTAT	AAATTATCGC	120
ACGATTGTCA	GCGCCTTTGT	GATTC AAGTG	GCTTTAGGGG	CGTTGGCTTT	ATATGTGCCT	180
TTGGGCAGAG	AAATACTGCA	GGTTTAGCT	AGCGGCATAC	AAAGCGTGAT	TGTTACGGC	240
TATGAGGGGG	TACGCTTTTT	ATTGGCAAT	CTCGCTCCAA	ACGCTAAGGG	CGATCAAGGG	300
ATAGGAGGCT	TTATCTTTGC	GATCAACGTT	TTAGCGATCA	TTATCTTTTT	TGCTAGCTTG	360
ATTTCACTTC	TATATTATTT	AAAAATCATG	CCTTTAGTGA	TCAACCTCAT	CGGCGGGGCG	420
TTGCAAAAAT	GCTTAGGCAC	TTCTAAAGCA	GAAAGCATGA	GCGCAGCGGC	TAATATTTTT	480
GTGGCGCACA	CCGAAGCGCC	CTTAGTCATT	AAACCCTATT	TGAAAAGCAT	GAGCGATTCA	540
GAGATTTTTG	CGGTCATGTG	CGTGGGCATG	GCTAGCGTTG	CGGGGCCTGT	GTTAGCCGGG	600
TATGCGAGCA	TGGGCATTCC	TTACCTTAT	TTAATCGCCG	CATCGTTTAT	GTCCGCTCCT	660
GGGGGGTTGT	TGTTGCTAA	AATCATTTAC	CCGCAAAACG	AAACCATTTC	TAGCCATGCA	720
GATGTTTCTG	CAGAAGAGCA	TGTCAATATT	ATAGAAGCTA	TCGCTAATGG	GGCAAGCACA	780
GGGCTTCATT	TAGCCTTGCA	TGTGGGGGCG	ATGCTTTTAG	CCTTTGTGGG	GATGCTCGCG	840
CTCGTTAACG	GGCTTTTAGG	GTTGTAGGG	GGATTTT TAG	GCATGGAGCA	TTTGTCTTTA	900
GGGGTGGTTT	TAGGCACGCT	TTTAAAACCT	TTGGCCTTTA	TGTTAGGCGT	TCCTTGAGGC	960
CAAGCCGGGA	TTGCCGGGGA	AATCATAGGC	ATTAAAATCG	CGCTCAATGA	ATTTGTGGGC	1020
TATATGCAAT	TATTCCTTA	TTTGGGCGAT	AACCCTCCTT	TAATCTTGAG	CGAGAAAACC	1080
AAAGCGATCA	TCACCTTTGC	GTTGTGCGGA	TTGCTAACT	TAAGTTTCACT	CGCCATGCTC	1140
ATTGGGGGGC	TTGGCAGTTT	AGTGCCTAAA	AAGAAAGATT	TCATTGCCAG	GCTTGCTTTA	1200
AAAGCGGTGC	TTGTAGGCAC	GCTTTCTAAT	TTCATGAGCG	CGACTATCGC	CGGGTTATTG	1260
ATAGGGTTAA	GCGCCAAT					1278

- (2) INFORMATION FOR SEQ ID NO:1225:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

877

(B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225

ACGCTATCCA	AAGAAGAGGG	ATTGATGCCA	CAAAACCAGC	TTGTGATCAC	CATCATTGAT	60
GAATCAGGCT	CTAAGCAACT	CAAATTTTCT	AAAAATTTAA	AACGCAACCT	CATCATTTCT	120
GTTGTCAITC	TTTTATTGAT	CGTGGGGCCT	GGCGTGGGGT	TTTTAAATTT	TTTAATCGCT	180
AAAATGGATA	CGATGACAAG	CGAGAGGAAT	GCGGTTTTAA	GGGATTTTAG	GGGTTTGAT	240
CAAAAAAATT	ACGCCCTAGC	GAAAGAGATT	AAAAACAAGC	GAGAAGAGCT	TTTTATTGTG	300
GGGCAAAAGA	TCCGTGGGCT	AGAATCCTTG	ATTGAAATCA	AAAAGGGGGC	TAATGGGGGA	360
GGGCATCTCT	ATGATGAAGT	GGATTTAGAA	AATTTGAGCT	TAAATCAAAA	ACATTTAGCA	420
CTCATGCTCA	TTCCATATGG	CATGCCCCCTA	AAAACCTATA	GCGCTATCAA	ACCCACTAAA	480
GAAAGGAACC	ACCCCATTTAA	AAAGATTAAAG	GGCGTTGAAT	CCGGGATCGA	TTTTATCGCG	540
CCATTGAACA	CGCCTGTGTA	TGCGAGCGCT	GATGGGATTG	TGGATTTTGT	GAAGACTCGT	600
TCTAATGCGG	GGTATGGGAA	CTTGGTGCGC	ATTGAACATG	CGTTTGGTTT	CAGCTCCATT	660
TATACGCACT	TAGATCATGT	CAATGTGCAG	CCTAAAAGCT	TCATCCAAAA	AGGGCAGTTG	720
ATTGGCTATA	GCGGGAAGAG	CGGTAATAGC	GGCGGCGAAA	AAATGCATTA	TGAAGTGCGG	780
TTTTTGGGTA	AAATTTTAGA	CGCAGAAAAA	TTCCTAGCAT	GGGATTTGGA	TCATTTTCAA	840
AGCGCTTTAG	AAGAAAATAA	ATTTATTGAA	TGGAAGAATC	TGTTTTGGGT	TTTGAAGAC	900
ATCGTCCAGC	TCCAAGAGCA	TGTGGATAAA	GACACCTTAA	AAGGTCAG		948

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226

GGGTTTTTGG	TGTTTTTAGA	CAGGCGTTTG	ATTGTGATGG	TTACGGACTC	TAAAGGGAGT	60
CGTTATATTA	ATGTGCATAT	CTTATTCCGC	CAAATCAGTT	TGTATGCGCT	GTTGAGCGTT	120
GTGGGATCTT	TATTGTTTTT	AGGCGTTTCA	TTACTGGTTT	TAAATAAAGA	AATTAAAAAC	180
ATTGAAAAAC	AGCATGCTTT	AATCACTAAG	GAATTTGAGA	AAAAAAGAGA	GACGAATGAA	240
AAGCTTTCTT	TGCAAAATGGA	TGAGTTTTTA	GACGATTTGC	AACTTTCAGG	GGAGCGCATC	300
AACGATTTAG	AAGAAGTGGT	GGGGGTGAAT	AGGCCTGAAG	AAGAAAAAGA	AGAGGGCAAT	360
TTTTCCAGCC	GCTTGGATGT	GGCTGGGATT	ACCGGCCTTC	AAAAAAGCTT	TATCATGCGC	420
CTTATCCCTA	ATGACTACCC	GCTAGAATCC	TATCGGCGCG	TTTCAGCCGC	TTTTAATAAA	480
AGAAATGCACC	CTATTTTGCA	TGTGTGTCAC	AACCATACCG	GGCTTGATTT	AAGCACCCTG	540
ATTAACACGC	CTGTGTATGC	GAGCGCGAGC	GGGGTAGTGG	GGTTAGCGAG	CAAGGGGTGG	600
AATGGGGGGT	ATGGGAATTT	GATTAAAGGT	TTCCACCCTT	TTGGTTTTAA	AACCTACTAC	660
GCCCATTTGA	ATAAAATCGT	CGTAAAAACG	GGCGAATTTG	TCAAAAAAGG	GCAGTTGATT	720
GGGTATAGTG	GTAATACAGG	AATGAGCACA	GGACCGCATT	TGCATTATGA	AGTGCGCTTC	780
TTAGATCAAC	CCATAAACC	CATGAGTTTC	ACCAATGGA	ACATGAAAGA	TTTTGAAGAA	840
GTTTTTAATA	AAGAAAGGAG	CATCAGATGG	CAATCTTTGA	TAACAATAAT	AAATCGGCTA	900
ATGCAAAAAC	AGGACCAGCG	ACTATCATCG	CTCAAGGCAC	CAAAA		945

(2) INFORMATION FOR SEQ ID NO:1227:

SUBSTITUTE SHEET (RULE 26)

878

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1380
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227

GATATTGAAT	TCGCCAATCT	TTATCATATT	CCTATTAAAG	TGATCACGCA	AAGCCCTCAA	60
AATTTGCCCC	ACACCAAAGA	AGAGATTTTA	AAAAATAGCG	GGGAGTGGAG	CGATCTTTCT	120
AGCTCACTGG	CCAGAAAAAA	AATCCTCCCT	TATTTTGACA	AAGAAAATCT	CGGTAAAAGG	180
GTCAATCACT	ACCGCTTGCA	AAATTGGGGG	GTGAGCCGTC	AAAGGTATTG	GGGAGCGCCC	240
ATTCTATGA	TTCATTGCAA	ACATTGCGGA	ATCGTGCCTG	AAACCCCACT	GCCGGTAACT	300
TTACCTGAAG	ACATTGTGAT	TGATGGGGAA	GGCAATCCAT	TAAAAAAGCA	TGCGAGTTGG	360
AGATTGCTC	AATGCCCCAG	ATGCCATAAA	GACGCTTTAG	TAGAAACAGA	CACCATGGAC	420
ACTTTTATCC	AATCCAGCTG	GTATTTCTTG	CGTTATACCA	CCCCCAAAA	TCAGCGTGAA	480
AATCAAGCGT	TTGATCAAAA	TTACTTGAAG	TATTTTCATG	CGGTGGACAC	TTATATTGGC	540
GGCATTGAAC	ATGCGATTTT	GCACTTGTTA	TACGCGCGCT	TTTTCACTAA	GGCTTTAAGG	600
GATTTGGGCT	ATCTTCATTT	AGATGAGCCT	TTCAAACAGC	TTATCACTCA	AGGCATGGTC	660
TTAAAAGATG	GTGCTAAGAT	GAGCAAATCT	AAAGGCAATG	TCGTTAGCCC	TAAAGAGATA	720
CTCAAAAAAT	ACGGGGCTGA	TGCCGTAAGG	CTCTTTATCC	TTTTTGCTGC	CCCGCCGGCT	780
AAAGAATTGG	AATGGGAATGA	CAACGCTTTA	GAAGGCGCGC	ACCGGTTTAT	CAAGCGCTTA	840
TACGATAAAG	CGAACGCCAT	TACCCCTACC	ACTTCTAAGC	CTGAATTTAA	AGAAGTTGGC	900
CTGAATGAAG	CGCAAAAATT	AGCCCGCAAA	AAAGTCTATG	AGGCGTTGAA	AAAATCGCAT	960
GAGATTTTCA	ATAAGGCTGA	AAGCGCTTAC	GCGTTTAACA	CTTTGATCGC	AAGCTGCATG	1020
GAGGCTTTAA	ACGCTTTGAA	CGCGCAAAGT	GATGAGCAAA	TTTTATGCGA	GGGTATTITT	1080
GTGTTGTTGC	AAATCTTAGA	GCCTATGATC	CCGCACACGG	CATGGGAATT	GAGCGAGAGG	1140
CTTTTAAAAA	GAGAGAATTT	CAAGCCTATA	GAAGTAGATG	AAAGCGCTTT	GATAGAAGAC	1200
TTTATGACTT	TAGGGCTTAC	CATTAATGGC	AAAAGGCGCG	CGGAATTGAA	AGTCAATATT	1260
AACGCTAGCA	AAGAAGAGAT	TATTATTTTG	GCTAAAAAAG	AATTAGAGAA	ATATTTAGAA	1320
AACGCGAGCG	TTAAAAAAGA	AATTTATGTG	CCTAATAAAC	TTGTTAATTT	TGTTACCGCA	1380

(2) INFORMATION FOR SEQ ID NO:1228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature

879

(B) LOCATION 1...1209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228

CTAAATTTGT	GGCTCAAATC	GCTTATGAGG	GGAAATTCAA	TAATGAAAAA	TAGTCATGGG	60
TTAAAGGCGT	TTTTAGAAAC	AAAGCCTAAG	GAATACCATA	AGTTCGACCC	TAGCCGTTTC	120
ATTCAAATTT	ATAAGGATTT	TAAAAACGCT	TTTTTTGAGA	TTCAAGCCAA	AGTCATTCAT	180
GTGGTAGGGA	CTAATGGTAA	GGGCAGCACA	GGCGGGTTTT	TAACCCTTTT	ATTAGCCGAT	240
CAAGGGTTTA	AAGTGTTCGA	TTTCACCTCC	CCTCATGTTT	TTGAATTCAG	GGAGCGCTTT	300
TATTTGAATG	GCTCTGTTGT	TAAAGAAAGC	GTTTTAGAAA	ACGCCCACCA	GCAATTGCAA	360
TCGCACGCTT	TCAGTAACGC	TTGCTCGTAT	TTGAATACG	CTACCTTATT	AGCTGTCATG	420
CTCGCTAAAG	ATTGCGATTA	TTTGGTTTTA	GAAGCAGGGC	TTGGGGGGGA	GTTTGACAGC	480
ACGAACGCTT	TGGAAAAAAC	CCTAAGCGTT	TTCAACCCCA	TTGATTACGA	TCATAAGGAA	540
TTTTTAGGGG	ATAGTTTAGA	AAGCATTGCG	ACTACTAAAT	TAAAAGCGAT	GGGCTCTCTT	600
AATATCATCG	CTCCCCAACA	AGAACTGGTT	TAAATGTGG	CTCAAAAAAT	CGCTAAAGAC	660
AAACACGCGC	AATTGATGTG	GGTTCAAAT	GAAATTTCAA	AAGGAGTGAG	CGATTATATT	720
GAACGCCACC	ATTTAGCCCA	TTTTTTAGCG	ATGAATTTAG	AAGTGGCTCT	AAAGGCGTTT	780
GAAACGCTAT	TGCCATGCAA	TAAACAAGAA	GTTTTAAAAA	ACCTAAAGCC	CCTAGATTTA	840
ATCGGCCGTT	GCGAGCTTTT	AAGCCCTAAC	ATTTTAATAG	ATGTGGGGCA	TAACCCCAT	900
AGCGCTAAAG	CCTTAAAGA	AGAAATCAAA	CGCATCTTTA	ACGCTCCAAT	CGTTTTGATT	960
TATAATTGCT	ATCAAGATAA	AGACGCTTTT	TTGGTGCTAG	AAATTTTAAA	GTCTGTGGTT	1020
AAAAAGGTTT	TGATTTTAGA	ATTGCATAAT	GAAAGAATTA	TCCAATTAGA	AAAACCTAAA	1080
GGGATTTTAG	AAACTTTAGG	GTTAGAACAC	GCCTTGTTTG	AAGAAGTGAA	AGAAAATGAA	1140
AATTATTTGG	TGTATGGCTC	ATTTCTGGTA	GCCAACGCTT	TTTATGAACG	CTATCCAAAG	1200
AAGAGGGAT						1209

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229

AGCGTGTTCA	GTCATAGCGG	GAGCGCGGAT	TTGTGGGAAA	ATTTGGGCGT	GAATATTGAA	60
ATGAACCCCA	TGCAATTAGA	AAATTGCTTC	AAACAATCGC	ATTTTGGGTT	TTTATTGCGG	120
CCTTTATACC	ATCAAAGTTT	TAAAAAATCC	GCCCCTTTAA	GAAAAGAGCT	TTTCACTAAA	180
ACGATTTTCA	ATTGCTTAGG	GCCTTTAATC	AACCCCTTAA	GGCCAAAAAT	CCAGCTTTTA	240
GGCGTGATG	ACAAATCCTT	GTGTAAGACC	ATGGCGCTAG	CGTTGAAGGC	TTTAGGCGTT	300
AAAAGGGCGA	TGGTGGTTAA	TGGAGGGGGG	ACAGATGAAA	TCGTGTTGCA	TGACATTACG	360
CATGCGTGCG	AATTGAAAAA	TAACGAAATT	TTAGAGTATG	ATTTGAGCGC	TAAAGATTTT	420
GATTTACCCC	CCTATGATTT	GAAAGAATTA	CAGATTGAAA	ACGCCAAAGA	AAGCGTTCAA	480
GCGTGTTTAG	ATATTTTAGA	AAATAAAGGC	AAAGATTTCG	ATACAATGGT	GGTTGCGGCG	540
AATGTGGCGA	GTTTGTTGTA	TTTGAGCCAT	AGGGCTAAAG	GATTTAAAAG	AGGGCGTGAG	600
CATGACTTTA	GAGCATTTAA	AAACCAAAGC	GCATTATGTG	CATTTACAAA	AAATCATAAG	660
GCTAAGCCAT	GCCTAGCGTG	T				681

(2) INFORMATION FOR SEQ ID NO:1230:

SUBSTITUTE SHEET (RULE 26)

880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230

AATTTGGTAG	TGAGTGTTC	TGCAACGAGT	GCGAATTAG	GCCCCGGTTT	TGATTGCTTG	60
GGTTTGAGTT	TGAATTTACG	CAATCGTTTT	TTTATTGAGC	CTAGTAATAT	CCATGCCGGTG	120
AAATTGGTTG	GGGAGGGTGA	AGGGATCCCT	AAATTTTAA	CCAACAATAT	TTTCACCAAA	180
GTGTTTTATG	AGATTTTAAA	AAAGCATGGG	AATGACGGCT	CGTTTAAATT	TTTATTGCAT	240
AATAAAGTCC	CTATTACAAG	GGGCATGGGG	TCTAGCTCAG	CGATGATTGT	GGGGGCGGTC	300
GCTTCAGCGT	TTGCGTTTTT	AGGGTTTGCT	TTTGATAGAG	AAAACATTCT	CAATACTGCT	360
CTAATTTATG	AAAACCACCC	GGATAATATC	ACCCCGGCGG	TGTTTGGGGG	GTATAATGCA	420
GCGTTTGTGG	AAAAAAAGAA	AGTGATAAGT	TTAAAACCA	AAATCCCTTC	TTTTTTAAAA	480
GCGGTGATGG	TGATCCCTAA	TAGGGTCATT	TCTACCAAGC	AATCGCGCCA	TCTCTTGCCC	540
AAGCGTTACA	GCGTGCAAGA	AAGCGTGT	AACCTTTCG	ATGCGAGTTT	GATGACGATG	600
GCGATTGTGC	AAGGGAAGTG	GGACTTGTG	CGTTGTGTT	CTAAAGACAG	GATGCACCAA	660
TATAAGCGCA	TGCAAACTTA	TCCCGTGTG	TTTGCGATCC	AAAAGCTCGC	TTTAGAAAAT	720
AACGCCCTTA	TGAGCACGCT	TTCAGGGAGT	GGTTCGTCGT	TTTTTAACAT	GTGTTATGAA	780
GAAGACGCTC	CTAAATTAAA	GCAGGTTTTG	AGCAAGAAAT	TCCCTAAATT	TAGGGTAGCG	840
GTTTTAGATT	TTGACAATGA	TGGAGTCCTT	ATTGAGAAAG	AC		882

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231

TTAGTATTCA	AAAAGCCCTT	TTTTAAAAAT	AGGTTACTAA	ACGTTACTAA	TAAGTTAAAA	60
TTCTGTAAAA	TAACCATAAT	GATTAAAGAT	TTTAACCACT	ATTGTAGAAA	AATAACGAGA	120
GGGTTTGTA	AAATTCCAC	CAAAAAACAA	GGAGCAAAAA	AGATGAAAAA	AGCGGGTTTT	180

SUBSTITUTE SHEET (RULE 26)

881

CTTTTITTTGG	CGGCGATGGC	TATCATTTGT	GTGAGTTTAA	ACGCCAAAGA	TCCGAAATGIG	240
TTGCGTAAGA	TGTTTTTTGA	GAAATGTTTG	CCTAATTATG	AGAAAAATCA	AAATCCTTCA	300
CCATGCATAG	AAGTCAAACC	CGACGCCGGC	TATGTGGTTT	TAAAAGATAT	TAACGGTCCG	360
TTGCAATATT	TGTTGATGCC	AACGACTCAC	ATTAGTGGCA	TGAAAACCC	TTTGTGCTT	420
GATCCTTCTA	CGCCTAACTT	TTTTTACTTG	TCATGGCAAG	CGCGCGATTT	TATGAGTAAA	480
AAATACGGAA	AACCCATTCC	TGATTATGCG	ATCTCTTTGA	CGATCAATTC	TAAAAAAGGG	540
CGATCGCAA	ACCATTTTCA	CATCCATATT	TCTTGCATTA	GCCTTGATGT	GCGCAAACAG	600
CTGGATAATA	ATCTAAAAAA	TATCAACAGC	CGTTGGTCGC	CATTATCAGG	TGGCTTGAAC	660
GGGCATAAAT	ATTTGGCGCG	TCGGGTAAAC	GAGAGCGAAT	TAGCGCAAAA	AAGCCCGTTT	720
GTCATGCTTG	CTAAGAAGT	GCCTAACGCG	CACAAACGCA	TGGGAGACTA	TGGCTTGGCG	780
GTGGTGCAAC	AGAGCGATAA	CTCCTTTGTC	TTGTTAGCGA	CACAATTTAA	CCCATTGACT	840
TTAAATCGCG	CTTCAGCCGA	AGAGATTCAA	GATCATGAAT	GCGCGATTTT	GCGT	894

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232

TATCATCGCA	CTAATACCAC	GATAAGGATA	ATTATCATGC	AAGATTTACC	CCCATGCCCT	60
AAACGCAACG	ACGCCTACAC	CTACCATGAT	GGCAGCGAGT	TCGTTTGCTC	TAGCTGTTTG	120
TATGAATGGA	ATGGAAATGA	AATTAGTAAT	GAAGAATTGA	TCGTTAAAGA	TTGCCATAAT	180
AATCTTTTAC	AAAATGGGGA	CTCGGTCATT	CTCATTAAG	ATTTAAAGGT	TAAAGGCTCA	240
TCTTTGGTGC	TTAAAAAAGG	CACTAAAATC	AAAAATATCA	AGCTTGTC	TAGCGATCAC	300
AATGTGGATT	GTAAAGTGGA	AGGGCAGAGC	TTGTCTTTAA	AATCTGAATT	CCTTAAAAAA	360
GCT						363

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

882

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233

AAGGGTTGTT	TTATGCGAGA	ATTTTTTAAG	AAACTTGGCA	CAGAATACGC	TTCCAAGCTG	60
TTTTTGCTTT	ATTGGCTTAG	ATGGATGTTG	AGTGCGTTGG	TGATGCTGCC	TTTTATGGAG	120
GTTTTTTATT	ATTTCAATTT	TCCGTGTGG	CTCAATCTTT	TCCTAGGGCA	AACCATTGGA	180
GCGGTGATTT	TTTTCAAGTT	GGATAAGTTG	ATTTTTTCTA	AAAAA		225

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234

TTCTTTAAAC	GCTATGAAAG	GTTAAGCATG	CAATATCTTT	CTTTGCTGTC	AGTGGTGTG	60
TTTTTGCCCT	TAATCGGTGC	GGTTTATGCG	GGGCTGTTTG	GGGCTAAAGC	TAAAGCGTTG	120
CATGTGGGCG	TTTTCAATTC	TTTGTGCGTG	CTGGTTTCTT	TCAATGGCGC	GGTGGTTCTT	180
TTCAATCAAG	CATGCGATCA	TCAAAGCTAT	GAAAAATATT	TGTTTGAATG	GATCGTGGTA	240
GGGAATTTTA	AAGTCGGCTT	TTCCCTCATG	CTGGATAATA	TCAATGCGGT	CATGATTGTC	300
GTGGTCACTC	TAGTTTCTTT	CTTAGTGCAT	GTGTATTCTA	TAGGCTATAT	GGAGCATGAT	360
ACAGGGTTTA	ACCGCTATTT	TTCTACCTT	AGCGGCTTTG	TGTTTTCCAT	GCTGGTGTG	420
GTGTTGAGCG	ATAATTTTTT	AGGGCTTTTC	ATTGGCTGGG	AAGGGGTGGG	GCTATGCTCT	480
TACTTGCTCA	TTGGCTTTTG	GTATCATAAA	AAAAGCGCGA	ATAACGCTTC	TATTGAAGCC	540
TTTGTGATGA	ATCGAATCAC	GGATTTAGGC	ATGCTCATGG	GGATTATTTT	GATCTTTTGG	600
AATTTTGGCA	CCCTCCAGTA	TAAAGAAGTC	TTTAGCATGC	TCAATAACGC	CGATTATTCC	660
ATGCTCTTTT	ACATTAGCGT	GTTTCTTTTT	ATTGGCGCTA	TGGGGAAGAG	TGCTCAATTC	720
CCTATGCACA	CATGTTAGC	CAACGCTATG	GAGGGGCCTA	CCCCTGTATC	CGCTCTCATC	780
CATGCAGCGA	CGATGGTAAC	CGCTGGGGTG	TATCTAATCA	TCAGAGCCAA	TCCTTTGTAT	840
AGTCCGCTGT	TTGAAGTGGG	TTATTTTATC	GCATGCTTAG	GAGCGTTTGT	GGCTCTTTTT	900
GGAGCGAGCA	TGGCTTTAGT	CAATAAGGAT	TTAAAACGCA	TCGTGGCTTA	TTCCACGCTT	960
TCTCAATTAG	GCTATATGTT	TGTAGCGGCC	GGGCTTGGGG	CTTATGCGAT	CGCGCTTTTC	1020
CACCTCTTTA	CGCATGCGTT	CTTCAAATCC	CTCCTTTTCT	TAGGCTCAGG	CAATGTCATG	1080
CATGCGATGG	AAGACAATCT	GGATATTACT	AAAATGGGCG	CTTTATACAA	GCCTATGAGG	1140
ATCACAGCTG	TCCTTATGAT	TATAGGGTCA	GTGGCTTTGT	GTGGGATCTA	CCCCTTTGCG	1200
GGCTATTTCT	CCAAAGACAA	GATTTTAGAG	GTCGCTTTTG	GGATGCACCA	CCACATTTTA	1260
TGGTTTGTTC	TTTTGATTGG	GGCGATCTTT	ACCGCTTTTT	ATAGCTTCAG	ACTCATCATG	1320
CTGGTGTTTT	TTGCACCCAA	ACAACATGAA	ATCAACCACC	CCCATGAAGG	CCAAAAATTT	1380
CATGCTTTTG	AGCATGCTAC	CGTAGGGGTT	TTTGGCGGTC	ATTGCCGGTT	TTTCAGAAGA	1440
GCCGTTTTTT	CATTTTATCT	CTCAAGTGAA	TTCTAGTGT	TGGAGAGTAT	C	1491

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

883

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235

AACAAGCCGA	ACAAGGGTGC	AGTATTGGAG	AAAACAAAGA	AGAGGCAGTT	GCTTCAAAAG	60
AAAACAAAGA	AGAGAATAAA	ACAGAAGCGG	CTGCCCCAAA	AGAAAATCAA	ACAGAAAACA	120
AGACAGAGGT	TAAAGAGAAA	AATTGAAGTC	CCTACC AAAA	CCACTTACTT	GTGCTTGAA	180
GAAGCGGGCA	TCAATTTAGA	AACTTATGAA	AAAATTCTCG	CTCTTTTGCA	AAAATCAAAT	240
AACACCTTGC	TAGTGGTTGG	CGAGGAAATT	TATAGCCACA	AACAAGCCCA	TAACATCGCT	300
AAAATGTTGC	GTTTATTAGC	CCAAAAAAGC	GCTATTAAAC	TCATTCTTAT	CCCCCAAGC	360
GCGAACGCTT	TAGGCATCGC	TTCTATTTGC	GAATTGAGCG	AAGAAGTTTT	TGAACATGAA	420
AAAATCGTAG	GCATTGCGCG	TCAAGGGGAT	TTCACTATCA	ATAGCGACGA	TAGGGTTTTT	480
GGGAAAGACG	CTGTCACTAA	AGTGGATTTT	ATTCTGCCCA	GTCTCAACCA	ACTAGAAGGC	540
ACGATCACTA	ATGTTGAAGG	GCGTGTGTTG	CCCTTAA AAC	CGGCTTTAAG	GTTTGAAGGC	600
TATGACTTGA	GCGATATCAT	GCAAGGCTTT	GGCTTTGTGG	AAGAAAACCT	CACAGAATGC	660
ACCCACA AAC	TCCCTACAGA	AGCGGGCTTT	AAAGCCTTAG	AGTTTGATCA	TCTAACC AAC	720
TATTTCATA	ACGACAGGGC	TAATCACAGA	GGCTATTAT	TAGGAACAAG	CCATTTTGAA	780
AATAGCGCTA	AAGAATCGAA	GCCACAGAAT	GCGAGCCTAT	CAAGCCTT		828

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236

GGAGGTTTTA	TGGCCAAACA	AGAATACAAG	CAACTTCCTA	AACGAGCCGA	AGTCCATAGC	60
GCGACCGAGC	AGTTTAAAGA	CACCATTAAA	ACGAGCTTGG	GTITGGATCT	ATTCAAAGGG	120
TTAGGGCTTA	CGATCAAGGA	ATTTTPTAGC	CCAAGCGTAA	CCATCCATTA	CCCTATGGAG	180
CAACTCCCTT	TAAAGCCACG	CTATCGCGCG	GTGCATCATT	TGCAACGGCT	TTTAGACTCA	240
GGCTCTGAAA	GGTGATAGG	CTGTGGGCTG	TGCGAAAAGA	TTTGACGAG	CAACTGCATA	300
AGGATCATCA	CGCATAAGGG	CGAAGACAAC	CGCAAAAAGA	TCGATTCTTA	CACGATCAAT	360
TTGGGGCGTT	GCAATTTATTG	CGGGTTGTGT	GCGGAAGTTT	GCCCAGAATT	GGCGATCGTT	420
ATGGGGAATC	GTTTGTAAAA	CGCCAGCACC	CAACGCTCCC	AATACGGCTC	TAAAAGCGAG	480

SUBSTITUTE SHEET (RULE 26)

884

TTTCTAACGA	GCGAACAAAGA	CGCTAAAAAC	TGCTCGCATG	CCGAATTTTT	AGGCTTTGGT	540
GCGGTAAAGCC	CTAATTATAA	CGAACGCATG	CAAGCCACCC	CTTTAGATTA	TGTCCAAGAA	600
CCTTCAAAAG	AAGAATCCAA	AGAAGAGTCT	CCAACAAGCC	CAGAAAGCCA	TAAGGGAGAT	660
GAAAATGTT						669

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237

ATTATGTCCA	AGAACCTTCA	AAAGAAGAAT	CCAAAGAAGA	GTCTCCAACA	AGCCCAGAAA	60
GCCATAAGGG	AGATGAAAAT	GTTTGAAC	ATTGCCTTTT	ATTTCTTTGC	GATCCTTACT	120
TTAAGCATGG	CGTTAGTGGT	GATCACAACC	ACAAATATCC	TCTATGCCAT	TACCGCTCTC	180
GCTAGTAGCA	TGGTTTTTAT	TTCTGCTTTT	TTCTTTTTAC	TGGACGCTGA	GTTTTTGGGC	240
GTGGTGCAAA	TCACGGTGTA	TGTGGGTGCG	GTCAATTGTGA	TGTATGCGTT	TGGCATGATG	300
TTTTTCAACT	CCGCTGCAGA	AGTAGTTGAA	CGCAAGCAAA	GCCCTAAAAT	CTTGTGCGTT	360
CTTTTCATTG	GCGTGCGCGT	GTGCTCACC	TTGATTTTAA	GCGCTCCTAG	CATTGGCGAA	420
AACCTTTCTA	AGCAAGTCAA	TTCCAACGCT	ATTGATGCGC	AAATCCCTAA	CATTAAAGCG	480
ATTGGTTATG	TGCTTTTCAC	CAATTACCTC	ATTCCCTTTG	AAGCGGCGGC	TTTAATGCTT	540
TTAGTCGCTA	TGTTGGAGG	CATCGCTACA	GGGATTCAAA	AAATCCATGG	GAAAAATCAC	600
ACGCAATTTA	TAAAGGAATC	TCTA				624

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238

SUBSTITUTE SHEET (RULE 26)

885

ATGAAACAAT	TTAAAAAGAA	ACCAAAAAAG	ATAAACGAT	CGCATCAAAA	TCAAAAAACA	60
ATCTTAAAGC	GTCTTTTATG	GCTTATGCCT	TTACTGATTG	GCGGGTTTGC	TAGTGGGGTG	120
TATGCCGATG	GAACAGACAT	TTTGGGGCTT	AGTTGGGGGG	AAAAAGCCA	AAAGGTATGC	180
GTGCATCGTC	CATGGTATGC	TATATGGAGT	TGCGATAAAT	GGGAGGAAAA	AACACAACAA	240
TTTACAGGAA	ACCAACTCAT	CACAAAAACT	TGGGCAGGGG	GTAATGCGGC	TAACACTACT	300
CACTCTCAAA	ACAACCAAGA	CATCACAGCC	AATTTAAAAA	ATGATAACGG	CACTTATTTT	360
TTAAGCGGTC	TGTATAACTA	CACCGGAGGG	GAATATAATG	GGGGGAATTT	AGACATTGAA	420
TTAGGCAGTA	ACGCTACTTT	TAATCTAGGT	GCGAGTAGTG	GGAATAGCTT	CACTTCTTGG	480
TATCCTAATG	GGCATACTGA	TGTTACTTTT	AGCGCTGGGA	CTATCAATGT	GAATAACAGC	540
GTAGAAGTGG	GCAATCGTGT	GGGATCGGGA	GCTGGCACGC	ACACCGGCAC	AGCCACTTTA	600
AACTTGAACG	CTAATAAGGT	TACTATCAAT	TCCAATATCA	GCGCGTATAA	AACTTCGCAA	660
GTGAATGTAG	GCAATGCTAA	CAGCGTTATT	ACCAATTAAT	CGGTTTCTTT	AAATGGGGAA	720
TACTTGCAGT	TCTTTAGC					738

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239

GTTTTACGCG	CAAGGGTGAA	GCGCTTTTTTC	ATCTTCTTAT	TCCTCTTTTTT	AATCTTGCAT	60
GAAATCTTAA	ACACAGAATT	AGCCCCTTTA	AATGGGATTT	CGCTCGCGCT	GGGCTATTTG	120
TGTTTGTTCA	TACTCGTTTT	GAGCGCTTCT	TTAATCTTTG	AAAAAGTCTT	ATCCAAGCAG	180
TATTTGCAAA	CCGCTAAAGA	TAAAATCGCC	TCTTTAAAAA	ATTTAAAAAGT	CATCGCCATT	240
ACAGGAAGCT	TTGGGAAAC	CAGCACCAAA	AATTTCTTGC	ATCAAATCTT	ACAAACCCAA	300
TTCAACGCGC	ATGCAAGCCC	TAAAAGTGTC	AACACCCTTT	TAGGCATTGC	GAACGATATT	360
AACCAGAATT	TAGACGACAG	GAGTGAAATT	TATATCGCTG	AAGCTGGGGC	AAGGAATAAG	420
GGCGATATTA	AAGAAATCAC	CCGTCTCATT	GAACCGCACC	TTGCCGTGGT	CGCAGAAGTG	480
GGCGAACAGC	ATTTAGAATA	TTTTAAAACT	TTAGAAAATA	TTTGGCAGAC	TAAAGCGGAA	540
TTATTGGATT	CCAAACGCTT	AGAAAAAGCC	TTTTGCTACT	CTGTGGAAAA	AATCAAACCC	600
TATGCCCTTA	AAGATAGCCC	TTTAATAGAC	TATTCTAGCC	TAGTTAGAAA	CGTCCAATCC	660
ACTTTAAAAG	GCACTTCTTT	TGAAACGCCT	ATCAATGGCG	TTTGGGAAAG	CTTTGAAACG	720
AAGGTTTTAG	GGGAGTTTAA	CGCCTATAAT	ATCGCTTCAG	CGATTTTAAT	CGCTAAGCAT	780
TTAGGCTTAG	AGACAGAAAG	GATCAAACGG	CTTGTTTTTG	AGCTTAAGCC	TATTAACCAT	840
CGTTTGCAAC	TGTTGGAAGC	GAATCAAAAA	ATCATTATAG	ACGATAGCTT	TAATGGGAAT	900
TTAAAGGGCA	TGTTAGAGGG	CATTCGTTTA	GCGAGCTTGC	ATCAAGGGCG	TAAGGTCATT	960
GTAACACCGG	GATTAGTGGA	AAGCAATACA	GAAAGTAATG	AGGCTTTAGC	GCAAAAAATA	1020
GACGGGGTTT	TATGATGTCG	TATCATCACA	GGGGAGTTGA	ATTCCAAAAAC	GATTGCTTCC	1080
AAATTGAAAA	CCCCCAAAA	AATCTTACTC	AAGGATAAGG	CGCAATTGGA	AAATATCTTA	1140
CAAGCCACCA	CGATTCAAGG	CGATTTGATT	TTATTCGCTA	CTGACGCCCC	TAATTACATT	1200

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2151 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

886

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240

TATGCTTAA	AGTCGTTGAG	ACAGGCTTAT	TTCTTTTCTC	AAAGCGTGTT	TGTAGGGCTT	60
TATCATGGGG	CAAGCATCTT	TGATTTAAAA	TTTGAAGTCT	ATCTTACTAT	GCTAATCTCT	120
TTAATGCCCT	TTGTGGCTAC	GATTTATATC	AATTTCCTAA	AAACCACAGA	AACTTCGCAT	180
GGCTATGCGA	GATGGGCTAA	TGTTAAAGAT	ATAGAATGCT	TAAAAATTTT	TAGCAAAGAG	240
GGCTTTTGTA	AAGTGCTGCA	TAGATTAGGG	GTGCAATTTG	ATAATGGCTT	TATTCTAGGT	300
AAATTTGGTT	TTCCAAAGCT	TAGAAATGTG	TGCTATGACA	AGCCCTTAGG	AACGATGATT	360
GTTGCACCCC	CTGGTGCTGG	AAAAACTGCA	TGTGTGGCTT	TGCCAAATTT	ATTGACTTTG	420
CCTAATAGCT	GTATTATCAC	TGATATTAAA	GGCGAACTAA	GAGATAAGAC	CGCAGGTAT	480
AGACAAAAAT	TCTTAAACAA	TAGAATTTTA	ATTTTAAATC	CTTATGGTGA	TGATAACACT	540
TGCTATTTC	ATCCTTTTGA	TAAAAGGATT	GTTGAAAAGA	TGACCTTTGC	GGAGCAATTA	600
AGGCATGTTA	AAGCAGTAGG	CGATGGTATT	TTTGTAGATG	AAGAAGACCA	TTGGGTATCT	660
AAAGCTAAAG	AGCTTTTGT	CTTTTGTGCT	CTTTTACAAG	TAGTAACCAA	AGGGCATAGC	720
TCTTTTATG	ATGTCTCTAT	CGCACCAGCT	AATGATTATG	CCCCCTTAAT	ACACCCTAAA	780
AGCCCTTATT	ACAAGCAACT	TTACCAACAC	GATAAAAAGA	CAGGCGAAGT	TATCTTAGAC	840
CCCAAAACTA	ACGCCCCCTAT	GAAAAATCCC	CAAGCTAATG	TTTTAAACT	CTTTTAAAT	900
CAAGTGCTG	ACCAAAAATA	CATAGATATG	AATGATGAAA	AAAACTATGA	CCCAAGAGAA	960
CCTGAACCCC	CTTATGGAAC	AAAAGGGGCG	TTAGATGAGA	TTATAAGGAC	AGATGCTAGG	1020
AGTTGGGCAA	ACACTCCTGA	TGATGAATTT	GGGAGCATT	TGTCTCTTT	TAAGCGTTTT	1080
ATGTATGTCT	ATAAGACCC	AAAAGTGCCT	GAAGCTACTT	CTAAAATGAG	CTTTGATTAT	1140
GAAGAATTAA	GAACGGGCAA	TATCAGTATT	TACATTGTAA	TCGCTCAAT	TGATATAGGC	1200
ACACTTTCTT	CTTTAGTAAG	AGCCTTTTTA	GAGAGTATTG	CTAAAAACCT	TATGGTCAAA	1260
GAAAGCTCTA	AACCTGAAGA	GCGTATTTT	ATCATTGCTG	ATGAATTTGT	TAGATTGGT	1320
AAGTTGCCTT	TCTTGTTAGA	AATGCCAGCA	CTTTGTCGCT	CTTATAATGT	TGTCCCTTA	1380
TTCAATCAGC	AAGATTATGC	TATGATTAGA	AAATACTATA	GCGATGATGA	TTTGAAAATC	1440
TTAAAAGGCG	TGGTGCATTA	TAACATTGTC	TTTAAGATGA	ATAGTGCTGA	AGATGCTGAG	1500
ATTGCTCTA	AGGAAGTGGG	CGAATTTACA	AGACGATCTA	AAAATTATTC	TACCGAAAAA	1560
GGTCAATTGG	TCTTTGGAGG	TAGCTCTTCT	TATAGCCATG	AGGGTAGAAA	CTTACTCACA	1620
GCCCAAGATA	TTATGAATAT	CAATTCAGAT	GAAGTCATTG	TTATTGTTAC	AGGGGCTAAA	1680
GCTACCCCTT	TAAAACCTCA	AGCTAATTAT	TGGTTCAAAG	ATAAAGAGCT	TTTAAAAAGA	1740
GCTAATTTGC	CTATTGATTT	AGAAGTAGAG	AGACAAAGAG	TTGAAGAGCC	TATACAACCC	1800
ACTACAGAGA	TTGAAACAAC	CCCTAATCAA	AACAAAGCTG	ACTTAGAACC	AAGTAATAAG	1860
GGGGAAGGAG	TAGAGAAATGA	GAGCAATGAG	AGAAACACTA	ACGAGAATAA	TCCCACTACA	1920
CCACAAGAGC	TTGAAAATTC	AACTTAAAA	GAAAGCGAGA	AAGACAATGA	AAGTCCCATT	1980
ACCTTAGAAA	ATGCTAATGA	AAATATAGAG	CAAGGAAATC	ACAATGAAAT	TGATGAGATT	2040
TTAAAAAAGC	CACTGAGTGA	AATCAGTATG	GAAGAGAAAA	GAGCCTTGTT	TAAGAAAAATG	2100
CAACAAAGCG	ATGAAGAAAG	CGAACAAGAA	GTTACACAAA	GCACCCAAAG	T	2151

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...7320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241

TATAATCATC	CAAAATTTAAG	CGTTGCTGAT	TTAGAATTAG	AGCAACAGAA	TTTAGGAGAA	60
CAAAATGGAA	AAGAGAGAAC	AAATCGCGCA	GATGAGCCGA	ATGGAAGTAG	AGCAGGAATT	120
CCGCAAGAAA	TTCACCGCAG	AAGCGAACCT	AGAGGACAGC	AAGAGGGAAT	GGAGCGATCG	180
AGTGATGAAG	ATCTTTTCACA	CCAAGACCCT	AGTTTATTTA	TTGAGTCTAG	AGAGCAGGGA	240
GGAACAAGAG	GAGTTTATCG	ATCTAGCGAC	CAACAGGCAG	TTTCAGAAGA	ATCCCATAGA	300
GAGCGAGATA	GAATACATGA	ACATGTATCT	AGAGGAGATG	GAGTATCAGC	AAGAGCGGAT	360
GCAAGAGCGA	ATAGCAATGG	AGCATCAAGT	CCAGCAAGCC	GAATGGAAAA	TGGAGCAAGA	420
AGCGAAGAAA	ATGGGAGATA	TCCCAGCGAT	GAGAGAGGAA	TACCACAGAC	ACCGCAATCC	480
CCATCTCATC	AACAAAATAG	CTCCAGAGAT	TTGGGGCTTT	CTCTCTCTAG	AGAACAGCCA	540
GGACAGACTG	GACGCTTACG	CCTTTTGTAT	CATGGACAGA	TGGGCTCATT	ATTTCCACAC	600
GACCATGAAA	ACCAAAGAAA	AAGGAGCGAT	AATGAGCTTG	ATAGACGCAG	TGATAAAGCA	660
AACGAAAATG	GAGACAAAAG	CCCTAGACAG	AATGGAAGCG	CAAATCAAGA	GAGCGCAAGG	720
AGTGAGCGAT	ATGGAATTGC	TCAAGGAAGC	TCAAATCAAT	CAGTATTATT	ACCTGCTCAA	780
AGCCGATTAC	ATCATGCAGG	ACTCAGCGCA	CAAAATGGAC	TTAGAGACCT	TGAAGAAAAC	840
AGGGATCAAG	AGGGAAGACT	TTTATCAAAT	TTAGATAATT	TAGAAAGCTT	GCTTAACGCT	900
ATTAGAAACA	ACACTATAGC	GAGTGAGCCT	GATTTTAGAT	CCAGGCTCTT	AGAAGCCATT	960
CAAAACAACG	ATCCTTTTAA	AGATAGCATT	GTGGGGGGCG	AACTCCTTAA	AGACCCTAGC	1020
ACTAAAATCT	TTTATGACAA	ATTCCAATTA	AAAATCAGCC	CTAAAAAAGT	CTTAGAGATT	1080
TTAGAAAATC	GCCTTAAAAA	ATCCATTGAA	ACAACGAACG	AAACGCTAAA	CGCATTCAAT	1140
GTGCTGGATA	GTCAAGCCAT	TGATTTAAAC	GCTATCTCTA	ATAGCGTAGG	ATTAAATCCC	1200
ACACAAGAGA	GCAAAATAAC	AGACAATAGC	GTAGAGTTGA	ATAACGCTCA	AGAACAAAAC	1260
GCGCAAGAGC	AAACCACACA	AGAACAAACC	ACACAAGAAC	AAACCACACA	AGAACAAACC	1320
ACACAAGAAC	AAACCACACA	AGAACAAACC	ACACAAGAAC	AAACCACACA	AGAGCAAGAC	1380
ACGCAAGAAA	ACGCGCCAAC	CACGATAAAA	CAAGAAACAC	CAATTACGCC	AGCCATCCCC	1440
CTTAATCCTA	AAATAGATTT	TAAACCGAGC	GAAGAAGTTT	TAATCAAGGG	AGCTAAAACT	1500
CGCTACAAGG	CTAACATTAA	AGCCATTGAG	CTTTTAAAG	AATTGCAAGC	CAAACAAGAG	1560
ATCTTTAAAG	GCGATTACTA	CGCCACTTTA	AAAGAGCAAG	AAATCCTAGC	GCAATTTAGC	1620
GGATGGGGCG	GGTTAGAGAG	CTACTTTAAA	AAGGCTCAAC	ACCCTGAGGA	ATTTAAAGAA	1680
TTAAACGCCT	TACTCACTAA	AGATGAATTC	AGAAGAGCTT	ATTTGAGCGC	AAGAGACGCT	1740
TACTACACCC	CTAAATTAGT	TATTGATAGC	ATTATCAAG	GTTTAGATCA	ATTAGGGTTT	1800
AATAACGACA	ACCATCCAAA	AAAAATCTTT	GAACCCAGTT	TAGGCACAGG	CAAATTTATC	1860
GCTCATGCGC	CAAGCGATAA	GAATTACCGC	TTTATCGGCA	CAGAATTAGA	TCCTATTAGC	1920
GCTAATCTTT	CTAAATTCTT	TTACCCTAAT	CAAGTCATCC	AAAACACCGC	TTTAGAAAAC	1980
TACCAATTCT	ATCAAGAATA	CGATGCGTTT	GTGGGCAATC	CTCCTTATGG	CAATCATAAA	2040
ATCTATAGCT	CCAATGACAA	AGAATTGAGT	AACGAGAGTA	TTCATAATTA	CTTTTATAGG	2100
AAAGCTATCA	AAGAATTGAA	AGATGATGGC	ATAGGAGCGT	TTGTGGTGAG	TTCTTGGTTT	2160
ATGGATGCTA	AAAACCCATA	AATGAGAGAA	CACATCGCAA	AAAACGCCAC	CTTTTATAGC	2220
GCGATAAGAC	TGCCTAATAG	CGTGTTTAAA	GCAACAGGCG	CTGAAGTTAC	GAGCGACATT	2280
GTGTTTTTTA	AAAAAGGCGT	TGAAAAAGCA	ACCAATCAAA	GCTTCACTAA	AGCTATGCCT	2340
TATTATGACA	AGATACTCAA	TAGCTTGGAT	GATGACACCC	TTTTTGCTTT	GCAAAACAAC	2400
CGCTTTGATA	GTTTTATTCC	TAGCGATCAA	CTTAAGATTG	TCAATGCGGT	TGCAAAACCAT	2460
TTTGTTTTCA	AACAAGAAAA	ATTGCAACGC	TGGTATGAAA	AAATAGACAC	CGCTAACTTT	2520
GGTACAGCA	GCAAGATTA	TAAGATCATC	AAAGACTTCA	TTGATAAAGT	TGGAAAGAAT	2580
AGCATCAATC	TCAACGAACA	AACCTTAAAT	GAATACTTTA	TCCACCACCC	TGAAAACATT	2640
CTAGGGCATT	TGAGTTTGGG	AAAAACCCGC	TATAGATTTG	AAACAAATGG	CGAACAAATT	2700
TACAAATACG	ACTTGCAAGC	CTTAGAAGAT	GAGAGCTTGG	ATTTATCCCA	AGCGCTTAAA	2760
CAAGCGATAG	AAAAATTGCC	TAAAGACGTC	TATCAATACC	ATAAGACTAC	CCTTAAACAA	2820
GACGTTCTTA	TTATTGATTG	AAGTAACGAA	CGCTATCAAG	AAGTTCAAAA	GCTTATCAAA	2880
AATTTAGAAA	GGAGGGAATT	AGTCAAGTGG	GATAATCTTT	ATTTCCAAC	AGAACAAAAT	2940
AATGAAATGG	GCATTTTTTT	AAAACCCACT	AAAATCAACT	CTAAAGTCCA	AGATTACGCA	3000
CTAAAGCCCT	ATTTTAAAAA	TAAAGACGCT	TTGAATGATT	TAACGAGCGC	GGAATTAAC	3060

888

CCCTTAAGCT	CTGATTTAGA	GCTAGAAAAC	AAGAGGGGCTA	AACTCAATCT	TGTTTATGAT	3120
GAATTTGTCA	AGAAATTTGG	CTATCTCAAT	GAGAAATAAAA	ATCGTAAGGA	CATCAGACAA	3180
GATTTGTATG	GCGCTAAAGT	CTTAGGATTA	TTGAAAAGACT	TTGAAAAGAA	AATAACCCCT	3240
AGAAGCGCTA	AAATGCAAAA	CATAGAACCA	AGGCAAGCTC	AAGCCAAAAA	AGCTCAAATC	3300
TTTTTTGAAA	GGACTTTAAA	CCCTAAAAAA	GAACCTTATTA	TCCTAACGC	TAAAGAGGCA	3360
TTAATTGCAA	GCATCAATCA	AAAAGGGGGT	TTGGACTTGC	ATTTTCATTAG	GGATCATTTC	3420
ACAACCCAAA	GTTTAGAAAC	CACGATTAAA	GAACTTTTAG	AGCAAAAACT	TATCTATAAA	3480
GACCACAAGG	ATAATGGCGG	CTATATTTTA	GCGAACGATT	ATTTGAGCGG	CAACGTGAAA	3540
AGAAAACCTCA	AAGAAGTTAA	AGAAGCCATC	AATCAAGGCG	TGGAGGGATT	AGAGGCTAAT	3600
GTGAAAGATT	TAGAGCTGAT	TATCCCTAAA	GATTTGAAAG	CCACTGAAAT	CATGGCTAAT	3660
ATCAACAGCC	CTTGGATACC	CACTCAGTAT	TTAGAAGAGT	TTTTAATGGA	ATTGAGCGCT	3720
AACCATTATG	AAAAGCAATA	CGCGATATAA	ATGACAGATT	ACCAACTAAG	CAATCTCAAA	3780
GAAGACATCA	AAATAGAACA	CCTAAGCGGT	GCTTATGAAG	TTTTTGTAG	AAACAATGAA	3840
TTAAACGAGC	TTTATGGTAT	CAGGCATATA	GACAAGCCGC	ATTCCTTATA	AGTGCCTTTT	3900
GAAAGCCTTT	TAAATAAAGT	CTTAAACAAC	AAGGATTTGA	GCGTTAAATA	CGCCCAAGTT	3960
GATCCTAATG	ACCCTAAAAA	AGAAATATTC	ATCACTGATG	AAGAGCAAAG	CAATCTCGCC	4020
AGACAAAAAG	CAGAAGAATT	GAAAGAAGCT	TTTAAAGACT	GGATTTATAA	AGATTATTCA	4080
AGAAGAACCC	ATTTAGAGCA	AATCTATAAT	GACACTTTCA	ACAACTTTGT	TTTAAAAACC	4140
TATGATGGCT	CGCAATTAGA	ACTAGAGGGC	TTTAACTACC	ATATCAGCTT	GCGCCCCAC	4200
CAAAAGAACG	CTATTTTTAG	AACCATCCAA	GACAGGGCGG	TGTGTTTAGA	CCATCAGGTT	4260
GGAGCAGGCA	AGACTTTGTG	CGCTATAGCC	AGCTGCATGG	AACAAAAACG	CATGGGATTA	4320
GTGAATAAAA	CGCTCATTCG	CGTGCCTAAC	CATTTAACCA	AGCAATGGGG	CGATGAATTT	4380
TATAAGGCTT	ACCCTAACGC	TAATGTGTTA	GTTGTTGATA	GCAAGGACAC	CAGTGAAAAA	4440
GAAAGAGAAC	TTTTATTCAA	TCAAATCGCT	ATGACCGTGT	GGTTATCGCG	GGTTATCGCG	4500
CACACCCATT	TGGAATTATT	GTCTAACCCCT	AGAGGAATCA	TAGAAGAATT	GAAAGAAGAA	4560
GAGCTAGTGA	ATGCTGAAAA	AAACTTTGAA	AGGCAAGAAT	TAGCTTATAA	AAATAACCCCT	4620
AGAGAACTA	AAAAACCCAA	TGAAAGAGCC	TTTAAAAACA	AGTTGGATAA	AATCCGTGCT	4680
AAATACGATG	CGAATTTAGA	AAAACAAGGC	TCTCATATTG	ATATTAGTCA	AATGGGGATT	4740
GACAATTTGA	TTGTGGATGA	AGCCCACTTA	TTCAAAAAATC	TAGCCTTTGA	AACTTCTATG	4800
GAAAAAATTG	CAGGACTTGG	TAACCAACAA	GGCTCTAATC	GCGCTAGAGA	TTTGTTTATT	4860
AAAACGCGCT	ACTTGCATCA	AAACGATAAG	AAAATCATGT	TTTTAACCGG	CACGCCTATA	4920
GCTAATTCCT	TGAGTGAAT	GTATCACTTG	CAACGCTATT	TAACCCCTGA	TGTGTTAAAA	4980
GAAAGAGGGT	TAGAATTCTT	TGATGATTGG	GCTAAGACTT	ATGGGGAAGT	GGTGAATGAT	5040
TTTGAATTAG	ACACTTCCGC	TCAAAGTTAT	AAAATGGTTA	ATCGCTTTTC	TAAATTTAGC	5100
GATGTGCAAG	GCTTAAGCAC	CATGTATAGA	GCTTTTGCGG	ATATTGTCTC	TAATGATGAT	5160
ATTTTAAAGC	ATAACCCCA	CTTTGTGCCT	AAAGTGTATG	GGGATAAACC	TATCAATGTG	5220
GTGGTGAAAA	GAAGCGAAGA	AGTGGCTCAA	TTCAATTGGAG	TGGCTTTAGA	AAATGGAAAA	5280
TATAGTGAAG	GCTCTATCAT	TGATAGGATG	CAAAAATGCG	AGGGCAAGAA	AAGCCAAAAA	5340
GGGCAAGACA	ATATCCTTTC	TTGCACCACA	GACGCTAGAA	AAGTGGCTTT	GGATTACCGC	5400
TTGATTGACC	CTAACGCTAA	AGTAGAAAAA	GAATTTTCTA	AAAGCTATGC	TATGGCAAAA	5460
AATATCTATG	AGAATTATTT	AGAAACTCAT	GCCACTAAAG	GCACACAAC	TGGTTTCATA	5520
GGGCTATCCA	CACCCAAAA	CCATAGCCAA	AAAGTCAGTT	TAGAAGCGCT	AGATAACGCT	5580
CACGAAATCC	AAAATAAAAA	TCCCTAGAT	AAAGCTCAAG	AACTTTTAGA	AAGCTTGTCT	5640
AGTTATGATG	AAAAGGGCAA	TCTTATCGCT	CCTAGCAAGA	AAGAATTAGA	GAACGAGCTC	5700
AAAGAGAAAG	AAGCTAAAAG	CGTCAATTTA	GATGAAGAGA	TAGCTAAAGG	CTGTTCGTTT	5760
GATGTTTATA	GCGATGTTTT	AAGGCATTTA	GTCCAAATGG	GTATCCCAAC	AAATGAAATC	5820
GCTTTTCATC	ATGACGCTAA	AACCGAAGAG	CAAAAGCAGG	ATTTGTTTAA	AAAGCTCAAT	5880
CGTGGCGGAG	TCAGGGTATT	ATTGGGCAGT	CCTGCTAAAA	TGGGCGTAGG	CACATAATGTG	5940
CAAGAAAGAT	TAGTCGCTAT	GCATGAATTA	GATTGCCCAT	GGAGACCTGA	TGAATTGTTG	6000
CAAATGGAAG	GGCGTGGGAT	AAGGCAAGGC	AATATTTTAC	ACCAAAATGA	TCCTGAAAAAC	6060
TTTAGAATGA	AAATCTATCG	TTACGCCACT	GAAAAGACTT	ACGATAGCCG	TATGTGGCAA	6120
ATCATAGAAA	CTAAATCTAA	AGGCATAGAG	CAATTTAGAA	ACGCGCACAA	ATTAGGCTTG	6180
AATGAATTAG	AAGACTTTAA	TATGGGTAGC	TCTAATGCCA	GCGAGATGAA	AGCAGAAGCG	6240
ACAGGCAATC	CCTTGATTAT	TGAAGAAGTC	AAATTGAGAG	CGGAGATTAA	AAGCGAAGAA	6300
TCAAAATACA	AAGCCTTCAA	TAAAGAGCAT	TACTTCAATG	AAGAAAGCTT	AAAAAACAAC	6360
GCTTCTAAAT	TGGATTATCT	AAAACAGGAA	TTGAAAGATT	TAGAAACGCT	TCAAAGATCC	6420
GTAATAATCC	CCACTCATAC	AGAGATCAAG	CTCTATGATT	TGAAAAATGA	AGAAAGTAAG	6480
GATTATAGG	TTATCAAAGT	TAAAGAGGTA	GAGCCTTTAA	AAGAAAAACG	CTCTATGAGT	6540
GAAGAATTAA	CGCACAAAGAA	ACTCAAAGAA	CAAAACAAGC	AAATAGCCGA	ACAAAATAAA	6600
GAAAGCTAG	ACGCTATTAA	AAAGCAATTT	GCAAGCAATT	TGAACACCTT	GTTTGTGAAT	6660
GAAGAAGAAG	ATTATAAGCT	TTTGAATATC	AAGGGCTTTG	TGGTGAATGC	TTATAAAACT	6720
AAGTATCAAG	TGGAGTTTAG	TTTAAAGCCCT	AAAGACAATC	CCAATATTGC	CTATAGCCCT	6780
AGCAATATGG	TTTATAAAAA	CGATACTATC	AACATGTTTA	GCTCTTATAA	TTTCTGCGCT	6840
GAGATCAAGT	TTGATGGGTT	TTTAAAAAGG	TTGGATAACG	CTATCACTAA	ACTCCCTGAA	6900
AAAATCAAGG	AATTAGAAAA	CTCCATTGAA	ATCACGAAAA	AAAATATCGC	TAAATACACA	6960

SUBSTITUTE SHEET (RULE 26)

889

AGATTAGTGG	AGCAAAAACC	TTCTTACCCA	CGACTAGAAT	ACCTGCAAGC	TTTAAAATGG	7020
GATCATAAAA	CTCTAATAGA	TGATTTAGCT	AAAATGAGCA	AAGACAGAAA	TTATAAGCCT	7080
GCGTTCAACC	CTAAATCTAA	AGAAGTCTTA	AAGAATTTGA	ACGCTGAAAA	AAGAGCGAGT	7140
TTAGAGAATG	AGAGGGAAGA	GCAAGGGGTT	AAGGGGAACA	CAAAGAGTCA	TGATGAAATA	7200
GAGCCAGCTA	CAGAACAAGT	GATTGAAAAA	GAAATAGAAA	AAGGAGATGA	AATCGCTAAT	7260
AATGTTGATT	ACTACGAGAA	CGAACAAGAA	GTGGAAATTA	CTAAATCAAT	GGGTAGAAGA	7320

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242

AGGGAGGGGG	CGATGAATTT	TTTTGACACC	CTTATGGGTA	TGTTTGTGTA	GCCATCTCAA	60
AAAGTAGCCA	AAAGTCTTGC	TGAACATGTG	GGTAGCTTTT	TTCATGCACA	ACTCATTTTA	120
AACACAATTA	TTACTATTTT	ATTTATGATA	TGGGCGTATA	AGCGTGTGAA	AGAGGGCGAT	180
ATGTTTGAGT	TTAAAACCGC	TATGGGTGTG	GTGTGATTTA	TAGCGTTTGT	AGGATTTATC	240
AATTGGGGGA	TTAAAAATCC	TAATGATTTT	AACACTTATT	TTATCAATAC	GATATTCTAC	300
CCATCTGAAA	AAC TAGCCAT	ACTTATCGCT	CAAAGCCTAA	ATGATGGCTT	AGAAATCCCC	360
ACTAACACTA	ATTTAAGTCC	TAGTGAAATT	TTTAGCATAG	GAAATTTAGC	CTCAAGTGCG	420
TATGCAATGA	TAGTTAATCT	GTGGGATAAT	GCTTTTGATG	GTATTAAACAT	GTTTAATTGG	480
CTCACAATGA	TACCTAAAAT	AATTATGTTT	TTTTTAGTGA	TTTTAGGGGA	ATTATGTGTT	540
TTAGGCTTAT	TGCTTATTAT	TGTGTTATTA	GTTACAGCAG	AAATTTTTTAT	GTGGTCAGCA	600
TTAGGTTTAA	TGTATTGCCC	TTTAGGTTTA	ATCCCCCAAA	CCAAAGGCAT	GTTATTTAGC	660
TATCTTAAAA	AGCTCATTTT	CCTTACTCTT	TATAAACCTT	GTATGATGTT	AGTAGCTTTT	720
TTTAATTATG	GAATAATCTA	TAAAGTCAAT	ACTTTAATCC	CCACTAAACA	CGAAGTCACA	780
CAAGGCTTTT	ATGGCAATGC	GGATAAAATG	GCAAATGAGG	GAAAAATTAT	TGATGTCTTT	840
GGCAATGTCT	TAAAAGGAGA	TTGGAACCTT	TATATAGCCC	ATAGTTCTAT	TGTAGGCTTT	900
TTAACCATTA	TTGTTTTAGG	TTCTGTGATT	TGTTTCTTTC	TAGTCAAACG	AGTGCCTGAT	960
TTTATCAATA	ATATCTTTGG	CACAAGTGGA	GGCGTGGGGG	CAGTAACAGA	AATGATGCAA	1020
AAAATTGGCA	TGACAATAGG	CGGAGCTGTA	TTTGGGGGTA	GTGCAGTTAT	GGTTGCTAAT	1080
CAAGTTAAGC	AAGCCTATCA	GAGTGCTGGG	GGCGGACTAG	CAGGACTTCA	AGCTGGAGCT	1140
AAAGCTTTTG	GGCTTGGAGC	AATCAGTGGA	GGGGCAAGTG	CTATGGCAAA	CCACAGGAGT	1200
GTTAAAGCTG	GGGTGAAACA	CTTTGTAGCA	AGTGTTAAAA	GTGGCTTTGG	ATTTGATAAT	1260
GATAAAAATA	ATAAA					1275

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

890

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243

AAGGAGCAAC	AAATGGCTTA	CAAACCTAAC	AAAAAGAAGT	TAAAAGAATT	AAGAGAGCAA	60
CCGAATTTAT	TTAGCATCTT	AGATAAGGGC	GATGTTGCAA	CAAACAATCC	TGTTGAAGAG	120
TCAGACAAGG	CCAATAAAAT	ACAAGAGCCA	CTCCCTTATG	TCGTGAAAAC	GCAAATCAAT	180
AAAGCAAGCA	TGATTCTCTAG	AGATCCTATT	GAATGGGCAA	AGTATTTAAG	CTTTGAAAAA	240
CGAGTCTATA	AGGATAATAG	TAAAGAAGAT	GTCAATTTCT	TTGCCAATGG	TGAGATAAAA	300
GAAAGTTCTC	GTGTTTATGA	AGCGAATAAA	GAAGGGTTTG	AAAGGCGCAT	CACTAAAAGA	360
TACGATCTGA	TTGATAGAAA	TATTGATAGA	AATAGAGAAT	TTTTTATAAA	AGAAATTGAA	420
ATTCTAACCC	ACACAAACAG	CTTAAAAGAA	TTGAAAGAGC	AAGGGTTAGA	AATCCAATTG	480
ACCCACCATA	ATGAAACGCA	TAAGAAAGCC	TTAGAAAATG	GCAATGAAAT	CGTTAAAGAA	540
TACGACCATC	TTAAAGATAT	TTACCAAGAA	GTAGAAAGAA	CAAAGATGG	TGGATTGGTA	600
AGAGAAATAA	TCCCCAGTAT	TTCTAGCGCT	GAGTATTTCA	AGCTTTACAA	CAAAGTGCCT	660
TTTGAATCAA	TAAACAATGA	AAATACCAA	CTGAATACTA	ACGACAATGA	AGAAGTTAAA	720
AAACTAGAAT	TTGAATTAGC	TAAAGAAGTG	CATATTTTAA	TCCTAGAGCA	ACAATTGCTT	780
TCAGCAACAA	ATTATTATTC	TTGGATAGAT	AAAGATGATA	ATGCGAATTT	TGCTTGGAAA	840
ATGCATAGGC	TTATCAATGA	AAATAAACTC	AAAGAAAACC	ATCTCAGCGC	CAATAACGCT	900
AATAAGATTA	AGCAATTTTT	CTTTAATAAT	GGTTCTATTT	TAGGCTGGAC	TAAAGAAGAA	960
CAAAGCGCTA	TACAAGAAAA	CAGAGATTAT	TCTTTAAGAA	GCGCTCTTTT	AAGTTTAGAA	1020
GAAATCGCTC	AAGCAAAAAT	TGAATTGCAA	AAATACTATG	AAAGCGTTTA	TGTTAATGGT	1080
GATGGGAATA	AAAGAGAAAT	CAAGCCTTTT	AAAGAAATTT	TAAGAGACAC	CAACAATTTT	1140
GAAAAAGCTT	ATAAGGAGCG	TTATGACAAA	TTGGTAAGCT	TGAGTGCAGC	AATCATTCAA	1200
GCTAAAGAGG	GTGGTAATGA	GCGACAAAAT	TCTAGTGCAA	ATAACAATAA	CCCTATTAAA	1260
AATACAATAG	AGACTAATAC	TTCTAACAAAT	ATTATTCAAA	ATAATGATAA	TATAATCATC	1320
CAAAAT						1326

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244

ATCAAACATT	ACAAACAATA	TGGCACAGGC	TTACATCTAT	TTAGGCATAG	TTTTGCAACA	60
CTCATTTATC	AAGAAACCCA	AGACTTAGTT	TTAACTTCAA	GGGCGTTAGG	GCATAGCTCC	120
TTACTCTCTA	CTAAGATTTA	TATTCATACC	ACACAAGAGC	ATAACAAGAA	AGTGGCTCTT	180
GTGTTTGATA	GTTTGATAGA	GAACAAGAAG				210

SUBSTITUTE SHEET (RULE 26)

891

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245

AAAAAGAGAA AATACATGCG TTTTAGAAGA GTTAAAAAGC AAAAAAATAA ACACAATAAG	60
GAGCATACAA GTATGGATT TACAACAAATT GATGAGCTAG AAAAGAAAGTT TGAAGAACAA	120
GAAGAACAAG CCCAAGATAC CCCCTAAAA CAAGAGCCTA GCACAAAGGA AGTAAAAATC	180
CCTAAAAAAA GGGGCGCTAA AAAAAGCTTG TTAGATGAAG ATAAGAAAAA GAGCTTTAAC	240
ATTGCCTTTA GTCCTTGTGT GATAAAGAA CTTAATGAAT TTTTGCTAGA ATTTGGCTCA	300
TTTAAAGAGA CACGAAGCAC TTTTATTGAA GAAGCGCTTA TTAGGCATTT AAAACACAGA	360
AAAAACACCC AAGAGCAAAA GCTTTTAAAG CAACTAGAAA GATTACAAA CAAAGAAAAG	420
GGCAATAATG AAAACAATGA ACTTGAA	447

(2) INFORMATION FOR SEQ ID NO:1246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246

CTTAATACTG ATAAAATAAC TAAATACTTG ATTATTATTG ATATATTTTT AAAACTTTAT	60
GTTATAATGA TAAGTGAGAT TATTAAGTTT CAATTAAAAG GAATAAAAAT GATTAGATTA	120
AAAGGTTTGA ATAAAACCTT AAAACAAGC TTATTAGCTG GGGTTTTACT AGGTGCTACT	180
GCTCCCTTAA TGGCAAAGCC TTTATTAGC GATGAAGACT TATTGAAACG AGTAAACTA	240
CACAATATCA AAGAAGATAC GCTGACTAGC TGTAATGCTA AGGTGGACGG CTCTCAATAC	300
TTGAATAGTG GTTGGAATTT ATCTAAAGAA TTTCCGCAAG AATATAGAGA AAAGATTTT	360
GAATGCGTAG AAGAAGAAAA ACATAAACAA GCCCTTAATT TAATCAATAA AGAAGACACT	420

892

AAAGATAAAG	AAGAACTTGC	AAAAAAAATC	AAAGAAATTA	AAGAAAAAGC	TAAAGTTTTA	480
AGGCAAAAAT	TTATGGCTTT	TGAAATGAAA	GAACACTCTA	AAGAATTCCC	AAATAAAAAG	540
CAACTTCAAA	CCATGCTTGA	GAACGCTTTT	GATAATGGAG	CTGAAAGTTT	TATTGATGAT	600
TGGCACGAAC	GCTTTGGGGG	TATAAGTAGA	GAGAATACTT	ATAAAGCACT	TGGCATTAAA	660
GAATATAGTG	ATGAAGGAAA	GATATTAGCC	TTTGGCGAAA	GAAGTTATAT	TAGACAATAT	720
AAAAAAGATT	TTGAAGAAA	CACTTATGAT	ACTAGACAAA	CCTTATCTGC	TATGGCTAAT	780
ATGAGTGGCG	AAAACGATTA	TAAAATTACT	TGGTTAAAAC	CCAAATATCA	GCTCCATAGT	840
TCAAATAATA	TTAAACCTTT	AATGTCAAAC	ACAGAGTTGT	TAAATATGAT	AGAGCTAACC	900
AATATCAAAA	AAGAATATGT	TATGGGCTGT	AATATGGAAA	TAGATGGTTC	TAAATATCCC	960
ATTCATAAAG	ATTGGGGATT	TTTTGGTAAG	GCAAAAGTCC	CAGAAACTTG	GAGAAATAAG	1020
ATTTGGGAAT	GTATTAAGAA	TAAAGTAAAG	TCCTATGACA	ACACTACCGC	TGAAATAGGA	1080
ATAGTTTGGA	AAAAAATAC	TTATTCTATC	TCTCATCAC			1119

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247

AAAGATTACA	AAACAAAGAA	AAGGGCAATA	ATGAAAACAA	TGAAGTTGAA	TGAATTTTTT	60
ACGCATAAGA	TAATCTATAA	AGACACCCCT	TAAAGTTTAA	AGGATACACT	AGAACAAGAA	120
ATCAGCCAAG	CTAGTTTACT	AGAGAAGTTA	ATCTTAGCTA	ATATCTTAGC	CAATATGGTG	180
TTTGCTAAGA	TAGCAATGA	GAATGCCCTT	AAAATTTCTT	TTTCACGCTT	GATGTGTAAG	240
TTTAGTCCTA	TTGATTATGA	AAGCACTATT	CCTAGTGATT	TTAAGCCTAT	AGATGAAGAA	300
GAATATGAAG	ATGATTTAGA	ATGGCTAAAT	GAAGAAAAAG	AAGATAGGCT	CTTTAATTAC	360
TATCTATTTT	TAAATGGTAT	TAAAGAAAGT	GATGTAGAAG	AAGTGTTTAA	TGAAAGTGTA	420
GAAATCTATG	ATGAGTGCTT	AATAGAAATC	GCTCAAAATG	TCCTTAAAGA	TAAATTTTCT	480
TATGACATTG	ACTTATTGCA	AGTTTATGTA	AAAGGTTATG	CTAAAGAGAT	TAGAGAATTT	540
TTGAGTTATA	AACCTATAAA	AGAAATCAAA	GACTTTAAAG	ACAAAGACAC	CGCACTTTAT	600
ATCAGCTTAG	GAAAAGACTA	TGACAAAGAA	AAAGAGCCAT	TTTCTAAAAA	ATTGCAACAA	660
TGTTTTAAAG	AGATTTTAGA	GAGCAAGGGT	ATT			693

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

893

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248

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ATGAAAGGTT TAACAATGAA AAAATTAGTT TTTAGCATGC TTTTATGTG TAAAAGCGTG      60
TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC      120
ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT      180
CAAGCTCAAG TCAATCAGTT ACAAAAAGTC AATAACATGA TAAATACGAC TAATTCCTTG      240
ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT      300
CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC      360
GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT      420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAT      480
GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT      540
GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG      600
TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC      660
AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT      720
AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT      780
GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA      840
GAAAATAAAG AGACAGGTAA ATGCGACCCT ATTAATAAATG TATTTAGGAC AACTCGCTTA      900
GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAACCAA AGCCTCCAAT      960
AAAGACGCTC AAAGCCAAGC CTACGCAAT TTCAATCAAA GGATTAAATT ACTTACTCTA     1020
AAATATTTAA AAGAAATTAC CAATCAAATG CTCCTTTTAA ATCAAACAAT GGCAATGCAA     1080
AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA     1140
AACCATATAG ACAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA     1200
TACTTTCAAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG     1260
GAT                                                                    1263

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(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1338 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249

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AAGCGTTGGT GGTATTTTCGT GCGAGCGTTT TTAACAGGA GTTTTGCTCC CTTACTCAAC      60
CCTAACGAGA ACCTTTTAGA TCAAGTTAAG TCTAGCATT TTTTAAAAA AGGGGTGTCT      120
TATTTTGACT GGGGGGCTTC AGGTTTGGCG AGTGCTTTAG TGGAAAAGCG CGTGAAATCC      180
TTACTGCCTT ATTATGCGAA CGCTCATCTC GTCGCTTCTA AACATGCGAT TTTAATGGGC      240
ATGCTTTTAA AAGAATGCCA AGAAAAGTTA AAGCGTTCTT TAAATTTGAG TGCTAATCAT      300
TGCGTCTTGA GCGCGGGGTA TGGGGCGAGT TCAGCGATTA AGAAATTTC AAGAAATTTA      360
GGGGTGTGTA TCCCTTCAAA AACGAAGAAA AATTTAGAGC CGTATTTGAA AGATATGGCT      420
TTAAAGCGTG TGATTGTAGG GCCTTATGAG CATCATCTA ATGAAGTTAG CTGGCGTGAA      480
GGCTTGTGTG AAGTGGTGCG TATCCCTTTA AATGAACATG GTTATTGGA TTTAGAAATT      540

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SUBSTITUTE SHEET (RULE 26)

894

TTAGAGCAAA	CTTTAAAAA	AACCCCTAAC	AGCTTGGTTT	CTGTGAGCGC	GGCTTCTAAT	600
GTAACGGGAA	TTCTTACGCC	TTTAAAAGAA	GTTTCATCAT	TGTGTAAGGA	ATATAGGGCT	660
ATTTTAGCTT	TGGATTTAGC	GAATTTTAGC	GCGCATGCTA	ACCCTAAAGA	TTGCGAATAC	720
CAAACCGGTT	TTTATGCGCC	TCATAAGCTT	TTAGGGGGCG	TTGGAGGGTG	CGGTCTTTTA	780
GGCATTTCCTA	AAGATTTGAT	TGACACGCAA	ATCCCTCCGA	GTTTTAGCGC	AGGGGGCGTG	840
ATTAAATACG	CTAATCGCAC	ACGGCATGAA	TTTATTGATG	AATTGCCTTT	AAGAGAAGAA	900
TTTGGCAGCG	CAGGATTGTT	GCAATTTTAC	AGGAGCGCTC	TAGCGTATCA	ATTAAGAGAT	960
GAATGCGGTT	TGGATTTTAT	CCATAAGAAA	GAAAACAACC	TTTTAAGGGT	GCTTGTGTAT	1020
GGCTTAAAAG	ACTTGCCCGC	TATTAATATT	TATGGGAATT	TAACGGCGAG	TCGTGTGGGG	1080
GTAGTGGCTT	TTAATATTGG	AGGGATTTCG	CCCTATGATT	TAGCGAGGGT	TTTAAGCTAT	1140
GAATACGCTA	TTGAGACCCG	GGCGGGTTGC	TCTTGCGCGG	GGCCTTATGG	GCATGATTTC	1200
TTGAATCTTA	ACGCTCAAAA	GTCAAGCGAT	TTTAAAGCTA	AACCCGGATG	GCTTAGAGTG	1260
AGTTTGCATC	TCACGCATTC	CATAAACGAT	ATTGATTATT	TGCTAGACAG	CTTGAAAAAA	1320
CGGGTGA AAA	AAATTGCGT					1338

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250

TATGTGATAG	AGCTTGACAT	TAACGCCAGC	GATAAATCGC	TCTCGCACAG	AGCCGTTATT	60
TTTAGCCTGC	TCGCTCAAAA	ACCTTGTTTC	GTGCGGAATT	TTTTAATGGG	AGAAGATTGT	120
TTAAGCTCTT	TAGAAATCGC	TCAAAATTTA	GGGGCTAAAG	TGGAAAATAC	CGCCAAAAAT	180
TCCTTTTAAA	TCACACCCCC	AACAACCTATA	AAAGAGCCTA	ATAAGATTTT	AAATTGCAAC	240
AATTCTGGCA	CTAGCATGCG	TTTATACAGC	GGGCTTTTAA	GCGCTCAAAA	AGGCCTTTTT	300
GTTTTAAGCG	GGGACAATTC	CCTAAACGCA	CGCCCCATGA	AAAGAATCAT	TGAGCCTTTA	360
AAGGCGTTTG	GGGCAAAGAT	TTTAGGGAGA	GAGGATAACC	ATTTTGCCCC	CTTAGCGATT	420
GTAGGGGGTC	CTTTAAAAGC	TTGCGATTAT	GAAAGCCCTA	TCGCTTCAGC	TCAAGTCAAA	480
AGCGCTTTTA	TTTAAAGCGC	CTTACAAGCT	CAAGGCATAA	GCGCCTATAA	AGAAAGCGAG	540
CTTAGCCGTA	ACCACACAGA	AATCATGCTT	AAAAGTTTGG	GGGCTAACAT	TCAAAATCAA	600
GACGGCGTTT	TAAAAATTTT	ACCCCTAGAA	AAACCCCTAG	AATCCTTTGA	CTTTACCATA	660
GCCAATGATC	CGTCTAGCGC	GTTTTTTTAA	GCTCTCGCTT	GCGCGATTAC	GCCAAAAAGC	720
CGCCTTCTTT	TAAAAAATGT	CTTGCTCAAC	CCCACTCGCA	TAGAAGCTTT	TGAGGTTTTG	780
AAAAAAATGG	GCGCTCATAT	AGAATATGTT	ATCCAATCCA	AAGATTTAGA	AGTTATTGGC	840
GATATTTACA	TAGAGCATGC	CCCTTTAAAA	GCGATCAGTA	TTGATCAGAA	TATCGCCAGC	900
CTTATTGATG	AAATCCCCGC	TTTAAGCATC	GCTATGCTTT	TTGCAAAAGG	CAAAAGCATG	960
GTGAGAAACG	CTAAAGATTT	ACGAGCCAAA	GAAAGCGATA	GGATTAAAGC	GGTTGTTTCT	1020
AATTTCAAAG	CTTTAGGGAT	TGAGTGCGAA	GAATTTGAAG	ACGGGTTTTA	TATAGAGGGA	1080
TTAGGAGATG	CGAGTCAATT	AAAGCAGCAT	TTTTCTAAGA	TTAAACCCCC	TATTATCAAG	1140
AGTTTCAATG	ATCACAGGAT	TGCGATGAGT	TTCCGTGTTT	TAACTTTAGC	GTTGCTTTTA	1200
GAAATTGATA	ATTTAGAATG	CGCGAACATT	TCTTTCCCAA	CCTTTCAGCT	TTGGCTCAAT	1260
CTATTCAAAA	AAAGGAGTCT	CAATGAAAT				1290

(2) INFORMATION FOR SEQ ID NO:1251:

SUBSTITUTE SHEET (RULE 26)

895

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251

AATGCGCGAA	CATTTCTTTC	CCAACCTTTC	AGCTTTGGCT	CAATCTATTC	AAAAAAGGA	60
GTCTCAATGG	AAATTAAAAT	GGCTAAGGAT	TATGGTTTTT	GTTTTGGCGT	CAAAAGAGCG	120
ATACAAATCG	CTGAAAAAAA	TCAAAACAGC	TTGATTTTTG	GCTCGCTCAT	TCATAACGCT	180
AAAGAAATCA	ATCGTTTGGA	AAAAAATTTT	AATGTGAAAA	TTGAAGAAGA	TCCTAAAAAA	240
ATCCCTAAAA	ATAAGAGCGT	GATCATAAGA	ACCCATGGCA	TTCTTAAACA	GGATTTAGAA	300
TACTTGAAAA	ATAAGGGGGT	TAAAATCACT	GACGCGACTT	GCCCCGTATGT	GATCAAACCT	360
CAGCAAAATTG	TGGAATCCAT	GAGTAAAGAA	GGGTATCAAA	TCGTGCTTTT	TGGGGACATT	420
AACCACCCTG	AAGTCAAGGG	CGTGATCAGC	TATGCCACTA	ACCAGGCTTT	AGTCGTCAAT	480
TCGTTAGAAG	AATTGCAAGA	AAAAAAATTG	CAACGGAAAG	TGGCTTTAGT	CTCTCAAACC	540
ACCAAGCAAA	CCCCAAAAC	CTTGCAAATC	GCTTCT			576

(2) INFORMATION FOR SEQ ID NO:1252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252

AAATTACCAA	TCCACGCATT	CGTTTAAATG	TGTTTAGCGA	TCCCCTCTAA	AGTCATAGCC	60
ATTAACGATA	ATGTGGCACT	CTTAGAGACT	TTGGGCGTTC	AAAGAGAAGC	GAGCTTGGAT	120
TTAATGGGCG	AGTCCGTTAA	AGTGGGCGAT	TATGTGCTAC	TACACATCGG	CTATGTGATG	180
AGTAAGATTG	ATGAAAAAGA	AGCCCTAGAA	TCCATTGAGC	TTTACCAAGA	AATGATCGCC	240
GAAGTGAACG	AAACGCATGA	A				261

(2) INFORMATION FOR SEQ ID NO:1253:

SUBSTITUTE SHEET (RULE 26)

896

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...738
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253

AAAGGAACAA	GCATGAGCGA	ACAACGAAAA	GAATCGTTAC	AAAATAACCC	TAATTTGAGT	60
AAAAAAGACA	TCAAAATCGT	GGAAAAGATT	TTGAGCAAGA	ACGACATTAA	AGCCGCTGAA	120
ATGAAAGAGC	GCTACCTTAA	AGAAGGGTCT	GTATGTGTGA	ATTTCATGAG	TTCTCCCGGT	180
AGCGGTAAAA	CCACGATGTT	AGAAAATCTA	GCGGATTTTA	AAGACTTTAA	GTTTTCGCTG	240
GTAGAGGGCG	ATTTGCAAAC	CAACAGGGAT	GCGGACAGGT	TGCGTAAAAA	AGGCGTGAGC	300
GCGCATCAGA	TCACCACCGG	CGAAGCGTGC	CATTTGGAAG	CGAGCATGAT	TGAGGGGGCG	360
TTTGATTTAT	TAAAAGATGA	GGGAGCGTTA	GAAAAAAGCG	ATTTTTTAAT	CATTGAAAAC	420
GTGGGAATC	TGGTTTGCCC	CTCAAGCTAT	AATCTAGGGG	CGGCGATGAA	TATCGTTTTA	480
CTCTCTGTCC	CAGAGGGCGA	TGATAAGGTG	CTAAAATACC	CTACGATGTT	CATGTGTGCG	540
GATGCGGTCA	TTATCAGTAA	GGCGGACATG	ATTGAAGTGT	TTAATTTTAG	GGTTTCTCAA	600
GTCAAAGAAG	ACATGCAAAA	ATTAAAGCCT	GAAGCGCCCA	TTTTTTTAAT	GAGCTCCAAA	660
GACCCTAAAA	GCTTGGAAAG	TTTTAAAAAT	TTCTTTTAG	AAAAAAGCG	TGAAAATTAC	720
CAATCCACGC	ATTCGTTT					738

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2871 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2871
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254

GGAAAAATAA	TGGCAAAGAA	AAAACAAGAA	GTAAGGAATA	ATGAAATTTT	TGTCGCTCAA	60
AAACTCGCTG	AAGAGGAATT	GAACGCTAAC	GAGATTAACG	ATCCGTTAGA	AATGCTGGAC	120
TTTAAAAGCT	TTGATGATAA	TAAGGAGCTT	TTAGATTACC	AACAGCAAGC	TTTGATTAC	180
GCTTTTAGAG	TGCTTGTTGC	TTATTTTAGA	GACTTCAAAG	AAAGTAAAAA	AGAATTTTAC	240
GCTTTTTATC	AAAAGCATTA	TTCAATTCGCT	AATTGCGATT	TCGCTAAAAA	GAAACTCAAT	300
CATTGTGTAA	AGAGCCATTT	TAAGGTAGAA	AATCATTGCG	TGCGTTTGA	AAATTTTCATC	360

SUBSTITUTE SHEET (RULE 26)

AACCGCCTAG	CCTTTTACAT	GGCCACAGGG	AGCGGTAAAA	CGATCGTCAT	TATCAAACCTG	420
GTAGAGCTTT	TAAGCGTGGC	TATGGGAATG	GGTTTGATCC	CTAAGAAAAA	TATCATGTTT	480
TTTAGCGCGA	ACGAGCATTT	AATCAAGCAA	TTTGAAAAAG	AAATTGAAAA	ATACAACCGC	540
AATAAGGACT	ATTCCAAACA	AATTGATTTT	AAAAACCTTA	AAAGCGTTAA	GAATAAGGAT	600
TTTTATCGTG	CTCCAAAAGA	TTCTTTAATG	AAAGAAATCG	CTCTTTTTTA	TTACCGCGCA	660
GATTTAATGA	GCGATGAAGA	AAGCAAGGAA	AACCTTTTTA	ATTATAAGGA	TTGTTGGGAT	720
AATGGGGAAA	ATTATGTGAT	TTTAGATGAA	GCGCATAAGG	GGAATAAGAC	TGAAAGCAAA	780
AGACAGGCGA	TTTTTAGCCT	GCTGCTTTTA	AAAGGGTTTT	TATTCAATTT	CAGCGCCACT	840
TTCACTGAAG	AAAGCGATCT	CATCACTGCG	GTGTATAATT	TGAGCGTGGG	CGAGTGGGTG	900
AAACTTGGCT	ATGGTAAAGA	GTCTGTTTTA	TTGAAGAAAA	ACAACCTAAA	CGCTTTTAAG	960
GAATTGAAAG	ATTTAAACGA	CAGGGAAAAA	GAAATCGCTC	TTTTAAAGGC	GTTATGTGCTT	1020
TTAGGCATGC	AAAAACGCTA	TAAAGTAGAA	GGCTATTTTC	ATGACCCCTT	AATGCTCGTG	1080
TTCAAGCATT	CTGTGAACAT	GGAAAACAGC	GATGCGGAAA	TCTTTTTTAA	AACTTTAGCG	1140
CGCGTGATTG	AAAATGATGA	TGAGAGCGAT	TTTTCAAAAG	CTAAAGACGA	TTTATTAGAG	1200
GAATTAAAGA	ATCCGGAATT	CCTTTTTTAGC	GATGGCAAAG	ATAAAGAAAA	AGACTATAAA	1260
ATTGAGGTCT	TTAAAGAGAG	TTTAAAGGGC	ATGGATTTTA	AAGGCTTAAA	AGAAGCAGTT	1320
TTTTATGCCA	GTAATGGGCA	TATGGAAGTC	ATCATTAAAC	CTAAAAACAA	CCAAGAAATC	1380
GCTTTTCAAG	TCAACACGAG	CGATAAAGTC	TTTTGCCTGA	TTAGAATAGG	CGATATTACA	1440
GAATGGATCC	GTGAAAAAAT	AAAGAGCGTG	AAGGTGGTGA	GTAAGAATTT	GAGCTTCAAA	1500
GAAGAGAGCT	ATTTAGCCCA	GATTGATAAG	AGCAGTATCA	ATATCTTAGT	GGGGTCTCGT	1560
GCTTTTGACA	CTGGGTGGGA	TAGCACAAGG	CCTAGCGTGA	TTTTATTTTT	AAATATAGGG	1620
CTTGATGATG	ACGCTAAAAA	GCTGGTGAAA	CAATCTTTTG	GCAGGGGCGT	AAGGATTGAA	1680
AGCGTCAAAA	ACCAACGCCA	AAGGTTAGCG	TATTTAGAGA	TAGATGAAGC	CATTAAAGAC	1740
AAGCTGAAAC	CAAAAGCTGC	AATGCTGGAA	ATGCTTTTTG	TGATACCTAC	CAACCATGCA	1800
AGCCTTGAAG	CGATTTTAAA	GTTCCAAAAA	GAGAGCGAAA	ATGGGGGTGA	GAATAGAGGT	1860
CCTTGGCGTG	AAATCAAATT	AGAAAAAACG	CGCATAGAGC	ATGCCTTATT	CGTGCCTTGC	1920
TACCGAAAAA	AACAAACCAA	CGCTCTTAAA	ATTTCTCAAA	GCGCTTCGTT	TAAAATGAGC	1980
GAAAAAATTT	TTAAGGATTT	AAAAGAGCAT	TTTCATTTAA	TGAGTGAAAA	GCATTTTATT	2040
TTAAAGCATG	AAATTTATGA	CCCTAAAGAT	TACGCGCTGT	TAAAAGAAAT	GATACAAACA	2100
GCGCATTTTA	AAAAGGTATC	AACCTGGCAT	TATAAAGATT	TAGATTACAT	GATTTCTGAA	2160
ATTAAAGGCA	AGCTATACCC	TAATCAAAAA	GTGCCTAAAG	ACGAGTTTAA	CGCCCTAGAT	2220
AATGAGAAAA	TCGTGCATTT	TAAAAGGGTT	AAAGTTAAGG	CGGATAAAAA	AGAAAAATTG	2280
ATTCAAAACCA	TCCAAGAAGT	GAAAGAGCAT	GCGCCTTTGG	ATAAAGAAAC	TTTAAGAAAA	2340
AAAATGCGCG	AGGCGGAGAT	CGATCCTTAT	GATACAGAAA	AACACAAACA	AGACAGAACG	2400
TTCAAAGTTG	GTGATGCAGA	GCTGTTAAAA	CTCAAAGAGC	ATTACTACAC	CCCGCTCATT	2460
AAAGCCAAAA	ACTGCGATTG	GCTTAAGCAT	GTGGTTAAGG	TAAAGAGCGA	GAGCGATTTT	2520
TTAGAAGAGT	TGTTAAAGAT	TACCGAAACG	CTGCAAGAAA	ACTATGATTT	TTGGGCGTTC	2580
AGCAAGATTG	ATGAGCATTT	AGACAATTTG	TTTATTCCTT	ATATAGACAA	CGCTACAGAA	2640
AGGCGCTTTT	TCCTTGATTT	TATCTTTTGG	CTGCAAAAAA	GCGGCACGCA	GATCATTGTC	2700
TTCAATTGATC	CTAAGGGGAG	CAAACACACT	GATTACGAGC	ATAAGGCAGA	TGCGTATCAA	2760
CTTTTGAAG	ATAAGGTTTT	TAACCCTAAA	GACGATCCCA	ATCTCAAAAT	CAAAGTGGTT	2820
TTAAATTTT	ATGGGGATAA	GGATGATGTG	GGGGAGCGTT	ATAGGGATCT	T	2871

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...747

898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255

TGCATGCGTT	TTTTATTTTAA	ATTCCTTTGG	CTTTTAGGGA	TTTTTCTTAT	TTTTTATTTT	60
TTAGACATTA	AAGGCAGCTC	TTCTTATATC	AGCGACCGGG	TTAAAAGCGC	CTTGATGAGC	120
GCGAAAAACA	GCTTACTAGA	CAACGTTCAA	GCGTATTTTT	TTCAAGCCCA	AAACATTAAG	180
GAATTTCAAA	AAGAACGCTT	GATTTTAGAA	GCTTTAAAAC	TAGAAAACGC	TGATTTGAAA	240
GAGCGTTTGA	ATAGTATTTA	TCCTTTAGAA	AATCCAAAAA	TGACTTATAC	CCCTACTTTC	300
ATGACTTCAT	TCATCAATTT	AGAAGACACA	CACAGCGTTT	CTCTCAACCC	TATTGTGAAT	360
TTAGAAGAAA	ACAAGATTTA	TGGCCTTGTC	TCTCACAACC	AAGCCATAGG	CATTGCCGTG	420
CTAGAAAAAG	GGCGCTTGAA	CGGGTTTTTG	AACGCCCCACA	AGCGGTGTGC	TTATAGCGTG	480
ATGATAGGCC	AAAATCAAGT	CTTAGGCTTT	ATAGGGACTA	ATTTCAAGCA	AGAATTAGTC	540
GTGATTTTCA	TTGTCCCAAG	CGCTGAAATC	AACATAGGCG	ATCAAGTGCT	AACGAGCGGG	600
CTAGATGGGA	TTTTTGGAGC	GGGGGTGTTT	GTGGGTGAAG	TTTCAAGCGT	TGAAGATCAT	660
TACACTTATA	AAAGCGCGGT	GTTGAAAAAC	GCTTTTTTAA	GCGAAGCCAA	ACTTTTAAGG	720
CATGTGTTTT	TAAGCGGTGT	GAAAAAC				747

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256

TGGTATTTTA	AAAAAGAAAG	AAATCCCATG	GTTATACATG	AAAAAATCAA	AAGCCGCTTT	60
TCTAGGAATT	GGTCTTTAAG	GAATAGGGGC	AGGCATTTTG	CATCTTCAAG	CGTGATTTTT	120
TTCTCACTTC	TTGTCATTAC	AGCGGTAAAT	AGAAGTAGTG	CAGTTGCTTG	GTTATTGATG	180
CCTGAACATT	TGATTGGGTG	GTTTTTGATT	TCTTTTAGTG	GGGAATTTGT	AGCAGACATG	240
GCGTTTGGCA	AAAAAAGTAA	GATTTTTTAA	ACCCGCTTTG	GAATTTCTAT	TGTGAGCGGC	300
GTTTCACTAT	TGCTTGGCGC	TTTACCAGCG	CATTTATTTT	TTGTATGGTT	TGGCTTTTAT	360
AATTGGTGGG	CTGCTTTTTT	TATAGAAGCG	GGAGCTGATC	TATTGGTGGG	CTGTGTGATA	420
CAAAAGATTT	TTTTTGGTAA	ATATTGGGTG	GATCGCTATT	AT		462

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

899

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257

TGGGCGAAAG GCGCTGGGGC TTTAGTGCTT GAAGAATACG AGAGCGCGAA AAAAAGAGGG	60
GCTAAAATTT ATGCAGAAAT TGCCGGGTAT GGCGAGAGCG GCGATGCTAA CCACATCACA	120
GCCCCAGCCC CTGAGGGTGA AAGGGCTTTT AAAGCCATGA AAATGGCTTT AGAAATGGCG	180
AAAGTGAAG TATGCTATGT GAACGCCCAT GGGGACAAGC ACGCATTA	228

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258

ACGCCCCATGG GGACAAGCAC GCATTATAAC GATTGGTATG AAAGCATTGC GTTAAAAAAT	60
GTGTTTGGCT CTAAAGAAAA AGTCCCTCCT GTTAGCTCCA CTAAAGGGCA GATTGGGCAT	120
TGCTTGGGTG CTGCGGGCGC GTTAGTAGCC GTTATTTCTA TCATGGCCAT GAATCAAGGG	180
ATCTTACCTC CTACCATTAA TCAAGAAACG CCTGACCCAG AATGCGATCT GGATTATATC	240
CCTAATACAG CCAGAGAAAA GCAAGTGAAT GCGGTGATGA GTAACTCATT TGGTTTTGGT	300
GGCACTAATG GTGTTGTGAT TTTCAAAAA GCC	333

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...567

900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259

GGCCCAATAC	AAAGCGCTCC	AGCAATGAAC	AAGCTTTTTT	TAGCTTTTAT	TGTTGGGGGA	60
ATGCTTTTAA	GTGCTGATGC	TTTAAACGAT	AAGATTGAGA	ATTTAATGGG	GGAGCGATCC	120
TACCACATGA	ACAAGCTTTT	TTTAGAGCGT	TTGTTTAAAA	ATCGTAAGGA	TTTCTATGAA	180
ATGGGGCGTT	TGGATTCTTT	AAAACACTCTC	AACACTCTCA	AAGAAAACGG	GCTTTTATCG	240
TTTAATTTTG	ACAAACCAAG	CGTGTTAAAA	ATCACTTTCA	AGGCTTCAAG	TAATCCCCTA	300
GCGTTTGCCA	AAAGCATCAA	CAATTCTTTG	AATATGATGG	GGTATTCGTA	TGTTTTGCCT	360
ATTAGAATGC	AAAGCTCTTC	AGGCGAGAAT	GTTTTTTCAT	ACGAGCTTAA	AACGGAATAC	420
GTTTTAGACC	CTAACATTTT	GATAGAGACG	ATGAAAAGGC	ATGGTTTTGA	TTTTATGGAT	480
ATTAGACGGG	TGTCTTTAAA	GGAGTGGGAA	TACGACTTTG	CCTTACAAAA	GATCAAGCTC	540
CCTAACGGCG	AGAGCCTTAG	TTTTGAG				567

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260

ATGGAACAGA	ATAAAAAAAG	TTTAGAAAAT	TTAGATCTTT	CTGATGTTCA	AAACATTTCT	60
AAAGATATTT	CTGGAACGCG	TTTAGAAGAA	TTATCGCTTA	AAAATTTAGA	TAAAAATTTG	120
CAGATTCTAA	AAGAAGTTGG	AGCGGCAGAA	ATTTGCAAGG	CGACTAAAAT	CGCTTCTAAA	180
AATATCCATT	CTATCTTGGA	AAAGCGCTAT	GAGTCTTTAT	CAAGGGTGCA	TGCTAGGGGT	240
TTTATACAGA	TTTTAGAGCA	CGAGTATAAA	ATTGATTTGA	GCGCATGGGT	GAAAGAATTT	300
GACAAAGTGT	GTGTTTTTAA	AGAGGGCGTG	GGAGAAGAGC	AAAAACAAGA	AACAAGCCCT	360
GAAGAAACAG	CAAAAAAACC	CCTTAAGGTT	GAATTGGATT	ACAGCATCAA	TCAAGCCAAT	420
ACTTCATTAT	CCAAAAAATC	TTCCAAATGG	AAACCCTTTG	TTATCGTTTT	AGGGGTGGTT	480
GTCATTATTT	TAGTGGTCGT	TATCATTCAA	AACAGCTCTT	CTTTAAAAGA	AGAGAGAGAG	540
CAAGAACGCG	CTATTAGCC	CGACACCAA	AATAATTCTT	TCAATGAAAC	TAATCCTACA	600
GAAGAAAAAA	AGTTAGAGCC	AACGCCTAAA	TTAGAAGAAA	AACACAAAGA	ACAAGACAAG	660
CAAGGCAAAG	AAGCGATCAA	AGAAAATCCT	AATACCATT	ACATTATCCC	TAAACGAGAT	720
ATTTGGGTAG	AAGTGATTGA	TTTAGATGAG	AAAAAAACT	CTTTTCAAAA	GGTTTTTAAA	780
AAAAGTTATC	CTTTAGAGGC	TAAAAACCAC	CGCTTGTTGT	TACGCTTTGG	GCATGGGCAT	840
CTTATTCTTA	AAAACAACCA	TCAAGAACAA	GATTATAACG	ACAGCAAAAC	TAGGCGGTTT	900
TTATACGAGC	CAAATAAAGG	TTTAACGCTC	ATCAATGAGG	CCCAATACAA	AGCGCTCCAG	960
CAA						963

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

901

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261

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AGGAGTGGGA ATACGACTTT GCCTTACAAA AGATCAAGCT CCCTAACGGC GAGAGCCTTA    60
GTTTTGAGTA GCGATCCTGT GGAGTTTAAG GAAGCGAGCG GGAAATATTG GCTGAGCGTG    120
AATCAAAACG CGTATTTTAAA AATAAGCTCC AATAACCCCTT TGTGGCAACC CAAAATCATT    180
TTTTATGATG AAAACTTAAA GATCATTCAA ATCATTGCTA AAGAAAACAG ACAACAAGAA    240
ATCGCTCTTA ACTTGCTTGA TGGCGTGCCT TTTATCCATA TCACTGACGC AAAAAACCCCT    300
ATCATTTTAA AAAATGGGAT TAGCGTGGTT TTTGATGCGA TGCCTT                    345

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(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262

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CGGTCTCTAG CGTGCTGGCT AAGATTGAGT CTCTTTAAGG GGATAATCAT GTTCGATTCA    60
ATCGTTTATT TTTTCAATAA GAGCGGGTTT GTTACCACGC TIGTTTTAGT TTGGATTTCG    120
CTTTATTTGG TGATGACTTT ATGGGTCTTT TTGTATAAAA GCATTGTATT AAAGATTGAA    180
CTCAGGCGCG AGATGCAATC TTTGTCTAAC ATTCTTAATG GAGCGCAAGA CGCTCAGAGC    240
ATTTTATGTT TAATAAAAAA AGAAATGATG AGACCAAAAG GTATTCTAAT GAATTGTTGC    300
AGGGCTTGGG AACACCAGGT TCTTAAGCAA AGCAGGACAG GTTTAGTGGT GTTGAGCATT    360
ATCTCTTCTA CAGCCCCCTT TATTGGTTTG TTGGGACGG TAGTTGAAAT TTTAGAAGCG    420
TTTAACAATT TGGGCGCGTT AGGTCAAGCT TCTTTTGGAG TGATCGCACC CATTATTTCT    480
AAGGCGCTTA TCGCCACCGC TGCAGGGATT TTAGCAGCCA TTCCAGCCTA TTCTTTTAC    540
TTGATCTTAA AGCGCAAGGT GTATGATTTA TCGGTTTATG TGCAGATGCA AGTGGATATT    600
TTGTCTTCTA AAAAAA

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(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

902

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263

AAGGTTTTTA	TGAATTACGA	TAACTATTGG	GATGAGGACA	AACCAGAACT	CAATATCACG	60
CCTTTAGTGG	ATGTGATGCT	TGTTTTATTG	GCTATTCTTA	TGGTAACGAC	GCCCCTCTC	120
ACCTATAAAG	AAGAGATTGC	CTTGCCTTCT	GGTTCAAAAA	CTGCTAGAGC	CACTCAAGAT	180
AAAGTGATAG	AGATACGCAT	GGATAAAGAC	GCAAAAATCT	ATATAGATAG	TCAAACCTAT	240
GAATACAAC	CTTTCCCGGA	CACTTTCAAT	TTGCTTTCTA	AAAAATACGA	TAAAGATACT	300
AGGGTGAGTA	TCCGTGCGGA	CAAGCGATTG	ACCTATGACA	AAGTGATTTA	TTTGTTAAAA	360
ACGATTAAAG	AAGCGGGGTT	TTTGAAAGTT	TCTTTAATCA	CAAGTCCT		408

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264

AAAGTAGGGC	CAATTTGCAT	GAGTAAGAGC	GCGATTTTTG	TTCTTTCTGG	CTTTTTAGCG	60
TTCTTGCTCT	ATGCTTTGTT	ATTATATGGT	TTGTTGTTAG	AAAGGCATAA	TAAAGAAGCA	120
GAGAAAATCC	TTTAGATTTT	AAATAAAAAG	GACGAACAAG	CCATTGACTT	GAATTTAGAA	180
GATCTGCCAA	GCGAGAAAAA	GAATGAAAAA	ATTGAAAAAG	TAACGGAAAA	ACAGGGCGAT	240
TTTTTAGAGC	CTAAGAAGA	ACCCAAAGAA	GAGCCTGAAG	AAAGCCTTGA	AGATATTTT	300
TCTTCACTCA	ATGATTTTCA	AGAAAGACAG	ACAAAACGC	TCAAAAAGAC	GAGCAAAAAA	360
ATGAACAAGA	AGAACAAAGG	CGTT				384

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

903

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265

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GGAAGAACAA TGAAATATTT ATGGCTTTTT TTAATATACG CTATAGGGCT TTTTGCAACA      60
GATAAAACGC TAGATATTAT TAAAACCATT CAAAAACTTC CTAAGATTGA AGTGCCTAC      120
TCCATAGATA ACGATGCCAA TTACGCTTTA AAATTGCATG AAGTCTTAGC GAACGATTTA      180
AAGACTAGCC AGCATTTTGA TGTTCCTCAA AACAAAGAGC AAGGTGCTAT CAATTACGCA      240
GAACTCAAGG ATAAAAAAGT CCATCTTGTA GCGCTTGTGA GCGTGGCGGT AGAAAACGGC      300
AATAAAATTT CACGATTAAT ACTTTATGAT GTGGATACAG GAACGCTCAA AAAGACTTTT      360
GACTACCCCA TTGTAAGTTT AGATCTATAC CCTTTTGCAG CGCACACAT GGCCATTGTG      420
GTGAATGATT ATTTAAAAGC CCCTTCTATC GCTTGGATGA AGCGCCTGAT TGTTTTTTCT      480
AAATACATTG GACCAGGAAT CACAAACATC GCACTAGCGG ATTATACGAT GCGTTATCAA      540
AAAGAAATCA TCAAAAACAA CCGACTCAAT ATTTTCCCA AATGGCGGAA CGCTGAGCAA      600
ACGGAGTTTT ATTACACGCA GATGGCGGAA AAACGCCCAT GGTTC      645

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(2) INFORMATION FOR SEQ ID NO:1266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266

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TTCCTGAGGG GGAAGTTTAT ACAGGAGAGG TTAAAAGCGT TGTGTTGCCA AGGAGTGGA      60
GGGGAATTTG GGGTGCTTTA TGGGCATAGC AACATGATCA CCTTGCTTCA GGCGGGAGTG      120
GTTGAGATTG AAACCGAAAA CCAAAAAGAG CACATTGCTA TCAATGGGGG TTATGCAGAA      180
GTTACTAATG AACGGGTGGA TATTTTAGCC GATGGAGCGG TCTTTATTAA AAAAGGATCA      240
GATGACAGAG ATGATGCTAT CTCTAGGGCT AAAAAGCTTT TAGAGGACGC AAGCTCTGAC      300
AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG ATTGAGTCTC TT      342

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(2) INFORMATION FOR SEQ ID NO:1267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid

904

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267

AAGCTTAGCA TGAGAGCGAT CGCTATTGTT TTAGCCAGAA GTTCCAGTAA AAGGATTAAG	60
AATAAAAATA TGATTGATTT TTTCAATAAA CCCATGCTCG CTTACCCATAT TGAAACAGCA	120
CTAAATTCCA AGCTCTTTGA AAAAGTGTTT ATCTCTAGCG ATAGCATGGA GTATGTCAAT	180
TTAGCCAAAA ATTATGGGGC GAGTTTTTTG AATTTACGCC CTAAAAATTT AGCAGACGAG	240
CAGGGCCACG ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGA	297

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268

ATCCCTCCGA GCACACCATT TCTTAACATT CTGCATGTTT TTAAACATTA TCGCTCCCAT	60
TATGGTAAAA TAAATACTTG CTTAAACACG CTAGGAGATT TGATTTTGCC ATTACCCGTT	120
TATTATGATA AAGACATTGA TTTAGGCGTT ATCCAATCCT TACAAGTGGG CATTATTGGC	180
TATGGCGTGC AAGGAGAGGC TCAAGCACTC AATTGAGGG ACTCTAAAGT GAAGGTGCGT	240
ATTGGCTTGT ATCAAGGGAG TTTGAGCGTT TCAAAAGCAA AAAAAGAGGG CTTTGAGGTG	300
CTAGGAGTCA AGGAATTAGT CCAACAATCT GATGTGATCA TGGCGTTACT TCCGGATGAA	360
TTGCATAAAG AAGTGTTAGA AAAAGAAGTG ATCCCTTTTT TAAAAGAGGG GCAAATTATA	420
GGCTTTGCTC ATGGTTTTAG CGTGCAATTC AATCAGGTTG TTCTCCCAAA AGGCGTGGGC	480
GCGATTTTAG TCGCACCAA AGGGCCCGGG AGCGCTTTAA GAGAAGAATA CCTTAAAAAT	540
AGGGGTTTAT ACCATCTAAT CGCCATAGAG CAAGAAAGCT CAATTCATAA CGCTAAAGCG	600
GTGGCTTTAA GCTATGCTAA AGCGATGGGT GGGGGGAGAA TGGGGGTTTT AGAAACGAGT	660
TTTAAAGAAG AATGCGAGAG CGATTTATTC GGCGAGCAAG CGGTCTTGTT CGGGGGGTAA	720
GAAGCGATCG TAAGAATGGG GTTTGAAACT TTAATCAAGG CAGGATAC	768

(2) INFORMATION FOR SEQ ID NO:1269:

905

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269

CAGACGAGCA	GGGCCACGAC	TTTAGAAGTG	ATGGCCTATC	ACATGAAAGA	ATTAGAATTA	60
AAAGATGAAG	ACATTGCGTG	TTGTTTGAT	GGCGTTTCAG	TATTTTAC	AGAAAAGCAT	120
TTACAAAACG	CTTTTGAAAC	TTTAAACAA	AATCAAAATA	CGGATTATGT	TTTCACATGC	180
TCTCCCTTTA	GCGCTTCGCC	TATCGTTCCT	TTAGCCTTGA	AAACGGCGTT	CAAATGGCTT	240
TTAAAGAGCA	TTCAAACACG	CGCACGCAAG	ATC			273

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270

ATGAAAAGCG	ATAAACCCCTT	TTTAGAACGC	TATTTTATG	ACCCCACTCT	TTTGCAAAAG	60
GGGTGATTT	TCGCGCTCTA	TCCTTTTCT	TTAATCTATC	AATGTATTGC	CACAATTAAA	120
CGAAAACCG	CTAAAAGCA	TGATTTTAAA	ATCCCCATTA	TCAGCATAGG	CAACTTGATC	180
GCTGGGGGAA	GCGGTAAAC	GCCCTTCATT	TTAGAAATCG	CTCCAAGATA	CCAAGAAGTG	240
GCGGTGTTT	CTAGAGGGTA	TCAACGGGAT	TCTAAAGGTT	TAGTGGTGGT	GAGCGTTAAA	300
GGAAACATTT	TAGTTCCTCA	AAAAACAGCG	GGCGATGAAG	CCTATCTTTT	AGCCTTAAAT	360
CTAAACAAG	CGAGCGTGAT	TGTGAGCGAA	AAAAGGGAGC	TAGGCGTTTT	AAAAGCCCTT	420
GAATTAGGAT	CAAAGATCGT	GTTTTTAGAC	GATGGTTTTA	GGTTTAATTT	CAACCAATTC	480
AATGCGCTTT	TAAAACCCAA	AGTCCCCCCC	TACTACCCCT	TTTGTGTTGCC	TAGCGGGTTG	540
TATAGAGAAA	ATATTAAAAG	CTATAAAGAA	GCCCATTAG	TCATTACAGA	AGATAAGGAT	600
TATCAAAGAA	TCACCTCTAT	CACTAACCCC	ACCAAACGCA	TGCTTTTAGT	AACGGCTATC	660
GCTAACCCCTA	GCAGGCTTGA	TGCGTTTTTA	CCCAAAGAAG	TGGTTAAAAA	ATTGTATTTT	720
AGAGACCATG	CCCTTTTGA	TTTGAAGCTT	TTAGAAAAAG	AGTTTATCA	AAATAACGCC	780
ACCTCCTTAT	TGTTACTTC	AAAAGATCTC	GTCAAATTAC	AAGATTGCAA	ATTGCCTTTA	840

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906

AGCGTATTGG ATTTAAACT AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT 900
ATCCTTTCTT ATCCTTGTA TATAAAGAA CATCTA 936

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271

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AAAGTGTGTG GGGTGCTATA TTTTAAACC AGTTTATTTA TTGCTCTTT GATTGTTTG      60
TGGTCTAAAA AATCCATGCT CTTTGTGGAT AACGCTAATA AAATCCAAGG CTTCCATCAT      120
GCAAGAACCC CACGAGCCGG GGGGCTTGGG ATCTTTCTTT CTTTGCCTT GGCTTGTTAT      180
CTTGAACCTT TTGAGATGCC TTTAAGGGG CCTTTGTTT TCTTAGGGCT ATCGCTAGTG      240
TTTTTGAGCG GTTTTTTAGA AGACATTAA CTTTCATTAA GCCCAAAAT ACGCCTTATT      300
TTGCAAGCTG TAGGGGTCGT TGCATCAT TCATCAACGC CTTAGTGGT GAGCGATTT      360
TCGCCCCCTT TTAGCTTGCC TTATTTTCAT GCTTTTTTAT TCGCTATTT TATGCTGGTG      420
GGTATCAGTA ACGCTATTAA TATCATTGAC GGGTTTAACG GGCTTGCATC TGGGATTTCG      480
GCGATCGCGC TTTTAGTCAT TCATTATATA GACCCTAGCA GTTTGTCTTG TTTGCTCGCT      540
TACATGGTGC TTGGGTTTAT GGTGTTAAAT TTCCCTTCAG GAAAGATTTT T          591

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(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272

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CAGTTTGTCT TGTGCTCG CTTACATGGT GCTTGGGTTT ATGGTGTTAA ATTTCCCTTC      60
AGGAAAGATT TTTTAGGCGA TGGGGGGGCG TATTTTTTGG GTTTGGTGTG CGGGATTTC      120
CTCTTGCAAT TGAGTTTGA GCAAAAATC AGCGTGTTTT TTGGGCTCAA TTTAATGCTT      180

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907

TATCCGGTCA TAGAGGTGCT TTTTAGTATC CTTAGGCGCA AAATAAAACG CCAGAAAGCC	240
ACCATGCCGG ATAATTGCA TTTGCACACC CTTTATTTA AATTCTTGCA ACAACGCTCT	300
TTCAATTACC CTAACCCCTT ATGCGCGTTT ATCCTTATTC TATGCAACCT GCCTTTTATT	360
TTAATAAGCG TTTTGTTCG CTTGGACGCT TATGCGCTCA TTGTGATTAG CCTAGTCTTT	420
ATCGCATGCT ATTTAATAGG CTATGCTTAT TTGAATAGGC AAGTTTGCGC TTTAGAAAAG	480
CGGGCGTTT	489

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273

ATGAATAAAA CCATAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA	60
AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA	120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA	180
GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC	240
AGCGTGGAAT ATAACGCGCA AATGTCCAAG	270

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274

GTCAAAAAGT CAAATAACAT GGTAGTAGAA TTAAAAACA TTGAAAAGAT TTATGAAAAC	60
GGGTTTCATG CTCTAAAAGG CGTGAATTTG GAATTGAAAA AAGGCGATAT TTTGGGCGTG	120
ATAGGCTATT CAGGGGCGGG GAAATCCACG CTCATTGCTG TGATCAATTG TTTAGAGCGC	180
CCCAGTTCTG GCGAAGTTTT AGTCAATGGG GTCAATCTGT TAAACTTAAA GCCTAAAGAA	240

SUBSTITUTE SHEET (RULE 26)

908

TTGCAAAAAG	CGCGCCAAAA	AATAGGCATG	ATTTTCCAGC	ATTTC AATTT	ATTGAGCGCT	300
AAAAACGTGT	TTGAAAACGT	CGCTTTCGCT	CTAGAAATCG	CCCGATGGGA	AAAAACTAAG	360
ATTAAATCAA	GGGTGCATGA	ATTGTTGGAA	TTAGTGGGGT	TAGAAGATAA	AGTGCATTTT	420
TATCCTAAAC	AGCTCAGCGG	CGGGCAAAAA	CAACGAGTGG	CGATCGCTAG	GAGTTTAGCG	480
AATTGCCCTA	ATTGTTGCT	TTGCGATGAA	GCCACATCCG	CTTTGGATTG	TAAAACCACG	540
CATTCTATTT	TAACGCTTCT	AAGCGGCATT	CAAAAAAGT	TTGATTTGAG	CATCGTTTTT	600
ATCACACACC	AGATTGAAGT	GGTTAAAGAA	TTGTGCAATC	AAATGTGTGT	GATCAGCAGC	660
GGCGAAATCG	TAGAAAGAGG	CTCGGTGGAA	GAAATTTTGG	CTAACCTTAA	ACATGCTGTT	720
ACTAAGAAT	TGCTTGCCAT	CAAAAACGAA	CATGCGGATC	AAAAATCGCA	AGACATTTAT	780
CGCATCGTGT	TTTtagggga	GCATTTAGAC	GAGCCGATCA	TTTCTAATTT	GATCAGGCGT	840
TTTAAAAATA	GACGT					855

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275

TTATTTTGCT	CCTGCCCTTA	TCAGCGCTTT	TTGATTGGCA	CAAGCATTGG	ATCTAGCGCG	60
AGCATTATCC	CGTTAGCCAT	TTGGGCCATT	CCTTTTGTG	TAAAGCTTTT	TGAAAATTCT	120
TTAATGAAG	TAGAGCATGG	CAAGATTGAA	ACCACTTTAA	GCTTGGGGGC	GTCTCATTGG	180
GAAGTCATTA	AAATGATGCT	TTAGAGAGC	CTGCCTTCTT	TAGTGAATAA	TATCACCATC	240
ACTTTAATTT	CTCTAATAGG	CTATTCGGCT	ATGGCTGGAG	CGTTAGGGGC	TGGGGGATTG	300
GGGGATTTAG	CCATTAGGAT	TGGCTATCAA	AGTTATAGGG	GCGATGTGCT	TTTTTATGCG	360
GTGCTCGTGA	TCATCGTTTT	AGTGCAAATC	ATTCAAAGCG	CGGGGGATTA	TGTGGTGAAA	420
CGCTTGAGAA	AGAATAAGTA	T				441

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

909

(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276

TCTTATTTT	TTTATAATCT	TAGGTTGTTA	AGTTTAGTTA	AAGGGAAAAC	CATGCTCCGC	60
TCTCTCTATA	GTGCCACTTC	AGGGATGCTC	GCCCAACAAA	CGCACATTGA	CACCACTTCA	120
AACAACATCG	CCAATGTCAA	TACCACCGGG	TTTAAAAAAT	CTCGCGCGGA	TTTAAACGAC	180
TTGTTTTACC	AAGCGATGCA	ATACGCCGGC	ACCAACACAA	GCAACACGAC	TTTATCGCCA	240
GATGGCATGG	AAGTGGGCCT	TGCGGTACGC	CCTAGTGCGA	TTACCAAAAT	GTTTTCGCAA	300
GGCAGCCCTA	AAGAAACGGA	GAATAATTTA	GATATTGCTA	TTACAGGTAA	AGGCTTTTTT	360
CAAGTCCAGC	TTCTGATGG	CACTACCGCT	TACACAAGGA	GCGGGAATTT	CAAGCTAGAC	420
GAGCAGGGCA	ATCTTGTAAC	AAGCGAGGGC	TATCTCCTCA	TCCCTCAAAT	CACTTTACCC	480
GAAGACACCA	CGCAAGTGAA	TATCGGTGTG	GATGGCACGG	TGAGCGTGAC	TCAAGGCTTG	540
CAAACGACTT	CTAACGTGAT	CGGCAAAATC	ACTTTGGCTA	ATTTTGTCAA	TCCGGCGGGG	600
CTTCATTCTA	TGGGGGATAA	TTTGTTTTCC	ATCACCACCG	CTAGCGGCGA	TGCGATTGTG	660
GGCAACCCGG	ATTCTCAAGG	CTTAGGCAAG	TTAAGGCAAG	GCTTTTGTGA	GCTTAGTAAC	720
GTGAGATTGG	TAGAAGAAAT	GACAGATCTA	ATCACCGCTC	AAAGGGCTTA	TGAAGCCAAT	780
TCTAAAGCA	TTCAAACCGC	TGATGCCATG	CTCCAAACAG	TCAATTCCCT	CAAACGC	837

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277

AAATGGCGCA	ACTCATCAAG	CGATAAAATG	GCTAAAAAGA	AAATTGCGAT	CAGCTGTGGG	60
GATATTCAAG	CGGTAGGCTT	AGAATTGATC	TTAAAAAGCC	ATAAGGAAGT	GAGTGCACCT	120
TGTGAGCCGT	TGTATCTCGT	TCATAGCGAA	CTTCTAGAAC	GAGCCAATCA	ATTGCTTGAT	180
AACGCTTATG	AAACTAAAC	GCTTAATGCG	ATCGCTATTG	ATGCCCCCTT	ACCCTTATTA	240
AACTCTAGCA	CGATAGGCAA	AGTCAGCACT	CAAAGCGGGG	CGTATAGCTT	TGAGAGTTTT	300
AAAAAGGCTT	GCGAGTTGGC	GGATAGTAAA	GAAGTGGATG	GCATTTGCAC	TTTGCCTATC	360
AACAAACTCG	CATGGCAACA	AGCTCAAATC	CCTTTTGTGG	GGCATACCGA	TTTTTTGAAA	420
CAACGCTACA	AAGATCATCA	AATTATTATG	ATGCTTGGGT	GTCAAAACT	CTTTGTGGGG	480
CTATTTAGCG	ACCATGTGCC	TTTAAGCGCG	GTTTCTCAAC	TCATTCAAGT	GAAAGCGTTA	540
GTTAAGTTTT	TATTAGCGTT	TCAAAAAAGC	ACTCAAGCCA	AAATCGTTCA	AGTGTGTGGT	600
TTCAACCCCC	ATCGGGGCGA	AGAGGGATTG	TTTGGGGAAG	AAGATGAAAA	GATTTTAAAA	660
GCCATTCAAG	AGAGCAACCA	AACGCTAGGT	TTTGAATGCT	TTTTGGGGCC	ACTGCCCGCT	720
GATAGCGCTT	TTGCCCCCAA	TAAACGCCAA	ATAACCCCTT	TTTATGTGAG	CATGAGCCAT	780
GATGTAGGGC	TAGCCCCCTT	AAAAGCGCTC	TATTTTGTATG	AAAGCATCAA	TGTGAGTTTG	840
AACGCTCCCA	TTTTACGCGC	TTCCAATGAC	CACGGCACGG	CGTTTGATAT	TGCTTATCAA	900
AATAAGGCGA	ACCATAAAAG	CTATTTGAAC	GCGATCAAAT	ACTTGGCT		948

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs

SUBSTITUTE SHEET (RULE 26)

910

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278

CAAGGTATAA	TTCAAGCAAA	AACACCACCC	AAAGATAAAG	ACATGATTTT	AAGCATTGAA	60
AGTTCTTGCG	ATGACAGCTC	TTAGCCCTT	ACAAGAATAG	AGGACGCCAA	GCTCATCGCT	120
CATTTTAAAA	TCTCTCAAGA	AAAGCACCAC	AGCTCTTATG	GGGGCGTTGT	GCCTGAGATT	180
GCATCGCGCC	TGCATGCTGA	GAATTTGCCG	CTTTTATTAG	AACGCGTTAA	AATAAGCTTG	240
AATAAGGATT	TTTCCAAAAT	TAAAGCCATC	GCTATCACTA	ATCAGCCAGG	TTTGAGCGTT	300
ACTTTAATAG	AGGGTTTGAT	GATGGCAAAA	GCCTTGAGCT	TGTCTTTGAA	TTTACCCTTG	360
ATTTTGGAAG	ATCATTTGAG	AGGGCATGTG	TATTCGCTCT	TTATCAATGA	AAAACAAACC	420
CGCATGCCTT	TAAGCGTGCT	GCTAGTCTCT	GGGGGGCATT	CTTTAATTTT	AGAGGCTAGA	480
GATTATGAAG	ACATTAAAAAT	CGTTGCCACG	AGTTTAGACG	ATAGCTTTGG	GGAGAGTTT	540
GATAAGGTTT	CAAAAATGCT	TGATTTAGGC	TATCCAGGAG	GCCCCATAGT	GGAAAAATTA	600
GCCCTTGATT	ATGCACACCC	AAACGAGCCT	TTAATGTTCC	CTATCCCTTT	AAAAACAGC	660
CCGAATTGG	CTTTTAGTTT	TTAGGTTT	AAAAATGCGG	TGCGTTTGGG	GTTTGAAAAA	720
AACGCCCAT	ATTGAACGA	TGAGGTAAAA	CAAAAGATTG	GCTATCATTT	TCAAAGCGCG	780
GCTATCGAGC	ATTTAATCCA	GCAGACTAAA	CGCTATTTTA	AAATCAAACG	CCCTAAAATT	840
TTTGGCATTG	TGGGGGGAGC	GAGCCAAAAT	CTAGCCTTAA	GAAAGGCGTT	TGAGGATTG	900
TGTGCTGAGT	TTGATTGCGA	GCTTGTTT	GCCCTTTAG	AATTTTGCAG	CGACAATGCC	960
GCCATGATAG	GGCGATCAAG	CCTAGAAGCT	TATCAAAAAA	AGCGCTTTAT	CCCTTTAGAA	1020
AAAGCCGATA	TTTCGCCAAG	AACGCTGTTA	AAAAATTTTG	AG		1062

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279

AGGAATAATA	TGGCATACAA	ATATGATAGA	GACTTGGAAT	TTTTAAAGCA	ACTGGAATCT	60
AGTGATTAT	TGGATTTGTT	CGAGGTGCTT	GTTTTTGGTA	AAGACGGCGA	AAAAAGACAC	120
AATGAAAAAC	TCACAAGCTC	CATAGAATAC	AAAAGGCATG	GCGATGATTA	CGCTAAATAC	180

SUBSTITUTE SHEET (RULE 26)

911

GCAGAAAGAA	TCGCTGAAGA	GTTGCAATAC	TATGGGAGCA	ATAGTTTTGC	GAGTTTCATT	240
AAAGGTGAAG	GAGTCTTATA	CAAAGAGATT	TTATGCCGATG	TGTGCGATAA	ATTAAAGGTC	300
AATTACAACA	AGAAAAGTGA	AACGACTTTA	ATTGAACAAA	ACATGCTTTC	TAAAATCTTA	360
GAAAGAAGCC	TAGAAGAAAT	GGATGATGAA	GAAGTGAAAG	AAATGTGCGA	TGAATTGTCC	420
ATAAAAAACA	CGGACAATTT	GAACAGACAA	GCCTTAAGCG	CGGCGACTTT	AACGCTGTTT	480
AAAATGGGAG	GCTTTAAATC	TTATCAATTA	GCTGTCAATG	TTGCGAATGC	GGTTGCAAAA	540
ACCATTCTAG	GGCGTGGTTT	ATCGCTTGCG	GGCAATCAAG	TGCTTACAAG	AACTCTGAGC	600
TTTTTAACAG	GCCCTGTTGG	CTGGATCATT	ACAGGCGTAT	GGACAGCGAT	TGATATTGCA	660
GGGCCGGCTT	ATAGGGTAAC	CATACCGGCA	TGCATTGTGG	TCGCCACTTT	ACGCCTAAAA	720
ACGCAACAAG	CCAATGAAGA	TAAGAAGTCG	TTGCAATAG	AATCCGTT		768

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280

GTTATAATAT	TTTTGCTATT	GTTTTTTTTA	GGAAATAAAG	TTTTCAGTAT	TTATTTGCTT	60
TTAGAGTCAT	TTTTGTGGGT	AATATTGACC	ACTTGGTGTT	GTTTGGTCAT	GCATGAAGAT	120
CAGACACAAA	AAGACATGGA	ACAACCTTATC	AATGGGATTG	ATAGGATTAT	TAAAGCAAAT	180
TCCGGTAAAT	CTTTACACCA	AGAAACACAA	CAAGCAAATA	AAACCGATAA	AGCATGGGAT	240
TTGGCGGCTA	ATGTTTTTCT	CATTGGTCTG	GTTGTTTTGG	CTGTTTTTCA	CATGATCAAG	300
CGA						303

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281

SUBSTITUTE SHEET (RULE 26)

912

CGCGTGAAAA	AAGTAGAATC	CATGAATGTG	GTGCCTTTCA	TTGACATCAT	GCTTGTGTG	60
TTAGTGATCG	TGCTCACAAC	GGCGTCTTTT	GTGCAAACCT	CAAAGCTTCC	TATTAGCATT	120
CCTCAAGTGG	ATAAGGATAG	CACTGATTCT	AAAGATGTGT	TGGACAAAAA	ACAAGTTACG	180
ATCGCTATTT	CTAATAAGGG	TTCTTTTTAT	TTTGACGATA	AAGAAATCAG	CTTTGAAAAT	240
TTAAACACA	AGGTTTCCAC	TTGGCTAAA	GACCCCCTA	TTGTCTTGCA	AGGCGATAAG	300
AAAAGCAATT	TGGACAACTT	TATCAAAGTG	GTGGATTTAT	TGCAACTAAC	AATC	354

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282

CTACACAGAC	AGGCGCAAGT	TAGAATTAGC	CTTACACAAA	CGACGACTTT	AGTGGCCACT	60
ATTGGCTCAA	ACGCCCCCTA	TATCGGTCTT	TTAGGGACGG	TTATGGGGAT	CATGCTCACC	120
TTTATGGATT	TAGGCTCAGC	TTCTGGCATT	GACACTAAGG	CGATCATGAC	TAATTTAGCC	180
CTTGCTTTAA	AAGCGACCGG	CATGGGGTTA	TTGGTAGCGA	TCCCTGCGAT	TGTGATTTAT	240
AACTTGTTAG	TGAGAAAAAG	CGAGATTTTA	GTTACCAAAAT	GGGATATTTT	CCACCATCCG	300
GTTGATACGC	AATCCCATGA	GGTTTATAGC	AAAGCC			336

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283

AACCATAAGA	TTAGGGGTTA	TGAAAAACGC	ATGGCATTAG	ACAAAAGGAT	TTGGATGCAT	60
TTTGATCTTT	TGCCTTTTGT	GTTTATCATC	CCCTTGTTGG	TGGTTTCTTT	TTTGTTGATT	120

913

TTTGAGAGTA	GTGCGGTTTT	GAGCTTGAAG	CAAGGGGTTT	ATTATGCCAT	AGGGTTTCTT	180
CTCTTTTGGG	TAGTGTTTTT	TATCCCTTTC	AGGAAACTCG	ATCGGTGGCT	CTTTGCGCTT	240
TATTGGGCGT	GCGTTAATTT	ATTAGCGTTA	GTGGATTTTA	TGGGATCGAG	CAAGCTTGGA	300
GCGCAGCGAT	GGCTAGTCAT	TCCTTTCAC	TCTATCACCT	TACAGCCTAG	CGAGCCTGTG	360
AAAATCGCTA	TTCTTTTATT	GTTGGCGCGA	TTTGATCAAA	ATCAACCCAC	CTCCTTTT	417

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284

TTTTGTGGGA	CACTAAAGGC	ATTGAAGATA	AAGATTACCA	CGACACCATG	CAAAGCATT	60
AAAAAGAAAT	GGAAGATTCT	TTTAAACAC	TTGATGAAA	AGAAGCCATT	GATGTGGCGT	120
ATCTGTGCGT	TAAGGAGACT	TCTTCTAGGG	TTCAAGAGAG	AGAGAGAGTT	ATTAAGCTTC	180
GCTAAACATT	GGAATATCCC	AACGATTGTC	GTTTTCACAC	ACACTCAAGC	CGAAGCCGGC	240
GATGCGTTTT	TCCAAGAAAC	TAAAGGGATC	ATAGACGAAG	AATGGGGGTT	TAAAGGTTTT	300
GTCAGAGCCT	ATGTGAGGGT	CAATTCCGTT	GCCTTTTCAT	TTAGGGGGTT	GAAAGTCCCT	360
GTTGAAGGTT	TAGAAGAATT	GGTAGATGAA	ACGAAAAAAT	GCCTTTCAGA	CGCTGAAAAA	420
AATAAGAAAA	GGCATTTCCT	GAGTATTCAA	AGAGTTAAGA	TTCAAGAAAG	AAAACAGGCT	480
ATGATAGAGG	AATGTAAAC	CATTATCCAT	GTTGCATCAG	GCGCTGCAGG	AGTTGCTGGG	540
CTTATCCCCA	TACCTTTTAG	CGATGCGCTC	GCTATCGCAC	CCATTCAAGC	AGGGATGATC	600
TATAAAATGA	ATGACGCTTT	TGGAATGGAT	TTGGATAAAT	CTGTGGGCGC	GAGTTTGGTC	660
GCAGGATTGT	TAGGCGTAAC	CGCTGTCCGG	CAAGTGGGGA	GGACTCTCGT	TAATGGTTTC	720
CTTAAATTCA	TTCCTGTTGT	GGGGAGTGTT	GCAGGGGGCG	CAACCGCTGC	TGTTATCACA	780
GAAGGCATTG	GGTTTGCCTA	TTTGAAAGTG	CTAGAAAAGT	GCTTTAATGA	TGAGACGGGT	840
GAAGTCAATT	TGCCTGGTGA	AGTTGGCATG	ATCACTTCTC	TCTTTAAGGA	GAATTATCTC	900
AAC TTGGATA	CAATCAAAAA	ATTAAACCA				930

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

914

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285

ATGAGGTCTT	GGATGAAGAA	AAAATACTTC	ACGCTTTTAT	TGCAAAGTAG	TGTGGTATTA	60
GCGGTTTTTA	TAGGGTGTTC	TTCTACCAGG	AATCATACTT	TTTCAGCCCT	TAGTAATCAA	120
GAAAATACAG	ACGATAAGCT	CCCAGTGGTC	CATTCCATTA	AAACGATTAA	CGATGTGAGT	180
TCAGTGGGCT	TTGAATGGTC	TAAAGTCGCT	GACACTTATG	ACATTGACGG	GTTTGTTTTG	240
TATCGTTTGA	AAAAAGACTC	CAAGCTTAAA	AGAATCGCCA	CCATTAAAAA	CCCTTATGCG	300
ACCCACTATT	ATGATGAGGG	GTTAGAAACA	GAGAGTTCC	ACACTTACCA	ATTAGCCACC	360
TACAAGGGCG	ATAAAATTTT	CAAACTTTCA	GAACCCATTT	TAGTAAAAAC	CTCCTTTTATC	420
AATCCTGTAG	AAAGCGTGTT	TGCAAGCCTT	GAATACCCTA	AAAGCGTGAA	AGTCTTTTGG	480
AGCCCGCACC	CAAAATCCAG	CGTTTCTAAA	TACATCATTC	AAAGGCAGAA	TAAAGACGGC	540
AAATTTTAA	ATGTGGGGGC	TGTAAAAAAC	CGCTTATTCG	TGGAGTTTTT	TGATAAAGAT	600
TTAGAAGATG	GGCAAAAATA	CCGCTACCAA	ATCATCGCCG	AAAATTTTCAT	GGGGGATAAA	660
TCCAGGCCTA	GCGTGATAGT	GGAGGGGAAA	ACCAAAGACT	TGCCCCAAGA	AATCGCTAAT	720
GTTAGAGTGA	ATCAAAAACCT	CACACGACAA	ATTGAAATGA	GTTGGGATAA	ATCCCCAGAA	780
GAAGATGTGA	TAGCTTATCG	CATTTACGCT	TCCAATAACC	GCAACGATAA	ATACAAATTC	840
ATCGCTCAAA	CCACCAACAC	TTCTTATGTG	GATAAGATAG	AAAAAGACAA	TCTCACTCGT	900
TATTATAAAG	TCGTCGCCGT	AGATAAAACG	CATCTTGAAG	GGGCGTTACC	CAAAGAGCCT	960
GCCATGGGTG	AAACCTCTGA	TAGGCCTGAA	GCCCCATCA	TCTACTAAAG	GACTATTCAA	1020
GACTCTTCGG	CCTTGATCCA	ATGGGAAAAC	AACCCAAGCC	CTAAAATAGC	CACCTATGCG	1080
GTGTATCGTT	TTGAAGCCAA	CTCCAAAACC	CCTTTGCGTT	TTGGGAATAT	CACACAAAAC	1140
CAGTTCGTGG	ATAAGGACAT	GAAAGTGGGC	GTGGCTTATC	GCTATCAGGT	GGTGAGCGTG	1200
GATAAAGATG	GTTTAGAGTC	GCACCCAAGC	AAAGAAGTGC	GTTTGTTTTT	AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286

CTTAAAAACA	CTCTAAAAGG	GTTATTGATG	CTGGATTTTG	ATTIGGTTCT	TTTTGGCGCG	60
ACTGGGGATT	TAGCCATGCG	AAAGCTCTTT	GTTTCGCTTT	ATGAAATTTA	TATTCATTAT	120
GGTTTTAAAA	ACGATTCTAG	GATTATCGCA	TCGGGGCGTA	AGGAGCTATC	CAATGAAGAG	180
TTTTTAGCGC	TTCTTTGTGA	AAAAACACAA	CTGCATTCAA	GAGAAAAGGG	TGAGGAATTT	240
TTAACCATA	TCAGTTATTT	GCGCGTCCGT	TTGGATAACC	CTAAAGACTT	TGAAGAAATG	300
AGTAAATCG	GTCAAAACAA	TAAGCCCTTG	ATTTTCTACT	TTTCTATCTC	CCCTAGTTTT	360
TTTGCAACGA	CCGCTCAAAA	TTTAGCCCAA	AACGCGCTCA	ATCACGCTAA	CACTCGTTTG	420
ATTCTAGAAA	AGCCTTTAGG	GCATGATTTA	AAGACTTGTA	AAGAGATTTT	CCAAAGCATT	480
AGCGCTTTTT	TTAAAGAAGA	ACAAATTTTT	AGAATCGATC	ATTATTTAGG	GAAAAAGGGC	540
GTTCAAAATA	TCCTTGAATT	GCGCCTGAAT	AACCTTATCT	TAAACATTTT	ATGGGATCAA	600
ATCAGCGCGG	TTGAAATCTG	CGTGTATGAG	ACTTTAGGGG	TGGAAGAAAG	GGGCGAATTT	660
TACGATAAAA	TCGGGGCTTT	AAGGGATATG	GTTCAAAACC	ATCTCTTGCA	AGTTTTTATCC	720
CTTATCGCTA	CAGATTTACC	CAACGATTTA	AAAGATTTGA	GGCAAGAAAA	ATCAAAGTTT	780

915

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287

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GGCATGGTTA AACACTATCT TTTCATGGCG GTTTCGCAGG TCTTTTTCTC CTTCTTTTAA      60
GTGCTGTTTT TTATCTCTTC CATTGTGTTA TTAATCAGTA TTGCAAGCGT AACGCTCGTG      120
ATTAAAGTGA GCTTTTTTGA TCTGGTGCAA CTCTTTTTGT ATTCCTTGCC AGGAACCACT      180
TTTTTTATTT TGCCGATCAC TTTTTTTGCG GCTTGCCTT TGGGGCTTTC AAGGCTTAGC      240
TATGACCATG AATTGTTAGT GTTTTTCTCT TTAGGGGTTT CGCCTAAAAA AATGACTAAA      300
GCGTTTGTGC CTTTAAGTTT GTTAGTGAGC GCGATTTTAT TAGCGTTTTT GCTCATCTTA      360
ATCCCCACTT CTAAGAGCGC TTATTACGGG TTTTTCGCTC AAAAAAAGA CAAGATTGAC      420
ATTAACATCA GAGCGGGTGA ATTCCGGCAA AAATTAGGCG ATTGGCTCGT GTATGTGGAT      480
AAGACTGAAA ACAATTCTTA TGATAATTG GTGCTTTTTT CTAATAAAG TCTCTCTCAA      540
GAAAGCTTTA TTTTGGCTCA AAAAGGCAAT ATCAACAATC AAAACGGCGT GTTTGAATTG      600
AATTGTGATA ACGGGCATGC GTATTTCACT CAAGGCGATA AAATGCGTAA GGTGATTTT      660
GAAGAATTGC ATTTGCGCAA CAAGCTCAAG TCTTTCATT CTAATGATGC GGCTTATTTG      720
CAAGGCACGG ATTATTTGGG TTATTGGAAA AAAGCCTTTG GTAAAAACGC TAATAAAAAT      780
CAAAAACGCC GTTTTCTCA AGCGATCTTA GTTTCCTTGT TCCCTTTAGC GAGCGTGTTT      840
TTAATCCCCT TATTTGGCAT CGCCAACCCG CGATTCAAAA CGAATTGGAG TTATTTCCAT      900
GTCCTTGGAG CGGTTGGGGT TTATTTTITA ATGTTGCATG TGATTTCTAC GGATTTGTTT      960
TTGATGACCT TTTTCTTCCC CTTTATTTGG GCGTTTATTT CTTATTTATT GTTTAGAAAA     1020
TTCATTTTAA AGCGTTAT

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(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288

ATCTTAATTG	AAGGGGTGTT	CATGCCCTAAG	CATTCTTTAG	AACAAATCAA	AGAAAAAATT	60
ACAGAGCGTA	GCAAAAAAAC	CAGAGAGCTT	TATTTAGAAA	ATACCTTCAA	CCCTAAAAAC	120
CAGCCCAAGA	TTGAGAGCTT	GGGTTGCGCG	AATATTGCGC	ATGTTACGGC	GAGCATGCCA	180
GAGCATTTAA	AAATGCCCTT	AGGTTCGCAT	AAAAGAAAGC	ATTTTGCGAT	TATCACCGCT	240
TATAATGACA	TGCTTTTCAGC	CCACCAACCT	TTTAAAAATT	ACCCTGATCT	GATTAAAAAA	300
GAGTTGCAAG	AGCATAACGC	CTATGCGAGC	GTGCTAGTG	GGGTGCCAGC	GATGTGTGAT	360
GGTATCACGC	AAGGTTATGA	GGGAATGGAA	TTGAGCTTGT	TTAGTAGAGA	TGTGATCGCA	420
TTAAGCACCG	CCGTAGGGTT	AAGCCATAAT	GTTTTTGACG	GGGCGTTTTT	TTTGGGCGTG	480
TGCGATAAAA	TTGTGCCAGG	CTTGCTCATA	GGAGCGTTAA	GCTTTGGGAA	TTTAGCGAGC	540
GTGTTTGTGC	CAAGCGGGCC	TATGTGTAGC	GGGATAGAAA	ATTATAAAAA	AGCCAAAGCG	600
CGCCAAGATT	TTGCAATGGG	AAAGATCAAC	AGAGAAGAGC	TTTTAAAGT	GGAAATGCAA	660
AGCTATCATG	ATGTGGGCAC	TTGCACTTTT	TATGGCACGG	CTAATCTTAA	TCAAATGATG	720
ATGGAGTTTA	TGGGGTTGCA	TGTGGCCAAT	TCAGCTTTTA	TCAACCCCTA	CAACCCCTTA	780
CGAAAGGTTT	TAGTAGAAGA	GAGCGCTAAA	AGATTAGCGA	GCGGGAAAGT	CCTGCCTTTA	840
GCCAAACTCA	TTGATGAAAA	AAGCATCTTT	AACGCTCTTA	TAGGCTTAAT	GGCAACAGGG	900
GGTTCTACTA	ACCACACTTT	GCAATTGATC	GCTATCGCTA	GATCTTGTGG	GGTGATCCTC	960
AATTGGGACG	ATTTTGACGC	AATCTCTAAT	CTCATACCCC	TTTTAGCTAA	AGTCTATCCT	1020
AACGGATCAG	CGGATGTGAA	CGCTTTTGAA	GCGTGTGGGG	GCTTAGCGTT	TGTGATCAAA	1080
GAATTGCTAA	AAGAGGGGCT	TTTATTTGAA	GACACTCATA	CCATTATGGA	TACAGAAACG	1140
CAAAAAGGCA	TGCAAAATTA	CACCAAAACC	CCCTTTTITAG	AAAACGACCA	ATTGGTGTAT	1200
AAAGACGCTG	TTAGTCATAG	CCTGAATACG	GATATTTTAC	GCCCTGTTAG	TGAGCCTTTT	1260
GCCGCTAATG	GAGGGCTTAA	AATCTTAAAA	GGTAATTTGG	GGCGGGCCGT	GATTAAAATC	1320
TCAGCCATTA	AAGATGAGCA	TAGGAAAGTT	AAAGCTAGAG	CGATTGTTTT	TAAAACCCAA	1380
AGCGAATTTT	TAGAACGCTT	TAAAAATAAA	GAATTAGAAA	GGGACTTTGT	GGCGGTCTTG	1440
CTTTTCCAAG	GCCCTAAGTC	TAACGGCATG	CCAGAATTGC	ACAAACTCAC	CACGAATTTA	1500
GGGGCTTTGC	AGGATATGGG	CTACAAGGTC	GCGCTCGTTA	CGGATGGGCG	CATGAGTGGG	1560
GCGAGCGGGA	AAGTGCCTAG	CGCGATCCAT	TTAAGCCCTG	AGGGGGCGTT	AAACGGGGCG	1620
ATCATTAAGA	TTAAAGATGG	CGAATTGATA	GAATTAGACG	CTCCTAATAA	CGCCTTGAAT	1680
GTGCTTGAAG	AGGATTTTGA	AAAGAGAGGC	ATCAACCCCT	TGTTTTTAGA	AACCTTAGAA	1740
AAATTAGAAA	AGCCTACTTT	TGGGTGGGTT	AGGGAATTAT	TTACAAGCTT	GAGATTGAAT	1800
GCCAATACCG	CTGAAGAGGG	TGGCATGAGT	TTTGGCATAA	AGGTA		1845

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289

AAATATAAAG	GAGATAAAAT	GCAAGATAAA	ATAATAGAAA	TTTTACAAAT	CAGCCCCATT	60
GTCCCTGTGG	TGGTGGTTGA	GAATATAAAA	GACGCTGTGC	CTTTAGCGCA	AAGCCTGATA	120
GAGGGGGGTA	TTCCAATCAT	AGAAGTAACT	TTGCGATCAA	ACTGTGCTTT	AGAGGCCATA	180
GAGCTTATCG	CTAAGAATGT	GCCAAAAATG	CGCGTGGGTG	CTGGCACGAT	ACTCAATCTC	240
ACTCAATTAG	AGCAGGCTCA	AAATAGGGGG	GCAGAGTTTT	TGATTAGCCC	GGGTCTTACG	300
ATTAAGCTTT	TAGAACACGC	AAAGAAAAAA	GACATGCCTT	TAATACCTGG	GGTTTCTAGC	360

917

AGCAGTGAAG TCATGCAAGC TTTAGAATTG GGTATAACG CTTTGAAATT TTTCCCGGCG	420
GAGTATTGCG GGGGCGTTAA ACTTTTAAAC GCTTTTAAAC GCCCTTTTAA AGGGGTGAAA	480
TTTTGCCCA CTGGGGGGAT TAGCGCAGAT AACATGCGTT CTTATTGGC TTTAGAAAAC	540
GTTGTGTGCG TGGGGGGGAG CTGGCTTACC CCTAAAGATT TAATTCAAAA CAAAGAGTGG	600
GATAAGATCA CAGAAATTG CAAGAGAGCG TTAGCTTTAA GA	642

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290

AATACCGCTA TTGTATCGTT TTTATGGTTT GCTTATGTTT CTATAGGTTT AACTAATTTT	60
GTAGCTGTTG GTTATATGGT ATCGTTGCTT GCGCGGCTTA AACGCACCCC TTGCACTAAT	120
CGCTTTTATC TTAAAGCACT ACTATTGCT ATATTCTATC ATGCAGTAAA TAATTTTCTA	180
ACGCAATGCC CGCCCCATCA AGTCCGGGAG TTTTTCAT CACGACATGC ACAGGGATGG	240
AAGCGAGAAA CGCTCCCATG CGCCCTTCG TTTCAAACG CGCTC	285

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291

AAGAAACGC CCCCTATTCT CTGCCGATTG CTCGGATTTT ACATTCTAAA AAAGTTACCA	60
CAGAGGTGTT TTATGCCAAA AACTGAAACT TACCCAAGAC TATTAGCCGA TATTGGCGGC	120
ACAAATGCCG GTTTTGGTTT GGAAGTCGCC CCACGACAGA TTGAATGCGT TGAAGTCTTG	180
AGGTGCGAAG ATTTTGAGAG CTTGAGTGAT GCGGTGCGAT TTTACCTTTC TAAATGCAAA	240
GAAAGCCTTA AACTGCACCC TATTATGGC TCTTTTGCTG TGGCTACGCC CATTATGGGG	300

918

GATTTTGTCC	AAATGACGAA	CAACCACTGG	ACTTTTCTA	TTGAAACGAC	ACGGCAATGT	360
TTGAATTTAA	AAAACTGCT	TGTCATCAAT	GATTTTGTG	CGCAAGCCTA	TGCCATTAGC	420
GCGATGCAAG	AAAACGATCT	AGCCCAAATA	GCGGGGATTA	AGTGTGAAAT	CAACGCTCCT	480
AAAGCGATT	TAGGGCCAGG	AACCGGGCTT	GGGTAAGCA	CTCTTATCCA	AAACAGCGAT	540
GGCTCTTTGA	AAGTCTTGCC	CGACGAAGGT	GGGCATGTGA	GCTTTGCCCC	TTTGTATGAT	600
TTAGAAATTT	TAGTGTGGCA	ATACGCCCCG	TCTAAATTCA	ACCATGTGAG	CGCGGAAAGG	660
TTTTTGAGCG	GTAGCGGCCT	GGTGTGATT	TATGAAGCCC	TGCTCTAAACG	CAAAGGCTTA	720
GAAAAAGTGG	CGAAGTTGAG	CAAGGCTGAA	TTAACCCAC	AAATCATTAG	CGAACGCGCT	780
TTGAATGGGG	ATTACCCTAT	ATGCCGATTG	ACCTTGGACA	CTTTTGTCTC	CATGCTTGCC	840
ACGCTCGCTG	CTGATGTGGC	TCTCACTTTG	GGGGCTAGAG	GGGGGGTGTA	TTTGTGTGGG	900
GGGATTATCC	CACGATTCAT	TGATTATTTT	AAAACCTCGC	CCTTTAGAGC	GCGTTTTGAA	960
ACGAAAGGGC	GCATGGGAGC	GTTTCTCGCT	TCCATCCCTG	TGCATGTCGT	GATGAAAAAA	1020
ACTCCCGGAC	TTGATGGGGC	GGGCATTGCG	TTAGAAAATT	ATTTACTGCA	TGATAGAATA	1080

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292

TCCAGGGAC	TGATTTTGA	TAAAAAGAAA	CAAAAATTTC	TAAAAGATTT	TAAAGCAGGA	60
GAATTATGT	ATCAATCCCA	TTTCAAACCA	TTAGTAGAAT	TTATAGCCGA	AGAGCTTCTT	120
AAAACTCGC	GCGCCAAAAT	CATTCAATCA	AACTGCAATA	AAGCCTTAAA	AGTGGTAGAA	180
GAATTACAA	ATACGATAAA	AACCACGATT	GAAAAACAGA	TCAATCCAGG	GATGAAAGAA	240
ACACAAGACC	CCCAACAAGA	AGCTCGCTTT	AATTTGGATC	GTTCTACAGA	TAAATTTATA	300
TCAGATTTGG	AAAAATCAGC	GTTCAAGAAA	ATCAATCAAT	TCGAATTTAA	TTTLAGAAAA	360
GAAATGCATG	AACGCATTGA	AAGAGGTATT	GGAAATAATG	AATGTAAAGA	AATTTTGGC	420
AATGAACTCA	AACAAAGAAA	GACAAAATTG	ATTGAAGACA	TAGAACGGCG	GTTCAAAGAA	480
TGCGAGGAAC	AATTCCTGG	AAGTGTAGGA	AAAAATATTG	AACAACCTGA	AGAAAGAGTT	540
AAAGATTCTC	TAGCGATTAT	AAAACGCATC	AATAACCTTG	GTCTTAATCC	TAATTCTAAT	600
TTTAATATGG	ATAGCGGCAT	TGATACAATA	GGCTTATTTA	GTTCAATAGG	AGGTTTGGTG	660
TTGCTTCTAT	TGACGCCTGT	AGTAGGTGAG	TTTGCGTTAA	TTGCAGGAGT	GGGTTTAGCA	720
TTAGTGGGGG	TAGGTAAATC	AATATGGAGT	TTTTTTGATT	CAGATTATAA	AAAATCCCAA	780
CAAAGAAAAG	AAGTGGATAA	GAATTTACAT	CAAATTTGCG	AAAAAATTGT	GCAGGATGTG	840
AAAAGCCGCA	TTGAAAGTTA	TAAAAATGGT	GCATTGGGAA	TGATTGAAGA	ACTCAACGCC	900
GGTTTTAACA	AACTTGTTGA	TCATTACGAA	CGCATGAAAA	GACAATTGGA	AGAAGCCCAT	960
GAAAAACTAG	GATACATCTA	TAATAGTATC	CATCTTACAA	TATCTAACCG	CCGCATACAA	1020

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

919

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293

AGTGCCTTAT	GGCACAAAGA	CCCCACCACG	ATCAAGCAAT	TTGGCTTAGA	GGCTTTGGAT	60
TTTTTCAAAC	CGCATGAGAT	TGAATTATTG	ATTGTGGCAT	GCAACACCGC	GAGCGCTCTG	120
GCTTTAGAAG	AGATGCAAAA	GTATTCTAAA	ATCCCTATTG	TGGGCGTGAT	TGAGCCAAGC	180
ATTTTAGCGA	TCAAGCGGCA	AGTGGAAGAT	AAAAACGCCC	CTATTTTAGT	GCTAGGGACA	240
AAAGCGACGA	TTCAATCCAA	CGCCTATGAC	AACGCCCTGA	AACAACAAGG	CTATTTGAAC	300
ATTTGCGATT	TAGCTACTTC	TCTTTTGTG	CCTTTGATTG	AAGAAAGTAT	TTTAGAGGGC	360
GAATTGTTAG	AAACTTGCA	GCATTATTAT	TTCCTCCCT	TAGAGATTTT	ACCCGAAGTG	420
ATCATTTTAG	GTTGCACGCA	TTTTCCCTTA	ATCGCTCAAA	AAATTGAGGG	CTATTTTCATG	480
GGGCATTTTG	CCCTTCCAAC	GCCCCCCTA	CTCATCCATT	CGGGCGATGC	TATTGTAGAA	540
TATTGCAAC	AAAAATACGC	CCTTAAAAAC	AATGCATGCA	CATTCCCTAA	AGTGAATTT	600
CATGCGAGCG	GCGATGTGAT	CTGGCTAGAA	AGACAAGCTA	AAGAATGGCT	CAAATTG	657

(2) INFORMATION FOR SEQ ID NO:1294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294

GGTATTAAAC	TAGGGGGTAT	TAACATGGCA	GGCACACAAG	CTATATATGA	ATCATCTTCT	60
GCAGGATTCT	TATCGCAAGT	CTCCTCAATC	ATCTCAAGCA	CAAGTGGTGT	CGCAGGGCCA	120
TTTGCAGGAA	TAGTAGCGGG	CGCTATGACA	GCAGCGATTA	TTCTATTGT	TGTGGGATTT	180
ACTAATCCGC	AAATGACCGC	TATCATGACC	CAATACAATC	AAAGCATCGC	TGAAGCTGTA	240
AGCGTGCTA	TGAAAGCCGC	TAACCAACAA	TACAGCCAAT	TGTATCAAGG	TTTAAACGAT	300
CAAAGCATGG	CTGTGGGAAC	AATATCT				327

(2) INFORMATION FOR SEQ ID NO:1295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

920

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295

TTTCAATTTG	AAAGGAAACG	CATGAAATTT	TTTACAAGAA	TCACGTACAG	CTACAAGAAA	60
GTTGTAGTAA	CTTTAGGGCT	AGTGGTAACA	ACCAATCCTT	TAATGGCGGT	CACCAGTCCT	120
GCAACAGGCG	TTACTGAGAC	TAAAAGTTTG	GTTATTCAGA	TCATTTCTGT	TCTAGCGATC	180
GTAGGTGGTT	GCCTTTTAGG	GGTCAAAGGC	ATAGCAGATA	TTTGGAAAAT	CTCTGATGAC	240
ATCAAAGAG	GTCAAGCGAC	TGTTTTTGCT	TACGCGCAAC	CCATAGCTAT	GTTAGCGGTG	300
GCAGGTGGCA	TTATCTATTT	GAGCACTAAG	TTTGGCTTCA	ATATTGGCGA	GAGTGGAGGA	360
GCTAGC						366

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2973 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296

AGCGGTATAT	CTATAAAGAG	AGGGGTGTTT	GTGGCAAGCA	AACAAGCTGA	CGAACAAAAA	60
AAGCTAGTTA	TAGAGCAAGA	GGTTCAAAAG	CGGCAGTTTC	AAAAAATAGA	AGAACTTAAA	120
GCAGACATGC	AAAAGGGTGT	CAATCCCTTT	TTTAAAGTCT	TGTTTGATGG	GGGGAATAGG	180
TTGTTTGGTT	TCCCTGAAAC	TTTTATTTAT	TCTTCTATAT	TTATATTGTT	TGTAACAATT	240
GTATTATCTG	TTATTCTTTT	TCAAGCCTAT	GAACCTGTTT	TGATTGTAGC	GATTGTTATT	300
GTGCTTGTAG	CTCTTGGAAT	CAAGAAAGAT	TACAGGCTTT	ATCAAAGAAT	GGAGCGAGCG	360
ATGAAATTTA	AAAAACCTTT	TTTGTTTTAAG	GGCGTGAAAA	ACAAAGCGTT	CATGAGCATT	420
TTTTCCATGA	AGCCTAGTAA	AGAAATGGCT	AATGACATCC	ACTTAAATCC	AAACAGAGAA	480
GACAGGCTTG	TGAGCGCTGC	AAACTCCTAT	CTAGCGAATA	ACTATGAATG	TTTTTTAGAT	540
GATGGGGTGA	TCCTTACTAA	CAACTATTCT	CTTTTAGGCA	CAATCAAATT	GGGGGGCATT	600
GATTTTTTAA	CCACTTCCAA	AAAAGATCTC	ATAGAGTTAC	ACGCTTCTAT	TTATAGCGTT	660
TTTAGGAATT	TTGTTACCCC	TGAATTCAAA	TTTTATTTTC	ACACTGTATA	AAAGAAAATC	720
GTTATTGATG	AAACCAATAG	GGATTATGGT	CTTATTTTTT	CTAATGATTT	CATGCCAGCC	780
TATAATGAGA	AGCAAAAGAG	AGAAAGTTTT	TATGATATTA	GTTTTTATCT	CACCATAGAG	840
CAAGATTATG	TACACACTCT	CAATGAACCC	GTTATGAATA	AAAAGCATTT	TGCAGACAAT	900
AATTTTGAAG	AGTTTCAAAG	GATTATTAGA	GCCAAGCTTG	AAAACTTCAA	AGATAGGATA	960

SUBSTITUTE SHEET (RULE 26)

921

GAGCTCATAG	AAGAGCTACT	GAGTAAATAC	CACCCCACTA	GATTAAAAGA	ATACACTAAA	1020
GATGGCATT	TTTACTCCAA	ACAATGCGAA	TTTTACAATT	TTCTTGTGGG	AATGAATGAA	1080
GCCCCTTTT	TTTGCAACAG	AAAAGACTTG	TATCTCAAGG	AAAAAATGCA	TGGTGGGGTG	1140
AAAGAAGTTT	ATTTTGCCAA	TAAGCATGGA	AAAATCTTAA	ATGACGATTT	GAGTGAAAAA	1200
TATTTTAGCG	CTATTGAGAT	CAGTGAATAC	GCCCCTAAAT	CACAGAGCGA	TTTGTTTGAT	1260
AAAATCAACG	CTCTAGACAG	CGAATTTATC	TTTATGCATG	CTTATTTCGC	TAAAAACTCA	1320
CAAGTTTTAA	AGGACAAACT	AGCTTTCACC	TCTAGAAGGA	TTATTATTAG	TGGAGGCTCC	1380
AAAGAGCAA	GCATGACTTT	GGGTGCTTG	AGCGAATTAG	TGGGTAATGG	TGATATTACG	1440
CTAGGCAGTT	ATGGTAATTC	TTTAGTGCTG	TTTGCTGATA	GCTTTGAAAA	AATGAAACAA	1500
AGCGTTAAGG	AATGCGTCTC	TAGTCTTAAC	GCTAAAGGTT	TTTTAGCCAA	CGCAGCGACT	1560
TTCTCTATGG	AAAATTACTT	TTTTGCCAAA	CATGCTCTTT	TTATCACGCT	TCCTTTTATT	1620
TTTGATGTAA	CTTCTAACAA	TTTTGCTGAT	TTCATAGCGA	TGAGAGCGAT	GAGTTTTGAT	1680
GGCAAAGAAG	ACAATAACGC	TTGGGGCAAT	AGCGTGATGA	CGTTAAAAAG	CGAGATCAAT	1740
TCGCCTTTTT	ATTTGAACTT	CCCATGCCCC	ACTGATTTTG	GTTTCAGCTTC	AGCAGGACAC	1800
ACTTTGATAC	TTGGCTCAAC	CGGTCAGGT	AAGACAGTGT	TTATGTCCAT	GACTCTAAAC	1860
GCTATGGGCG	AATTTGCCTA	TAATTTTCCT	GCTAATATCA	GCAAAGACAA	GCAAAGCTC	1920
ACTATGGTTT	ATATGGATAA	AGATTATGGC	GCTTATGGGA	ATATTGTGTC	AATGGGTGGG	1980
GAGTATGTCA	AGATTGAGCT	AGGGACAGAT	ACAGGATTAA	ATCCTTTTGC	TTGGGCAGCT	2040
TGTGTGCAAA	AAACAAATGC	AACAATGGAG	CAAAAACAAA	CAGCTATTTC	TGTTGTCAAA	2100
GAGCTTGTTGA	AAAACCTAGC	AACTAAAAGC	GATGAAAAAG	ATGAAAATGG	CAACAGCATC	2160
TCTTTTAGCC	TAGCAGATTTC	TAATACGCTT	GCAGCGGCAG	TAACCAACCT	TATCACAGGA	2220
GATATGAACC	TAGATTATCC	TATCACTCAA	CTTATTAATG	CTTTCGGGAA	AGACCACAAT	2280
GATCCTAATG	GGCTTGTGCG	GCGATTAGCG	CCTTTTGTGA	AATCAACCAA	TGGTGAATTT	2340
CAATGGCTTT	TTGACAATAA	AGCAACAGAT	CGCTTAGATT	TTTCAAAAAC	GATTATTGGC	2400
GTTGATGGGT	CAAGTTTCTT	AGACAATAAT	GACGTTTCGC	CTTTTATTTG	TTTTTACCTT	2460
TTGCTCGTA	TCCAAGAAGC	AATGGATGGG	CGTAGATTTG	TCTTAGATAT	TGATGAAGCG	2520
TGGAAATATT	TAGGCGATCC	AAAGGTCGCT	TATTTTGTGA	GAGACATGCT	AAAAACTGCA	2580
AGGAAAAGAA	ACGCTATTGT	TAGACTTGCG	ACTCAAAGCA	TCCTGATCT	TTTGGCTTGC	2640
CCTATTGCTG	ATACGATTAG	AGAACAATGC	CCTACAAAAG	TTTTTTTGGG	AAACGATGGG	2700
GGTAATCTTT	CTGATTACCA	AAGATTAGCC	AATGTTACAG	AAAAAGAATT	TGAAATCATC	2760
ACTAAGGGGC	TGGATAGGAA	AATCCTCTAC	AAACAGGATG	GAAGCCCTAG	CGTTATCGCT	2820
AGTTTAAATT	TGAGAGGCAT	TCCTAAAGAA	TATTTGAAAA	TTTTATCCAC	AGATACTGTA	2880
TTTGTCAAAG	AAATTGACAA	GATTATCCAA	AACCATAGTA	TCATAGATAA	ATATCAGGCC	2940
TTGAGGCAAA	TGTATCAACA	AATAAAGGAG	TAT			2973

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297

TTTTTAGTAG	CATTAATGAT	ACCAAATTTA	GATATAGAAG	GAGAAACAAT	GACTAACGAA	60
GCCATTAACC	AACAACCACA	AACCGAAGCG	GCTTTTAAAC	CGCAGCAATT	TATCAATAAT	120
CTTCAAGTGG	CTTTTATTAA	AGTTGATAAT	TTGTTCGCTT	CATTTGATCC	TAATCAAAAA	180
CCAATCGTTG	ATAAGAATGA	TAGGGATAAT	AGGCAAGCTT	TTGAGAAAAA	CTCGCAGCTA	240
AGGGAGGAAT	TCGCTAATAA	AGCGATCAAA	AATCCTACCA	AAAAGAATCA	GTATTTTTC	300
AGCTTTATCA	GTAAGAGCAA	TGATTTAATC	GACAAAGACA	ATCTCATTGA	TACAGGTTCT	360

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922

TCCATAAAGA	GCTTTTCAGAA	ATTTGGGACT	CAGCGTTACC	AAATTTTAT	GAATTGGGTG	420
TCCCATCAAA	ACGATCCGTC	TAAAAATCAAC	ACCCAAAAAA	TCCGAGGTTT	TATGGAAAAT	480
ATCATACAAC	CCCCTATCTC	TGATGATAAA	GAGAAAGCGG	AGTTTTTGAG	GTCTGCCAAA	540
CAAGCTTTTG	CAGGAATTAT	CATAGGAAAC	CAAATCCGAT	CGGATCAAAA	ATTCATGGGC	600
GTGTTTGATG	AATCTTTGAA	AGAGAGGCAA	GAAGCAGAAA	AAAAATGGAGA	GCCTAATGGA	660
GATCCTACTG	GTGGGGATTG	GCTTGATATT	TTTTTATCAT	TTGTGTTTAA	CAAAAAACAA	720
TCTTCCGATC	TCAAAGAAAC	GCTCAATCAA	GAACCAGTTC	CTCATGTCCA	ACCAGATGTA	780
GCCACTACCA	CCACTGACAT	ACAAAGCTTA	CCGCCTGAAG	CTAGGGATTT	GCTTGATGAA	840
AGGGGTAAAT	TTTCTAAATT	CAGTCTTGGC	GATTAGAAC	TGTTAGATGT	TGAGGGAGTC	900
GCTGACATTG	ATCCTAATTA	CAAGTTCAAC	CAATTATTGA	TCCACAATAA	CGCTCTGTCT	960
TCTGTGTTAA	TGGGGAGTCA	TAATGGCATA	GAACCTGAAA	AAGTTTCATT	GTTGTATGGA	1020
AACAATGGTG	GTCTTGAAGC	TAGGCATGAT	TGGAACGCCA	CCGTGGGTTA	TAAAAACCAA	1080
CGAGGCGACA	ATGTGGCTAC	ACTCATTAAT	GTGCATATGA	AAAAATGGCAG	TGGGTAGTCT	1140
ATAGCAGGTG	GTGAGAAAGG	GATTAACAAC	CCTAGTTTTT	ATCTCTACAA	AGAAGACCAA	1200
CTCACAGGCT	CACAACGAGC	ATTGAGTCAA	GAAGAGATCC	AAAACAAAGT	GGATTTTCATG	1260
GAATTTCTTG	CACAAAATAA	TGCTAAATTA	GACAACCTGA	GCAAGAAAGA	GAAAGAAAAA	1320
TTCCAAAATG	AGATTGAAGA	TTTTCAAAAA	GACTCTAAGG	CTTATTTAGA	CGCCCTAGGG	1380
AATGATCACA	TTGCTTTTGT	TTCTAAAAAA	GACAAAAAAC	ATTTAGCTTT	AGTTGCTGAG	1440
TTTGGTAAATG	GGGAATTGAG	CTACACTCTC	AAAGATTATG	GGAAAAAAGC	AGATAAAGCT	1500
TTAGATAGGG	AGGCAAAAAAC	CAGTCTTCAA	GGTAGCCTAA	AACATGATGG	CGTGATGTTT	1560
GTTGATTATT	CTAATTTCAA	ATACACCAAC	GCCTCCAAGA	GTCTTGATAA	GGGTGTGGGT	1620
GCTACGAATG	GCGTTTCCCA	TTTAGAAGCA	GGCTTTAGCA	AGGTAGCTGT	CTTTAATTTG	1680
CCTAATTTAA	ATAATCTCGC	TATCACTAGT	GTGTAAGGC	AGGATTTAGA	GGATAAACTA	1740
ATCGCTAAAG	GATTGTCCCC	ACAAGAAGCT	AATAAGCTTG	TCAAAGATT	TTTGAGCAGC	1800
AACAAAGAAT	TGGTTGGAAG	AGCTTTAAAC	TTCAATAAAG	CTGTAGCTGA	AGCTAAAAAC	1860
ACAGGCAACT	ATGACGAGGT	GAAACAAGCT	CAGAAAGATC	TTGAAAAATC	TCTAAAGAAA	1920
CGAGAGCGTT	TGGAGAAAGA	TGTAGCGAAA	AAATTTGAGA	GCAAAAGCGG	CAACAAAAAT	1980
AAAATGGAAG	CAAAATCTCA	AGCTAACAGC	CAAAAAGATG	AGATTTTTCG	GTTGATCAAT	2040
AAAGAGGCTA	ATAGGGATGC	AAGAGCAATC	GCTTACGCTC	AGAATCTTAA	AGGCATCAAA	2100
AGGGAATTGT	CTGATAAACT	TGAAAATATC	AACAAGGATT	TGAAAGACTT	TAGTAAATCT	2160
TTTGATGAAT	TCAAAAATGG	CAAAAATAAG	GATTTTCAGCA	AGGCAGAAGA	AACACTAAAA	2220
GCCCTTAAAG	GCTCGGTGAA	AGATTTAGGT	ATCAATCCAG	AATGGATTTT	AAAAGTTGAA	2280
AACCTTAATG	CAGCTTTGAA	TGAATTCAAA	AATGGCAAAA	ATAAGGATTT	CAGCAAGGTA	2340
ACGCAAGCAA	AAAGCGACCT	TGAAAATTCC	ATTAAAGATG	TGATCATCAA	TCAAAAAGATA	2400
ACGGATAAAG	TTGATAATCT	CAATCAAGCG	GTATCAGTGG	CTAAAGCAAC	GGGTGATTTT	2460
AGTGGGGTAG	AGCAAGCGTT	AGCCGATCTC	AAAAATTCTT	CAAAGGAGCA	ATTGGCTCAA	2520
CAAGCTCAAA	AAAATGAAGA	TTCAATACT	GGAAAAAATT	CTGCACTATA	CCAATCCGTT	2580
AAGAATGGTG	TAAACGGAAC	CCTAGTCGGT	AATGGGTTAT	CTAAAGCAGA	AGCCACAAC	2640
CTTTCTAAAA	ACTTTTCGGA	CATCAAGAAA	GAGTTGAATG	CAAAACTTGG	AAATTTCAAT	2700
AACAATAACA	ATAATGGACT	CGAAAACAGC	ACAGAACCCA	TTTATACTCA	AGTTGCTAAA	2760
AAGGTAAAAG	CAAAAATTGA	CCGACTCGAT	CAAATAGCAA	GTGTTTGGG	TGATGTAGGG	2820
CAAGCAGCGA	GCTTCCTTTT	GAAAAGGCAT	GATAAAGTTG	ATGATCTCAG	TAAGGTAGGG	2880
CTTTTCAGCTA	ACCATGAACC	CATTTACGCT	ACGATTGATG	ATCTCGGCGG	ACCTTTCCCT	2940
TTGAAAAGGC	ATGATAAAGT	TGATGATCTC	AGTAAGGTAG	GGCTTTCAAG	GGAGCAAAAA	3000
TTGACTCAGA	AAATTGACAA	TCTCAACCAG	GCGGTATCAG	AAGCTAAAGC	AAGTCATTTT	3060
GACAACCTAG	ATCAATGAT	AGACAAGCTC	AAAGATTCTA	CAAAAAAGAA	TGTTGTGAAT	3120
CTATATGTTG	AAAGTGCAAA	AAAAGTGCCT	ACTAGTTTGT	CAGCGAAATT	GGACAATTAC	3180
GCTACTAACA	GCCACACACG	CATTAATAGC	AATGTCAAAA	ATGGAACAAT	CAATGAAAAA	3240
GCGACCGCA	TGCTAACGCA	AAAAAATTCT	GAGTGGCTCA	AGCTCGTGAA	TGATAAGATA	3300
GTTGCGCATA	ATGTGGGAAG	TGCTCCTTTG	TCAGCGTATG	ATAAAATTGG	ATTCAACCAA	3360
AAGAATATGA	AAGATTATTC	TGATTCGTTT	AAGTTTTCCA	CCAGGTTGAG	CAATGCCGTA	3420
AAAGACATTA	AGTCTGGCTT	TGTGCAATTT	TTAACCAATA	TATTTTCTAT	GGGATCTTAC	3480
AGCTTGATGA	AAGCAAGTGT	GGAACATGGA	GTCAAAAATA	CTAATACAAA	AGGTGGTTTC	3540
CAAAAATCT						3549

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

923

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298

GCCTAAGTT	TGGCTTCAAT	ATTGGCGAGA	GTGGAGGAGC	TAGCTAAATT	GATCAACAAT	60
AATAATAACA	ATAAAAAACT	GAGAGGCTTT	TTTTTGAAAG	TTCTCTTAAG	TCTCGTTGTT	120
TTCAGTTCGT	ATGGGTCAGC	AAATGACGAT	AAAGAAGCCA	AAAAAGAAGC	GCTAGAAAAA	180
GAAAAAACA	CTCCCAATGG	GCTTGTTTAT	ACGAATTAG	ATTTTGATAG	TTTAAAGCG	240
ACTATCAAAA	ATTTGAAAGA	CAAGAAAGTA	ACTTTCAAAG	AAGTCAATCC	CGATATTATC	300
AAAGATGAAG	TTTTTGACTT	CGTGATTGTC	AATAGAGTCC	TTAAAAAAT	AAAGGATTTG	360
AAGCATTACG	ATCCAGTTAT	TGAAAAAATC	TTTGATGAAA	AGGGTAAAGA	AATGGGATTG	420
AATGTAGAAT	TACAGATCAA	TCCTGAAGTG	AAAGACTTTT	TTACTTTCAA	AAGCATCAGC	480
ACGACCAACA	AACAACGCTG	CTTCTATCA	TTGCACGGAG	AAACAAGAGA	AATTTTATGC	540
GATGATAAGC	TATATAATGT	TTTATTGGCC	GTATTCAATT	CTTATGATCC	TAATGATCTT	600
TTGAAACACA	TTAGCACCAT	AGAGTCTCTC	AAAAAATCT	TTTATACGAT	TACATGTGAA	660
GCGGTATATC	TA					672

(2) INFORMATION FOR SEQ ID NO:1299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299

AATAATGCTA	AAAATAAGAA	TAAAGGAGTC	AAAAGTATGA	AAACGAACTT	TTATAAAATT	60
AAATTACTAT	TTGCTTGGTG	TCTTATCATT	GGCATGTTTA	ACGCTCCGCT	TAACGCTGAC	120
CAAAACACGG	ATATAAAGA	TATTAGTCCT	GAAGATATGG	CGCTAAATAG	CGTGGGGCTT	180
GTTTCTAGAG	ATCAGCTAAA	AATAGAGATC	CCTAAAGAAA	CCCTAGAGCA	AAAAGTGGCC	240
ATACTCAATG	ACTATAATGA	TAAGAATGTT	AATATCAAGT	TTGACGACAT	AAGTTTAGGG	300
AGTTTCCAAC	CTAATGATAA	TCTAGGTATC	AATGCGATGT	GGGGCATTCA	AAATCTTCTC	360
ATGAGCCAAA	TGATGAGCAA	TTACGGTCCA	AACAATTCTT	TCATGTATGG	CTATGCGCCA	420
ACATACTCAG	ATTCATCGTT	TTTACCACCG	ATCTTAGGGT	AT		462

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1554 base pairs

924

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300

CCTTTGGTTA	AAATAAGGTT	ATTTGATTTT	ACTATAAGGT	TGTTTAAACC	TGAATTTAC	60
ATTTTIGATT	TTTTAAAAGG	GATTAGAGTT	CTTATGATTG	AATGGATGCA	AAATCATAGA	120
AAGTATTTAG	TGGTTACGAT	ATGGATAAGC	ACGATCGCTT	TTATTGCCGC	CGGAATGATA	180
GGTTGGGGGC	AATACAGCTT	TTCTTTAGAT	AGCGATAGCG	CTGCCAAAGT	GGGACAGATT	240
AAGATTTCTC	AAGAAGAATT	AGCCCAAGAA	TACCGCCGCC	TTAAAGACGC	CTATGCTGAG	300
TCTATCCCTG	ATTTTAAAGA	ACTCACCGAA	GATCAAATCA	AAGCCATGCA	TTTAGAAAAA	360
AGCGCGCTAG	ATTCGCTCAT	CAATCAAGCT	TTATTGAGGA	ATTTGCGCTT	AGATTTAGGG	420
CTTGGTGCTA	CCAAGCAAGA	AGTGGCCAAA	GAGATCAGAA	AAACGAACGT	TTTTCAAAAA	480
GATGGCGTTT	TTGATGAAGA	ATTGTATAAA	AATATCTTAA	AACAAAGCCA	TTACCGCCCC	540
AAGCATTTTG	AAGAAAGCGT	TGAAAGGCTT	TTAATCCTTC	AAAAAATCAG	CGCTCTATT	600
CCCAAAACCA	CCACCCCTTT	GGAGCAATCC	AGTCTATCGC	TTTGGGCAAA	ATTGCAAGAC	660
AAATTAGACA	TTCTTATCCT	AAATCCTAAT	GATGTTAAAA	TCTCTCTCAA	TGAAGAAGAG	720
ATGAAAAAAT	ATTATGAAAA	CCATAGAAAG	GATTTTAAAA	AGCCCAAGAG	CTTTAAAAAC	780
CGCTCTTTAT	ATTTTGAACG	TAGTTTAGAA	AAAACGTGAT	TGAAAGAGTT	GGAGGAATAC	840
TACCATAAAA	ACAAGGTGTC	TTATTTGGAC	AAAGAGGGGA	AATTACAGGA	TTTTTAAAGC	900
GTTCAAGAGC	AAGTCAAGCA	TGATTTAAAC	ATGCAAAAGG	CGAATGAAAA	AGCCTTAAGG	960
AGCTATATCG	CTCTAAAAAA	GGGGAACGCA	CAAAACTACA	CCACGCAAGA	TTTTGAAAAA	1020
AACAACCTCC	CCTATACTGC	TGAAATCAGC	CAAAACTCA	CCGCTCTCAA	GCCCCCTGAA	1080
GTCTTAAAC	CAGAGCCTTT	TAAAGATGGT	TTTATCGTGG	TGCAGCTTGT	CTCTCAAATT	1140
AAAGACGAAT	TGCAAAATTT	TGATGAAGCC	AAAAGCGCTC	TTAAACCCG	TCTGACTCAA	1200
GAAAAAACCC	TTATGGCGTT	GCAAACTTTA	GCTAAAGAAA	AGCTTAAGGA	TTTTTAAAGG	1260
AAAAGCGTGG	GTTATGTAAG	CCCTAATTTT	GGAGGCACTA	TCAGTGAAC	TAACCAAGAA	1320
GAGAGCGCGA	AGTTTATCAA	CACCCTTTTT	AACCGCCAGG	AAAAAAAAGG	GTTTGTAACC	1380
ATAGGTAATA	AAGTGGTGCT	TTATCAAATC	ACAGAGCAAA	ATTTCAATCA	CCCTTTTAGT	1440
GCAGAAGAAA	ACCAATACAT	GCAGCGTTTA	GTCAATAACA	CTAAAACGGA	TTTTTTTGAT	1500
AAAGCGTTGA	TAGAAGAATT	GAAAAACGCG	TATAAGATAG	TCAAATACAT	TCAA	1554

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

925

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301

AAAGGTAAGC	TAGGCCTATT	TTACTATTTT	TCAGACTTAC	TAGAGTCGCT	AATTTGCTTT	60
TCAAACTCTT	GTGTGAAGGC	CTGTTGTTGC	TTTTCTTTCT	TTGAAAGGCG	TCGTTTTTTC	120
TTGGGCTTTT	TTTCCTTTTT	TGAAGAAGTC	TCTGGCTCTT	TTGAAGCTGT	TTCTTTGAGC	180
GTGTTAGCGT	TAGTCATAGG	GTCTAGATCT	GGGTTAGAAG	AATTCGTGT	CTTAGAAGAG	240
CTTATAAATT	CAGGGCTATC	AGTATGGCTT	TCAAGCTCCC	CACTGCTCCT	CTTTTGGAAT	300
GCTGCCTTAG	TGTCTTTCTC	AGCTTGTTCT	TCCATTTTTT	TAAGAACGAT	TGCATCCACT	360
TTTCTAGCCT	TTTCTTTTTG	GCTCACCCCTA	ACCATGCTGA	TCAAGTATTT	GATATACCCA	420
TCATACATGT	CCCCAACTG	CTCATGCAA	GCCCCAAAT	CTGAGCCTTT	G	471

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302

GGGCTTTTGA	AGCCTTTAGA	AGAAACCGAA	ATCAAGGCCT	GTAACAAAGA	TATTTTACCC	60
TTAAAGCCTT	ATGAAAAGC	CAAATTGATT	GCTTATATCC	CCCAAGTGA	ATATTATGCG	120
TTTAATTCA	GCGTGTGGA	TTTGTCCTTA	ATGGGGAAAG	CGACGCATTT	GAATCTGTTC	180
GCTATGCCTA	AAGCTAAGCA	CATTAAAGAA	GCCACGAGCG	TTTTAGAGCG	CTTGGATTTA	240
GAGTCCTTAA	AAGATCAAGG	CATTAAACGAT	TTGTCCGGCG	GTCAAAGGCA	GATGGTACTT	300
TTAGCCAGAA	GCTTGTGCA	AAGAACGCCC	TTATTGTTAC	TGGATGAGCC	TACGAGTGCG	360
TTAGATTTAA	AAAACCAAGC	CCTTTTTTTT	GATGCGATTA	AAGATGAGAT	GAAAAACGA	420
GAATTGAGCG	TTTTAGTCAA	TATCCATGAT	CCCAATTGG	TTGCCAGGCA	CTCCACGCAT	480
GTGGTCAATG	TCAAAGATAA	AAAACCTTTT	TTGCAAGCTT	CCACGCCAAT	CGCTATGACT	540
TCACACAATT	TAAGCGCGCT	TTATGACACG	CCCCTAGAAG	CGATCTGGCA	TGATGATAAG	600
CTTGTGGTGT	ATGCCGTTG					618

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

926

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303

AAAAAAAAAA	AAAACGATGA	AAAGCATATC	GCTAAGCACT	TTGTAGCGGT	ATCCACCAAT	60
AAAGAAGCCG	TGCAACAATT	TGGCATTGAC	GAGCATAACA	TGTTTGGATT	TTGGGATTTT	120
GTAGGGGGGC	GTTATAGCTT	GTGGTCGGCT	ATTGGCTTAT	CCATTATGAT	CTATTTAGGG	180
AAGAAAAATT	TTAACGCCCT	TTTGAAAGGG	GCGTATTATA	TGGATGAGCA	TTTAGAAAC	240
GCCCTTTTG	AAAGCAATTT	ACCCGTTTTA	ATGGGATTAA	TCGGCGTGTG	GTATATCAAT	300
TTTTTCCAAT	CCAAAGGCCA	CTTGATCGCC	CCTTACGAC			339

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304

CACAACAAGA	CACGAATGAA	AAGAGCGAAA	CGGAGGAAAT	TTATCACTAA	ATTTTCACGC	60
TACTACACCC	CAAGCGTTTT	ATTCATCGCC	TTAATGATCG	CTGTATTACC	GCCCTTGTTT	120
TCTATGGGGA	GCTTTGATGA	GTGGATTAT	AGGGGGCTTG	TGGCTTTAAT	GGTGAGCTGT	180
CCTTCGCGCT	TAGTGATTTC	TGTGCCTTTA	GGGTATTTTG	GAGGCGTGGG	AGCGGCGAGC	240
CGAAAGGGGA	TTTAAATGAA	AGGAGTGCAT	GTTTATAGAG	TGCTTACCCA	AACTAAAAGC	300
ATCGCCTTTG	ATAAAACCGG	CACTTTGACT	AAAGCGTTTT	TTAAAGTGGT	GGATATTGTG	360
CCGCAAAACG	GGCATTCTAA	AGAAGAAGTT	TGCATTACGC	TTCTTGCTCG	CAGCTTTTAT	420
CCACGCACCC	GATCGCTTTA	TCCATTCAAA	AAGCATGCCA	AGAAATGT		468

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

927

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305

CGCTCCACTC	TAGCGAGCGC	TGATGTGGGG	ATTGGCATGG	GGAAAGGATC	AGAATTGAGC	60
AAGCAAAGCG	CGGACATTGT	GATCACTAAT	GACTCCTTAA	GCTCTTTAGT	CAAAGTTTTA	120
GCGATCGCTA	AAAAAACTAA	AAGCATTATT	TGGCAAAATA	TCTTGTTTCG	TTTGGGGATT	180
AAGGCGGTTT	TTATCGTGCT	AGGGCTTATG	GGGGTAGCGA	GCTTGTGGGA	AGCGGTCCTT	240
GGCGATGTGG	GGGTTACGCT	TTTAGACTTA	GCCAAATCCA	TGCGCACGAT	GAGGGCT	297

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306

CACCAATCTT	TTAAAAGAGC	GTTTGAACCA	AGAAGAAAAG	GGCGAGTTTT	TAGAATAATG	60
GGTTTTGAAA	AAAGCATTTT	AGACAATTG	AACGGAGCGC	AAAAAATTGC	CGCATGCCAC	120
ATTCAAGGGC	CTTTATTGAT	TTTAGCGGGA	GCTGGGAGCG	GTAAGACTAA	GACTTTAACG	180
AGCCGTTTAG	CGTATTGAT	TGGCGCTTGT	GGCGTGCCTA	GCGAAAACAC	TTTAACGCTC	240
ACTTTCACCA	ATAAAGCGAG	TAAAGAAATG	CAAGAAAGGG	CTTTGAAATT	GTTGAAAAAC	300
CAAGCCCTTA	TCCCCCCTT	GCTTTGCACT	TTCCATCGTT	TTGGTTTGCT	GTTTTTAAGG	360
CAACACATGA	ATCTTTTAAA	AAGGGCGTGC	GATTTTTCGG	TGCTAGATAG	CGATGAAGTG	420
AAAACGCTCT	GCAACAGCT	CAAAATTTCA	AATTCAGGG	CGAGCATTTT	TCAAATCAAA	480
AACGGCATGA	TGGATTGAG	CGTGCAAGAT	AGCGAATGTT	ACAAAGCGTA	TGAGCTTTAT	540
CAAAACGCGC	TCAAAAAGA	CAATTAGTG	GATTTTGACG	ATTTGCTTTG	TTTGAGCCTT	600
AAGATTTTAC	AAGATAATGA	AAACTCGCC	AAAGAGACCA	GCGAACGCTA	CCATTACATT	660
ATGGTAGATG	AGTATCAAGA	CACGAACGCC	CTGCAACTGG	AATTTTAAA	ACAATTGAGT	720
TTACAGCACC	ATAATTTGTG	CGTGGTGGGC	GATGACGATC	AGAGCATTTA	TGGGTTTAGG	780
GGGGCTGATA	TTTCTAACAT	TTTAAATTTT	TCCAAGCATT	TTAAAGGGGC	TAAAATAGTG	840
AAATTAGAGA	CCAATAACCG	CTCTAGCGCT	GAAATCTTAG	CGTGGCGCTA	TTCCCTGATC	900
AGCCATAACC	AACACCGCCA	CATTAAAACG	CTTCAAAGTT	TCAAAGGTTT	GCACAAAAGC	960
GTGATTTGTA	AAGAATACCC	CACGCAAAAA	GAAGAGAGCC	TGGATGTGGC	TTATCAGATT	1020
CAAAGCCCTT	TTAAGAAGG	GCGAGAATTT	AGAAAATATC	GCTATTTTGT	ATCGTTTAAA	1080
TGG						1083

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

928

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307

TTTGTGCTGA	ATGAAGAGCA	AAATTCATTA	GAAGAAAAAG	GGGGCGAAAA	CAAAAACGAA	60
AAAGAAACCC	CCCTAAGGG	CATTCAATTCT	AAAATCCCCCT	CTTTGAAGCA	GGCTTIGGAG	120
CAGACGATTA	GTAAAAACAA	AAGCTCTAAA	GAGTTTTTCA	AACAGCTTCT	ACACAATAAA	180
AAAAAGCTTT	ATATCGCGCT	TGGAATATTG	CTTTCACCTCA	TCGCGCTCAT	TGTGGCTTTG	240
AGTTTGTITAC	TAGGGCATAA	AAAAGAAAAAT	AAACAAACTT	CTTTACAAAC	TAATACCGCC	300
ACCACCAATA	ACGAAAACGCC	TAACGACACC	AATAACGCAG	AAGCCGAAGG	GCAAATAGAA	360
AATTTAGACT	TGCCTGATTT	AATCGGCAAA	GACTCTTTGA	AAAGAAACGA	TGAAAGCCAA	420
GTGGATGCGA	TGATGCAAAA	AGCGAGCCTT	TTGTATGAGC	AAGGGCAAAA	AGATGAAGCC	480
TTGCATTTGT	TTGATAAGAT	CGCTTCTTTC	TCGCAAGGGA	TTGCGAGCCA	TAATCTAGGG	540
GTGATTAAAT	TCAAAGAAAA	GGATTTTAAT	GGGGCGTTGG	ATTTGTTTGA	TTCCAGTATC	600
GCTTCTAAAG	AAAACGCGAG	CGTGAGCGCG	ATTGATGCGT	TAGTTACGGC	TTATCATTTG	660
CAAGATGCGG	ATTTGTATTA	TCATTATCTA	AAAATTGTAA	GAGACACTTT	GTATAAAGAT	720
TACAAAAAGT	CTTTTATTC	CTACGCTTAC	GCACTCAAAT	CCTACTACGC	TGGAGAGTAT	780
TTTGAAGCCC	TTTCGCCCTT	AATGCACCCT	AATTCCAACG	CCTTTTAAAG	GCCTAATGCG	840
CGCTTAGCGT	CTAAATGTTT	TTTGATGTTT	AAAGATGAAA	CGAACGCTTA	CAAGCAATTG	900
CAAAAAAGTG	CGAACGCCCA	AGATGAGCTT	GCTTTAGGGC	TTTTGCAGGC	CCGTTTGGGT	960
ACTTACAAGC	AGGCTTTGGA	GCATTTGCAG	CATTATTTGC	ACAACTACCC	TAAAGATTTA	1020
AACGCTTTAA	TGGCTTTGGA	ATTGGTGAGT	TGAAAATGCG	GCGATACCCCT	TAAAGCGAGC	1080
GAAGCCTTAA	AATTAGCCAG	CCATACGCAA	GAAGACACGC	TATTAGCCAA	CTCTTTTAC	1140
CCCATAAGC	CCACTATAAA	CCCTATGTTT	TTAGACAAAG	AAAGGGCCAA	AGAGCGTTTT	1200
TGGAACACGC	AATATTTTGA	AGGTAAAGG	GATTTTATCT	ACCGCTTGCT	GTTTTATTAC	1260
GCTCCTTTTA	AGGTTTTAGA	CTCTAAAGAA	ACCTTAGGCG	TGATTGAAGA	GGGGCTGTTT	1320
CTTTTAGATT	CTGACACGCA	AAAGGATTTA	GAGGGGGCAA	GCCTTGCTTT	TAAAGGGGGG	1380
CGTTTGATGG	CGATAGCGGA	TAAAAACGCG	CTCAAGGGGT	TGAAAGAATT	AGAAAAGAAG	1440
CGTCTAAAAA	AAGCCCTTTC	TTTTTTTGAT	TTGTCTTTAA	AAAATAGCCC	CAATAACGCG	1500
CTTTTGCAAT	ATAATGTGGG	CTTGATTTAT	GCGCAATTGG	AAAATTACCA	CAAAGCTTAT	1560
TTCCATTTTT	TAAGGGCTTT	CCATTGGAAT	TCTGCGGATT	ATTTGAGCGC	GGTTTTTGCG	1620
GTTTTAGCCT	CGCATTTCAC	CCATGAAGAC	ACCACGGAGT	TTTTAAGAGA	AATCACCGAG	1680
AATTTTTATA	GTATGATTTT	TTCTAGCCCC	ACGCAAAAAG	CTTTACTCTC	TTCCGCTCATC	1740
GCTTATTTGA	ATTACCGCAC	CAATTGGGAT	ATGGACTGGC	TCAAAAACGC	CCCTAAAAAG	1800
CTCCCTTTTT	ATTACGCGCT	AGAAGCGGTG	TTGCTAAAG	AGAGCAAGGA	TAAAAAATTG	1860
ATGGTGCAAT	CTTTTGGGAA	TTTAAAAAAA	ATGCTCCCTA	AAGATCTCAT	CTCTAATATT	1920
TTTTATGAAA	TCGCTCTGTA	TTACGATGCG	AGCATCCGCC	ACACTTTAAG	CATTTACACC	1980
CTTTTAGATT	CGCATAAAAT	CAGTTGGGAT	CAAACCATGC	AAGGGCCCAT	TTTAGGGCGT	2040
CATTTCTACA	CTTACATGGG	ATTTATGGTC	AATGATCTGG	ATCATCAAGA	AAGATTGTTA	2100
GAGCAAAAAA	TCGCCAGTTT	AGAAAGGGGC	GAAGCCCCTA	ACGATTGGTT	GGAAAAATTTA	2160
GCGCTAGTGA	GTTTGTTCFA	AGGCCAGTAT	GAAAAAGCGA	GCGCGTTGTA	TCAAAACTTA	2220
ATTGATGGGC	TTAAGGATAA	CGAGGCGCGT	TTAAAAATCC	TAGCGGGTTT	AACCTATATC	2280
GCGCAAAATA	ATTACAATAA	CGCCGCTTTA	TGGCTAGAGC	TTGGGAAATT	AGACGATCCG	2340
AATAATGAAA	ATATCCGTTA	CGCTTAGGG	TTGTTGTATC	AAGAAGAGGG	AGACTTGAAA	2400
TCAGCGCTAA	ACCATTTTTT	AGCCATTAAA	ACCTCTGATT	TTTCGTCGCC	TTATTTTGAT	2460
TTTGAATTTG	ACACCAATCT	TTTAAAAGAG	CGTTTGAACC	AAGAAGAAAA	GGGCGAGTTT	2520
TTAGAA						2526

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

929

- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308

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AAGGTTACTA CTACCATGAT AAAAGCAATC ATTGGAAAAA TCATCGGCAC TAGAAACGAT      60
CGCTGGATCA AACATAACAA AAAAAAAGTC CTAGCCATCA ACGCCTTAGA GCCTACTTAT      120
GAAAAAATGA GCGATGTTGA GCTGCAAAAC GCTTTTGAAG AATTAAAAAA ACGAGTGCGA      180
TCCGTAGAAA AAGATTTGCA AGAAAAAACC CTTTTAGAAG TTTTACCAGA AAGCTTTGCT      240
ATCACTAGAG AAGCGAGCAA AAGGATCTTA AAGATGCGCC ATTTTGATGT GCAACTCATT      300
GGGGGCGATG TCTTAAACGA TGGCAAGATC GCTGAAATGA AAACCGGAGA GGGTAAGACT      360
TTGGTTCGCTA CTTTAGCGGT GGCTTTGAAC GCTATGAAAG GCGAGAGCGT GTATGTGGTA      420
ACCGTTAATG ATTACTTAGC CCATAGGGAT TCTAAAGAAA TGGAGCCGTT GTATCAATTC      480
TTAGGTTATA GCGTAGGCAC GATCACTGCG AGCGTGCGAG ATGATGATGA GCGCTTAGAA      540
ATTTATTCTA AAGACATTGT TTATGGCACT AATAATGAAT TTGGCTTTGA TTATCTAAGG      600
GATAACATGA AATATTCTTT AGAGCATAAA GTGCAAAAAT CCCATGCGTT CGCCATTGTT      660
GATGAAGTGG ATTCCATTTT AATTGATGAA GCGAGAATC CTTTAATCAT TTCAGGGCCT      720
GTGGATAGGC GCATGGAAAA TTACAACAAG GCTGATGAAG TCGCTAAAAG CATGCAAGTG      780
GAAGTGGATT TCACCATAGA CGAAAAAACC CGCGCGATT TAATCACTGA AGAGGGGATT      840
AAAAAAGCCG AAAATCTCTT TGGCGTGGAT AATTTATACA AAATTGAAAA CGCCGCCCTA      900
TCGCACCATT TAGACCAAGC CTTGAAAGCG AATTACCTCT TTTTATATGA TAAAGATTAT      960
ATTGTAGCCA ATAATGAAGT GGTGATTGTA GATGAATTA CCGGCCGTT GTCTGAGGGG     1020
AGGCGCTTTA GTGAGGGCTT ACACCAGGCT TTAGAGGCTA AAGAGGCG     1068

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(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309

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AAGCTTTTTT TAAACCCCT AAAAGAAACG AGCCTTGCCC TTGTGGGAGT GGCAAAAAAT      60
ATAAAGATTG TTGCGCTAAA AGCGGGCCTA AAAAGGGCTT ATTTGCCAAA TAGATCCTTA      120

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SUBSTITUTE SHEET (RULE 26)

930

ATCTTTTTTC	TTATCAAGCG	TTATTTGCGT	TTTGATAAAA	GCCAGCCTTT	CATTAGTATC	180
ACTGCTTTGT	TAGCCTTTTT	TGGCGTGGCG	GTTGGCGTGA	TGGTTTTAAT	TGTGGCTATG	240
GCGATCATGA	ACGGCATGAG	TAAGGAATTT	GAAAAAAGC	TTTTTGATG	GAACTACCCC	300
TTAAGGCTCT	ATACCACAAG	CCCTTATGGG	ATCAGCGAAG	AAGTGGTTCA	AGCTTTAGAA	360
AAAAAGTTCC	CTAATTTGCT	TTTTAGCCCC	TATTTGCAAA	CCCAAAGTCC	GATTAAAAGC	420
GCGCATTCCA	TGAATGGCGG	CGTGGTGTTC	GGGGTTGATT	TTTCTAAAGA	AAGGCACATC	480
AATGAAGTTT	TAAATGACGC	CTTAAAAAAC	ATTAATGAAA	ACGATCTCTT	CAAAAACCTT	540
TTTAATTTGA	TCTGTTGGGA	AAGCTTGAGA	TACAGCTTGA	ATTTAGATCT	CAATCAAAAA	600
GCCGATTTGT	TTTTACCCGA	ATTAGAGCCA	ACAGGTCTCA	CGCTCTCCCC	CATCATGAAA	660
CGCTTTACTA	TCAAAGGCGA	TTTTGATTCA	GGGCTAAAAT	CCTATGACAT	GAGCTACATG	720
TATGCGAGCC	TTCAAGCTAT	AAGCGCGATC	AGGAGATTAC	CCTTAGGGCT	TTATGATGGG	780
GTGCATGTCT	ATTCTAAAAC	GCCCATGAAG	GATATTGAAA	AATTACGCAA	CGCTTTAAAA	840
ACAATCAACC	ACCATGGCAT	AGGCATTGAA	GGGTGGTGGC	AACAAAACGG	GAATTTTTTC	900
TCGGCGATGG	AATTGGAAAA	AAGAGCGTTA	TTCATTGTGC	TCATGCTCAT	TATTTTAATG	960
GCGTCTTTGA	ATATCATCAG	CTCGCTTTTA	ATCGTGGTGA	TGAACAGGCG	TAAAGAAATC	1020
GCCTACTCT	TTAGCATGGG	GAGCAGTCAA	AAAGAAATCC	AAAAACCTT	TTTTTATTG	1080
GGTAATATCA	TTAGT					1095

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310

AGAGGCGTGA	GCATTAAAGA	AGAGAGCCAA	ACCTTAGCCG	ATATTACTTT	CCAAAATTAT	60
TTCAGGATGT	TTTCTAAACT	TTCAGGCATG	ACAGGCACGG	CTCAAACCGA	AGCCACAGAA	120
TTTTTAGAAA	TCTACAATTT	AGAAGTGGTG	TCCATCCCTA	CTAATCTAGC	GATCAAGCGA	180
AAAGATTTGA	ACGATCTGAT	CTATAAGAGT	GAAAAAGAAA	AATTTGACGC	TGTGATCCTT	240
AAAATTAAAG	AATTACACGA	TAAGGGTCAG	CCCGTTTTAG	TCGGCACGGC	TAGCATTGAA	300
AAGAGTGAAA	CCTTGACACG	TTTACTCAAA	AAAGAGCGCA	TCCCTCACAC	CGTTTTAAAC	360
GCCAAGCAAC	ACACTAAAGA	AGCTGAAATC	ATCAAAGACG	CCGGGCTTAA	AGGGGCGGTT	420
ACGATTGCGA	CCAACATGGC	AGGCAGGGGC	GTTGATATTA	AGCTCACTGA	TGAAGTTAAA	480
GAACCTGGGG	GGCTGTATAT	CATTGGCACT	GAAAGGCATG	AGAGCCGTAG	GATTGACAAT	540
CAATTAAAGG	GGCGAAGCGG	GCGTCAAGGC	GATCCGGGAG	TGAGTCAGTT	TTATTTGAGC	600
TTAGAAGACA	ATCTGTTACG	CATTTTTGGG	AGCGATAGGA	CTAAGGGGGT	GATGGAAAAA	660
TTAGGGCCTA	AAGACGGCGA	ACACATTGAA	TTCAAGCTCG	TTACAAGAGC	GGTGGAAAAAC	720
GCGCAAAAAA	AAGTGAGAG	CTTGCAATTT	GACAGCCGTA	AGCATTGTGT	AGAATACGAT	780
GATGTGGCTA	ATGAGCAACG	AACAAGCGTG	TATAATCTTA	GAGATGAATT	ATTAGACATC	840
AATTACGATA	TTAGCGCTAA	AATCGCTGAA	AACAGAGAAT	ACGCGCTCAA	TCAAATCTTT	900
TCTAAACTCA	AAGCCTTTGA	CCATCAAAAC	CTGTCTGAAG	AGGAACTTTT	AGGGCTTAAA	960
AACATTTTAA	AAGAAGATTT	TAACGCTAGC	GTTGAATTAG	AAGATTTAGA	AAAAGCCTCC	1020
CCTATTGAAA	TATTTGTGGC	TGAAAACTC	AAAAGCGGAT	TA		1062

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

931

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311

ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT	60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC	120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CGGTGGATAG GGGGCGCAAT	180
ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA TCAAACATTT GCGCTTGATT	240
TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAAT TGGGAGGTAA TAAGGATATG	300
AAAACGGTTG AAATCGGAAG C	321

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312

AAAAACCAAA TACTTCAAAT CCCACTGCTT CCACCCCCC CCAATAATGA AGAGCTTTTA	60
AAATCTATTA CAGATCTTAA AGATCGCCTT AAAAAATTAG AAGATCTTAA ATTAGAAGAC	120
TTTGAACCCC TTAGAAAACCT CTCTCATTTT ATAGTTATAG GTAATTTGTT TGGAAAATCC	180
TCTAACGACA CCCAAGAAAA CCCAAAAGAC GCTTTAAAAA CCACCAATTT CCACGAGAAA	240
CACACCAAAC CGACTGAAAC CACCGAACTA GTTGAAGAAA ATAAAGCGCT AACCACAGAA	300
AAAGAAAGGC TAGAAAGAGA AAATAAAAAC CTAAGTGCAG ACAAAGAAAA CCTAACTAAA	360
GAAAAAACCG AATTACAAAA ACAAGTGAAT GAGTTAAAAA ACTCTAAGCA AGTTTTAGAA	420
AATGAAAAAG CCGATTGGCT AAGAGAAAAA GAAATCTAA CCAAAGACAG AGAAAACCTA	480
ACTAAAGAAA AAACAGAGCT GACTGAAAAA AATAAAGTGC TAACCACAGA AAAAGAAAGG	540
TTAGCCACAG AAAAAGAAAA CCTAACTAAA GAAAAACCG AATCAGAAAA ACAAGTGAAT	600
GAGTTAAAAA ACTCTAAGCA AGTTTTAGAA AATGAAAAAG CCGATCTGAC CAACGAAAAC	660
ACCAAGCTAA AACAGATAA AACAGATCTG ACTGAAAAAA ATCAAAGGCT AACCACAGAA	720
AAAACAGAAT TAAATAACAA GATTACTGGG TTAGCCACAG AAAAAGAAAG GTTAGCCGCA	780
GACAAAGAAA ACCTAACTAA AGAAAGCAGA CAAAGAAAAA CTAAC	825

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313

GCGCTTTCTA	ATTGTTTGAG	CTTGTCAGTT	AGGCGTTGGT	TTTCTTTCTC	TAAATTGGTG	60
CATCGTTTTT	CTAGAAAACC	ATGCGCATCT	TGCAATCGCG	CTCGCTCTTG	TTTCGAGACTA	120
TCTCGCTCAT	TAGTGAGCGC	GGTAACTTGG	TGTTGAGCT	TGTCGTTTTC	GGTGGTTAGT	180
GCTTTATTTT	CTTTAGTCAG	CTCGGTGATT	TTATGGGTTA	GCTCGGTGTT	TTCTCTTTTT	240
AGCCTTTCTT	TTTCTGTGT	CAATCTCTT	TTTCTTCAG	TCAGCCGATC	TCTGGCTGCT	300
AATAAGCGTG	TGTTTTCTT	AGCTAAAATG	TCTTTTCCG	TTTTCAGTTC	TGCTTTTTCT	360
TTAGTGAGCT	TGTTATTGTT	TTGCCATAAT				390

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314

ATGGGAACGC	TCATTGAAAA	ATGGTTTGGC	TTCTCTCAAA	TCAGAGAAGA	ATTAGAAGCT	60
CGCATCAGTG	AGTTAGAAGA	CGAAAACACC	GAATTGTTAA	GAGAAAGAGA	ATACTTAGCT	120
GCAGAAACTA	GCGAGTTAAA	AGACGCTAAC	GATCAATTAC	GGCAAAAAAA	CGACAAGTTA	180
TTCATAACAA	AAGACAAGCT	AACCAAAGAA	AACACCGAGT	TATTCGCAGA	AAACGAAAGC	240
TTATCTGTAA	AAATCAGCGG	GTTAGAACAC	TCTAACGATC	AATTATGGCA	AAACAATAAC	300
AAGCTCACTA	AAGAAAAAGC	AGAACTGAAA	ACGGAAAAAG	ACATTTTAGC	TAAAGAAAAC	360
ACACGCTTAT	TAGCAGCCAG	AGATCGGCTG	ACTGAAGAAA	AAAGAGAATT	GACACAGAA	420
AAAGAAAGGC	TAAAAAGAGA	AAACACCGAG	CTAACCCATA	AAATCACCGA	GCTGACTAAA	480

933

GAAAAATAAG	CACTAACCAC	CGAAAACGAC	AAGCTCAACC	ACCAAGTTAC	CGCGCTCAC	540
AATGAGCGAG	ATAGTCTCGA	ACAAGAGCGA	GCGCGATTGC	AAGATGCGCA	TGGGTTTCTA	600
GAAAAACGAT	GCACCAATTT	AGAGAAAGAA	AACCAACGCC	TAAGTGACAA	GCTCAAACAA	660
TTAGAAAGCG	CTCAAAAAAG	C TTGGAAAAC	ACTAACAATC	AATTACGGCA	AGCTTTAGAA	720
AACTCTAATG	TCCAATTAGC	ACAAGCTAAA	GAAAAAATAG	CCATAGAGAA	AAGCGAGCTG	780
GAGCGAGAAA	TCGCACGCTT	GAAGAGCTTA	GAGGGTATGG	AAGCCAAAAG	CGATCTGGAC	840
TTACACAACA	GGCGTTTAGC	GAGCGCAAAC	GAGGATTTAA	AACGCCAAAA	CCGAAAATTA	900
GAAGAAGAGA	ACATCGCCCT	CAAAGAGAGG	GTTGATGGCT	TGAACGAGCA	GCTCTCCAAA	960
TTGCAACCAC	AAAAACCACA	A				981

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315

TTTAAACCA	TTGAACGAAA	CGATTTTAAA	TTAAACGGAT	TGACAAAAAT	TTTACAAAAC	60
AAAGGATATA	AAATGAAAAC	AATTAAAAAT	GGTATTATGA	TCGGCACACT	CGGTGCGTTG	120
TTATTGAGCG	GTTGTTCTAG	CTTTGATGCT	CAGCGTTTCG	CTTGCTCCTC	TAAAGACCAT	180
TCTTCAAAAG	ACGCTTCTAC	CAAAAAGAA	GCGCAATACA	TTCTTAAGGG	CTTTTTTGAC	240
CCTTATTCTT	CTAACTTAAA	CCATTGGGAT	TCTACATTC			279

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316

AGCTTAAATA	AGGGTCTGGC	ATTGTTTTTA	GTCAAAAAAA	TAGGCGTGGT	AATAATGATT	60
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SUBSTITUTE SHEET (RULE 26)

934

TTAGTCTGCT	TTTTAGCTTG	CTCGCAAGAG	AGCTTTATCA	AAATGCAAAA	AAAAGCCCCA	120
GAGCAAGAAA	ATGACGGCTC	TAAACGCCCC	AGCTATGTGG	ATTGCGGATTA	TGAAGTCTTT	180
AGCGAAACGA	TTTTTTTACA	AAACATGGTG	TATCAGCCTA	TAGAGGAAAG	AAACGCTTTT	240
TTCCAAGTGA	CTAAAGATGA	AGACAATTCT	TTTAACCCCTG	AAAATTCCGT	GATTTTACTG	300
AATGAGCCAA	GCGATAATAG	TGAAAAAAAC	CTACTCTCAT	ACCCAAACGA	TCCCAATAAC	360
AATGAAGACA	ACGCTAATAA	TAGTCAAAAA	AATCCGTTCC	TTTACAAGCC	CAAAAGAAAA	420
ACAAAAAACC	CAAACTCAT	TGAATATTCC	CAACAAGATT	TCTACCCCTT	AAAAAATGGG	480
GATATTATCA	TGAGTAAAGA	AGGGGATCAA	TGGTTGATAG	AAATCCAATC	CAAAGCCTTG	540
AAGCGTTTTT	TAAAAGATCA	AAACGATAAA	GATCGCCAGA	TCCAACTTTT	CACTTTTAAT	600
GACACTAAAA	CGCAAATCGC	GCAAATTAAAG	GGCAAATTTT	CTTCGTATGT	TTATACCACC	660
AATAACGGTA	GCTTGAGTTT	AAGGCCTTTT	TATGAATCGT	TTTGTGTTAG	AAAAAGAGC	720
GATAATGTTT	ATACGATAGA	GAATAAGGCT	TTAGATACTA	TGGAGATTTC	AAAGTGTCAA	780
ATGGTGTTAA	AAAAGCATT	AACCGATAAA	TTAGACAGCC	AGCATAAAGC	CATCAGTATT	840
GATTTGGATT	TTAAAAAAGA	GCGCTTTAAG	AGCGATACGG	AACTCTTTT	AGAATGTCTT	900
AAGGAAAGT						909

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317

GCATGGTTAA	AAAGTAGGGT	TTTAATGAAA	CGCCTTGCTG	TTGCGCTTAT	TTTGGTGTG	60
GGAGTGGTGT	GGGGGAAATC	CTGCGCTAAG	TGGGCAAAAAG	ATTGCTCAAA	AGAGATGCGG	120
ATTGAAAAGA	CCCAAACCAA	AGATGAAAAA	ATTTTAGTGT	GTGGGATGAG	CGATATATTG	180
CTTTCAGATA	TGGATTATAG	CTGTCTCTCA	GCCAGACAAA	ACGCGTTAGA	GAAAGTGATG	240
GAAGCTTTCA	AGGGGGATAG	AATAGAGATT	AAGGCTGGTG	AGCTAAAGGC	CACTTTTATT	300
GATACGGATA	AAGTTTATGT	GCTTCTAAGA	ATCACTAAGA	AGCATGTCCG	TTTAATGAAT	360
GAG						363

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

935

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318

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GGATTGATAA TGAAAAAGAT TATTCTTGCA TGCCTTGTTG CTTTGTGTTG TGCCAATTTA      60
AGCGCAGAGC CTAAGTGGTA TAGCAAGGCC TATAACAAAA CAAACGCCCA AAAAGGCTAT      120
CTTTATGGGA GTGGTTCAGC CACTTCTAAA GAGGCTTCTA AACAAAAAGC GTTAGCGGAT      180
TTAGTGGCGT CTATTAGCGT GGTGGTCAAT TCACAAATCC ACATTCAAAA AAGTCGTGTG      240
GATAATAAGT TAAAATCCAG CGATTACAA ACGATCAACT TAAAAACCGA TGACTTGGAA      300
TTGAATAATG TAGAAATTGT CAATCAAGAA GCGCAAAAAG GGATCTACTA CACCAGAGTG      360
AGGATCAATC AAAACTTGTT TTTGCAGGGT TTAAGGGATA AGTATAACGC TCTTTATGGG      420
CAGTTTTCCT CTTTAATGCC TAAGGTTTGC AAAGGGGTTT TTTACAAACA ATCCAAGAGC      480
ATGGGGGATT TATTGGCTAA AGCGGCGCCT ATGGAAGGA TTTTAAAAGC GTATTCTGTC      540
CCGGTGAGTT CGTTAGAAAA TTATGAAAAA ATCTATTACC AAAACGCTTT CAAACCTAAA      600
GTGCGAATCG CTTTIGATGA TAACAGCGAC ACAGAGATTA AAAACGCTCT CATGAGTGCT      660
TACGCTAGAG TGCTAACCCC TAGCGATGAA GAAAACTTT ATCAAATCAA AAATGAAGTT      720
TTCACGGACA GTCTAATGG CATCACACGC ATTAGAGTGA TTATTAGCGC GAGCGATTGT      780
CAAGGCACGC CTGTATTGAA TAGGAGTCTT GAAGTGGATG AAAAGAATAA GAATTTTGCT      840
ATCACGCGCT TGAATCTTT ACTTTATAAA GAATTGAAAG GTTATGCCAA TAAAGAAGGA      900
CAAGGCAATA CAGGGCTA

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(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319

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CCCCAAGAG TTGTTTTTAG GGTGCGATTC TTGCTCGCTA TCCCCCAAAT TTTAGTGGGC      60
TTAAGGATTG CGGTGGTGAT GCTAGTAGCG ATGGCTGGAA TCGGGGCACT CATGGGGGCT      120
GGGGGTTTGG GGCAGGCGAT TTTTAGAGGG CTAAACACGC AAAATACCAC GATTTTAGTG      180
GCGGGCAGCT TTATTATTGC TCTTTTAGC GTTTTAGCGG ATCAATTGTG GAGCGTGTGT      240
CAGCATGAAA ACGCCTTGCA ACGCCTATTT TCTCAAAACG CCACCCAAA ACAAAAAAGA      300
AGAGTTTATG TTAATTTAGC GGTGTTTCTT TTTTATTGCT TAGCGAGCGC TTTATGGCTC      360
ATTCTAGAA GTGCCATAGA AGAAAAGCCC TTAGTCGTGG CGACAAAACC TAGCAGCGAG      420
CAGTATATTT TGGGCGAAAT TTTAAGCCTT TTGTTAGAAA AACACCATAT CCTATCAAG      480
CGAGCGTTTG GCATTGGTGG GGGGACGATG AATATCCATC CGGCATTGAT TAGGGGCGAT      540
TTTGATTTGT ATGTGGAATA TACCGGCACC GCTTGGGTGA ACACGCTCAA AAACCCTTTG      600
ACTCAAAAAG TGGATTTTGA AACGATTAAA AAGCGTTATG AGAAGGAATT TAATCTTTTG      660
TGGGTGGGAC TTTTGGGCTT TAATAACACC TATCTTTAG CGATTTCTAA AGAAGACGCT      720
CAAAAATACG CAATTGAAAC TTTAGCGGAT TTAGCCTTTC ATAGCCCGAA TTTTGATTTT      780
GGAGCGGAGT TTGATTTTTT TGAAAGAGAG GACGCTTTTA AGGGCTTAAT CAAAGCTTAT      840
CGCTTTCATT TTAGAAGTTT GCATGAAATG GATATTAATT TGCGTTATAA AAGTTTGTAA      900
TCCCATAGA TCAACGCTTT AGACGTCTTC ACTACAGACG CTCAAATCAA AGAGCTGGAT      960
TTAAGGTGC TGAAGGACGA TAAAGGGTTT TTTCTTAATT ATCAGGCCGG TATTGTT      1017

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936

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320

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GGAGCAAAAA TGAAAAAAT TGGTTTGAGC TTGTGTTTGG TTTTGAGTTT GGGTTTTTTA    60
AAAGCCCATG AAGTGAGCGC TGAAGAGATT GCGGATATTT TCTACAACT CAACGCCAAA    120
GAGCCTAAAA TGAAATCAA CCACACGAAG GGGTTTTGCG CTAAAGGCGT GTTCCTCCCT    180
AACCCGCAAG CAAGAGAGGA TTTAGAGGTG CCACTACTCA ATGAAAAAGA AATCCCTGCG    240
TCTGTAAGGT ATTCTTTAGG GGGCGTGGCG ATGCACGATA AAAGCAAGGT TAGGGGAATG    300
GCGTTAAAC TAGAAATCA AAACGCTAGT TGGACAATGG TGATGCTCAA TACAGAAATC    360
AATTTTGCCA AAAACCCTGA AGAATTCGCC CAATTTTTTG AAATGAGACT TCCTAAAAAT    420
GGCCAAGGTA GA                                     432

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(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321

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CATGAGTTTT TAGCTATTAA TGAATTGATG TTTGACGTGT TTTTGCCCAG CAGATTGAAA    60
CAAAAAGAGC TTTTAGAAAA AATTGAGGTG ATCCAAAAGT TTTTCCCTAA TTTTCCCAAA    120
GAAACGCTTT TAAACAATTA CAAAAAGAA AATTCGCTCT ATAACCATAA CCTCATTAAT    180
GTGGTGGGCT TCATTCCCTA TGCCACCATG CAATCCCTTT ATACCAAACT CATCCAAACT    240
CAAGGCATTT TTGTGCGCCC TTTAGACAAG CGCTACTACC CTAATAACGC TTTAGCTTCG    300
CATGTTTTAG GTTATGTGGG GGTGGCAAGT TTACAAGATT TAAAAGACGA TGAAGAGAAT    360
CAATACAGCC AGATTGTAGG CAAAACCGGC ATTGAAAAAG AATACAACAA GTTTTACAA    420

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937

GGCAAGGTGG	GTTATAAAAT	CATACATGTC	AATGCGCTCA	ATCAAGAATT	AGCCACCTTA	480
GAGGTCGTGC	CACCACGCTC	CAATAACCAC	TCGCAATTGA	GTTTAGACAA	ACGCTTCCAA	540
AAAGAAGCAC	ACAAGCTCTT	TGTAATAAG	AGAGGGCCTA	TTTTAGTGAT	GGATGCAGAA	600
AATGGGGAAT	TGCTCGTTGC	AGGAAGTTAC	CCTGAATACA	ATTTGAACGA	TTTTGTAGGC	660
GGGATCAGTC	AAGACAAATG	GCAAAACTC	CAAGATGATA	TTTATAACCC	TTTATTAAAC	720
CGCTTCGCTA	ATGCCTTGTA	TCCGCCGGA	TCTGTGGTTA	AAATGGGCGT	GGGGTTAAGC	780
TTTTTAGAAA	ACCTTCATAT	CACAGAAAAC	ACCACTATCC	CCACACCGCC	TTTTATTGAA	840
GTGGGCAAGC	GCAAATTCAG	GGACTGGA	AAAACAGGGC	ATGGCAATTC	TAATTTGTAT	900
AAAGCCATTA	GGGAGTCCGT	GGATGTGTAT	TTTTATAAGT	TGGGCTTGA	AATCTCTATA	960
GAAAAACTCT	CTAAAACCTT	AAGGGAAGTG	GGCTTTGGGG	AAAAAACGGG	CGTTGATTTC	1020
CCGAATGAAT	TGTGTTGGGAT	TGTGCCGGAT	AATTTGTGGA	AGCTCAAACG	CTTCAATCAA	1080
GACTGGCGCG	TGGGGACAC	GCTCATTACT	GCTATTGGGC	AAGGCTCTTT	TTTAGCCACG	1140
CCTTTGCAGG	TGTTAGCCTA	CACAGACTC	ATTGCGACAG	GCAAACCTGGC	AACGCCTCAT	1200
TTTGCTATCC	ATAACCAACA	ACCGCTCAAA	GACCCCTGA	ATAGTTTTCA	AAAAAAGAAG	1260
CTCCAAGCCT	TGCGCGTGGG	CATGTATGAA	GTGTGTAACC	ATAAAGACGG	CACCGCTTAT	1320
CATTCCACAA	GAGGTTCTAA	GGTTACCTTA	GCGTGTAATA	CCGGCACCGC	GCAAGTCGTA	1380
GAAATCGCTC	AAAACATCGT	CAATCGCATG	AAAGAAAAGG	ATATGGAATA	TTTCCATCGA	1440
TCCCATGCGT	GGATTACGGC	ATTCTTGCCC	TATGAAAAAC	CCAAATACGC	TATCACTATT	1500
TTAGTAGAAC	ATGGGGAGGG	AGGGTCAAAA	CTAGGGGGCT	TGTTAGTGAA	AATGAGCAAC	1560
AAACTCTATG	AGCTTGGCTA	TCTT				1584

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322

ATTAATTTTG	TTAATAAAGG	GGTTTTTATG	AACATATTCA	AGCGTATTAT	TTGCGTAACC	60
GCTATTGTTT	TAGGTTTTTT	TAACCTTTTA	GACGCCAAAC	ACCACAAAGA	AAAAAAGAA	120
GACCACAAA	TCACTCGTGA	GCTTAAAGTG	GGCGCTAACC	CTGTGCCGCA	TGCGCAAATC	180
TTGCAATCAG	TTGTGGATGA	TTTGAAAGAG	AAAGGGATCA	AATTAGTGAT	CGTGTCTTTT	240
ACGGATTATG	TGTGTCCTAA	TTTAGCGCTC	AATGACGGCT	CTTAGACGC	GAATTACTTC	300
CAGCACCGCC	CTTATTTGGA	TCGGTTTAAT	TTGGACAGAA	AAATGCACCT	TGTTGGTTTG	360
GCCAAATATC	ATGTGGAGCC	TTTAAGATTT	TATTCTCAAA	AAATCACAGA	CATTAAAAAC	420
CTTAAAAAAG	GCTCAGTGAT	TGCTGTGCCA	AATGATCCGG	CCAATCAAGG	CAGGGCGTTG	480
ATTTTACTCC	ATAACAAGG	CCTTATCGCT	CTCAAAGACC	CAAGCAATCT	ATACGCTACG	540
GAGTTTGATA	TGTCAAAAA	TCCTTACAAC	ATCAAAATCA	AACCCCTAGA	AGCTGCGTTA	600
TTGCCTAAGG	TTTTAGGGGA	TGTGGATGGG	GCTATCATAA	CAGGGAATTA	TGCCTTGCAA	660
GCAAAACTCA	CCGGAGCCTT	ATTTTCAGAA	GATAAGGACT	CGCCTTATGC	TAATCTTGTA	720
GCCTCTCGTG	AGGATAATGC	GCAAGATGAA	GCGATAAAAG	CGTTGATTGA	AGCCTTACAG	780
AGCGAAAAGA	CCAGGAAATT	CATTTTGGAT	ACCTATAAGG	GGGCGATTAT	CCCGGCTTTT	840

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs

938

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323

ATGATGATAA	CCAAACAATC	GTATCAAAGA	TTGCGTTTAA	TGCGGGTTTT	TGTGTTTTCG	60
CTTTCGGCGT	TTATTTTTAA	CACCACGGAG	TTTGTCCCTG	TTGCACTTCT	GTCAGACATT	120
GCGAAAAGCT	TTGAAATGGA	GAGCGCAACA	GTGGGGCTTA	TGATCACTGC	TTATGCATGG	180
GTGGTGTCTC	TTGGCTCATT	GCCCTTGATG	CTGCTTAGCG	CTAAAATTGA	AAGGAAACGC	240
TTATTGCTTT	TTCTTTTCGC	TCTTTTATT	TTCAGCCATA	TCCTTTCAGC	GTTAGCGTGG	300
AATTTTTGGG	TGCTTCTCCT	TTCTCGTATG	GGTATCGCTT	TTGCCCACTC	TATTTTTTGG	360
TCCATCACGG	CTTCTTTAGT	CATTCTGTGC	GCGCCAAGAA	ACAAAAACA	ACAGGCCTTA	420
GGGCTGTTAG	CGTTAGGGAG	TTGCTTAGCG	ATGATTTTAG	GGTTGCCGCT	TGGGAGGATC	480
ATTGGGCAAA	TTTTGGATTG	GCGATCCACT	TTTGGCGTGA	TTGGGGGCGT	TGCGACTCTT	540
ATAATGCTGC	TTATGTGGAA	ATTGCTCCCG	CATCTACCGA	GTAGAAACGC	CGGCACGCTC	600
GCAAGTGTC	CTATATTAAT	GAAACGCCCG	CTTTTAGTGG	GGATTTATTT	GCTTGTGATC	660
ATGTTATTTT	CTGGGCATTT	CACCACCTAT	AGCTATATTG	AGCCTTTTAT	CATTCAAATC	720
AGCCAATTTT	CTCCTGACAT	TACAACGCTA	ATGTTGTTTG	TGTTTGGGTT	AGCAGACGTG	780
GTGGGGAGTT	TTTTGTTCCG	CCGTTTGAT	GCGAAAAATT	CAAGAAAAAT	TATCGCTTTT	840
GCAATGGTTT	TAGTCATTTG	CCCGCAACTC	TTGCTTTTTG	TGTTTAAAAA	CTTAGAGTGG	900
GTGATCTTTT	TGCAGATTTT	CTTGTTGGGG	ATTGGGATTA	CTTCACTCAC	CATTACGTTA	960
CAAAATGAGG	GTATTCAC					978

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324

AAGGGCATTTC	AAAAGAAACA	AAATCTTAAA	GAGGTGGCTT	TAGACGCTTT	CTTGCCTAAA	60
AGCATCAATT	ACTACCATTT	TAACGGCTCT	CTCACCGCTC	CTCCTTGAC	AGAGGGGGTG	120
GCATGGTTTG	TCATAGAAGA	ACCTTTGGAA	GTTTCTGCCA	AACAATTGGC	TGAAATCAAA	180
AAACGCATGA	AAAATTCGCC	CAACCAACGC	CCCGTCCAGC	CTGACTACAA	CACCGTGATC	240

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939

ATTAAAAGCT CGGCTGAGAC CCGC

264

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325

AGGATAATTA AAATGAAAAA AACTTTTTTG ATCGCTTTAG CGCTTACGGC TTCTCTTATA	60
GGCGCTGAAA ACACCAAATG GGATTATAAA AATAAAGAAA ATGGCCCGCA CCGCTGGGAC	120
AAATTGCACA AAGATTTTGA AGTGTGCAAA AGCGGTAAAA GCCAATCGCC CATCAACATT	180
GAGCATTACT ACCACACGCA AGATAAAGCC GATTTGCAAT TCAAATACGC CGCTTCTAAA	240
CCTAAAGCGG TCTTTTTTCAC CCACCATACT TTAAAGGCTT CGTTTGAGCC GACTAACCAC	300
ATCAATTATA GAGGGCATGA CTATGTGTG GATAATGTGC ATTTCCACGC CCCTATGGAG	360
TTTTTAATCA ATAATAAAAC CAGGCCTTTG AGCGCGCATT TCGTGCATAA AGACGCTAAA	420
GGCGGTTTGT TGGTGTTAGC GATTGGGTTT	450

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326

ATGCCTGTTA TAAGAGTTTT AGTAATGCTT GCAACAATGA TGATGAAATT AGTAAAAACG	60
GCAAAAGAAA AGAAAGTTTT TAAGAATGTG GGAATATCTA TAATGGGGAT TGCTTTTTTG	120
GAAGCGATAA AAGACTCGAT AAAAAACAA ATTAAAAAAA GCGATTGGAT ATGCGGGAAT	180
GTTAAGACTG CGGATGATTA TTAAAAACG CATCCTAACT CATGGTTTAA TTCAGCAATA	240
GGTGTAAACAG CGATAACAGC CATGCTTATG AATGTGTGTT TTGCTGATGA CCAATCCAAA	300
AAAGAAGTGG CTCAAGCTCA AAAGGAAGCT GAAAACGCTA GGGATAGAGC GAACAAGAGT	360

940

GGGATAGAAC	TGGAACAAGA	AGAGCAAAAG	ACAGAACAAG	AAAAACAAA	GACAGAACAA	420
GAAAAACAAA	AGACAGAACA	AGAAAAACAA	AAGACAGAAC	AAGAAAAACA	AAAGACAGAA	480
CAAGAAAAAC	AAAAGACAAG	CAATATAGAG	ACTAACAATC	AAATAAAAGT	AGAACAAGAA	540
CAACAAAAGA	CAGAACAGGA	AAAACAAAAG	ACAAACAATA	CGCAAAAAGA	TTTGGTTAAC	600
AAAGCAGAAC	AAAATTGCCA	AGAAAATCAT	AATCAATTCT	TTATTAAAAA	ATTAGGAATT	660
AAGGCTGGCA	TTGCTATAGA	AATAGAAGCT	GAATGCAAAA	CCCCTAAACC	CACAAAAACC	720
AATCAAACCC	CTATCCAGCC	AAAACACCTC	CCAAACTCCA	AACAACCCCA	TTCTCAAAGA	780
GGATCAAAAAG	CGCAAGAGCT	TATCGCTTAT	TTGCAAAAAG	AGCTAGAATC	TCTGCCCTAT	840
TCACAAAAAG	CTATCGCTAA	ACAAGTGGAT	TTTTATAGGC	CAAGTTCTAT	CGCTTATTTA	900
GAAGTAGATC	CTAGAGATTT	TAACGCTACA	GAAGAATGGC	AAAAAGAAAA	TTTAAAAATA	960
CGCTCTAAAG	CTCAAGCTAA	AATGCTTGAA	ATGAGGAGTT	TAAAACCAGA	CCCACAAGCC	1020
CACCTTTCAA	CCTCTCAAAG	CCTTTTGCTC	GTTCAAAAAA	TATTTGCTGA	TGTTAGTAAA	1080
GAAATAAAAG	TAGTTGCTAA	TACCGAGAAA	AAAGTAGAAA	AAGCGGGTTA	TGTTTATAGT	1140
AAAAGGATG						1149

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327

AATAAAAGGA	AGAACATTAA	AGAAGTTTAT	GCGGGCGAGA	TTTGCGCGTT	CGTGGGCTTG	60
AAAGACACGC	TGACTGGGGA	CACGCTTTGC	GATGAAAAGA	ATGCGGTGGT	TTTAGAGAGA	120
ATGGAATTTC	CTGAGCCGGT	CATTCACATC	GCTGTGGAGC	CTAAAACGAA	AGCAGACCAG	180
GAAAAAATGG	GCGTAGCGTT	AGGCAAGCTT	GCTGAAGAAG	ATCCAAGCTT	TAGGGTGATG	240
ACTCAAGAAG	AAACCGGTCA	AACCCTTATT	GGTGGTATGG	GTGAATTGCA	CCTAGAAATC	300
ATCGTGGATA	GATTGAAGAG	AGAATTTAAG	GTGGAAGCTG	AAATCGGTCA	GCCGCAAGTC	360
GCCTTTAGAG	AGACTATCCG	CTCAAGCGTG	AGCAAAGAGC	ATAAATACGC	TAAGCAAAGT	420
GGTGGCCGTG	GGCAATACGG	GCATGTGTTT	ATCAAGCTTG	AGCCTAAAGA	GCCTGGCAGT	480
GGGTATGAAT	TTGTGAATGA	AATTTCTGGG	GGCGTGATCC	CTAAGAATA	TATCCCTGCC	540
GTGGATAAGG	GTATCCAAGA	AGCGATGCAA	AATGGCGTTT	TGGCAGGCTA	TCCGGTGGTG	600
GATTTTAAAG	TTACCCTTTA	TGATGGGAGC	TACCATGATG	TGGATTCTTC	AGAAATGGCG	660
TTTAAATCG	CTGCTCTAT	GGCGTTTAAA	GAAGCGAGTC	GTGCGGCTAA	CCCAGTTTAA	720
CTAGAGCCTA	TGATGAAAGT	GGAAGTGGAA	GTCCCTGAAG	AATACATGGG	CGATGTGATT	780
GGCGATTTAA	ACAGAAGAAG	AGGGCAAATC	AATTCATATG	ACGATAGATT	AGGTTTGAAA	840
ATCGTGAATG	CTTTCGTGCC	GTTAGTGGAA	ATGTTTGGTT	ATTCTACGGA	TTTGCGATCA	900
GCCACTCAAG	GGCGTGGGAC	TTACTCTATG	GAGTTTGACC	ACTATGGCGA	AGTGCCTAGC	960
AATATCGCTA	AGGAAATCGT	GGAAAAACGC	AAAGGC			996

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

941

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328

TCTAAAGGG	CGTTCGCAAG	CTCTTTAGTG	TCTTCTAAGC	TGTTTTTGAG	GGACAAAGAA	60
ACTCGTAAAA	GGGGTTTAGA	AACCGTAGGG	GGGCGGATAG	CCCCCACTAA	AAACCCCTTT	120
TCTTTCAAAA	AATATTGGGC	GTTTAAAAGA	GCGGGATTGT	TTTCAAACCTC	TAGGGTAAAA	180
AATCCTGTAG	GCGTTCTAAC	GCCTAAAGTT	TCAAAAATAA	TCTGTTGGTG	TTTGCTAAGC	240
TCATTTTTTA	ATTCTTGTTT	TTGCGCGATA	AAGTATTCTA	AATGGGCCAA	AGTCAAAGCG	300
GTGTCTAACA	GGCTTAAAGC	GGTGTA				327

(2) INFORMATION FOR SEQ ID NO:1329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329

ATAAGGAATG	CCACCATGTT	TGGGAATAAG	CAGTTACAGC	TTCAAATCAG	TCAAAAAGAT	60
TCTGAGATTG	CGGAGTTAAA	AAAAGAAGTC	AATCTCTATC	AAAGCCTTTT	AAATTGTGTC	120
TTGCATGAGG	GTTTTGTAGG	TATTAAAAAC	AATAAAGTCG	TTTTTAAAAG	CGGGAATCTT	180
GCAAGCTTAA	ACAATTTAGA	AGAACAAAGC	GTTTCATTTA	AAGAAAACGC	AGAAAGCGTT	240
AATTTACAAG	GGGTTTCTTA	TTCTTTGAAA	AGCCAAAATA	TTGACGGCGT	GCAGTATTTT	300
TCATTGGCTA	AAAAAACAGG	GGGTGTGGGG	GAATACCATA	AAAATGATTT	GTTTAAGACT	360
TTTTGCACGA	GCTTAAAAGA	GGGCTTAGAG	AACGCGCAAG	AAAGCATGCA	GTATTTCCAT	420
CAAGAAACAG	GCTTGCTCTT	GAATGCGGCT	AAAAATGGCG	AAGAGCATTG	TAATGAAGGA	480
TTAATAACCG	TTAATAAAAC	GGGTCAAGAC	ATTGAATCGC	TTTATGAAAA	GATGCAAAAC	540
GCCACTTCGT	TAGCGGACTC	CCTCAACCAA	CGGAGCAATG	AAATCACTCA	AGTCATTTCT	600
TTGATTGATG	ATATTGCAGA	GCAAACCAAT	CTCTTAGCCC	TAAACGCCGC	TATTGAGGCC	660
GCACGAGCGG	GTGAACATGG	CAGAGGGTTT	GCGGTGGTGG	CTGATGAGGT	GAGAAAGCTC	720
GCTGAAAAAA	CCCCAAAAGC	CACTAAAGAA	ATCGTGTCG	TGGTTAAAAG	CATGCAACAA	780
GAAGCGAAGC	ATATTCAAAC	CAACACCCAC	GATATTAATT	CTATTGTAGG	CTCTATTAA	840
GGTGATGTGG	AAGAGCTTAA	ATCCACCGTA	AAAAATAACA	TGATTGTGCG	GCAAGCCGCA	900
AAATACACCA	TCTACAATAT	CAATAACCGG	GTGTTTTGCG	GTCTGGCTAA	ACTCGATCAT	960
GTGGTCTTTA	AAAACAATCT	TTATGGCATG	GTCTTTGGTC	TCAATTCCTT	TGACATTACC	1020
AGCCATAAGA	GTTGCCGTTT	AGGCAAATGG	TATTATGAGG	GTGCGGGTAA	AGAAAACTTT	1080

SUBSTITUTE SHEET (RULE 26)

942

GCTAACACTT	CAGGCTATAG	AGCTTTAGAA	AGCCACCATG	CGAGCGTGCA	TGCTGAAGCT	1140
AATGATTTCG	TTAAAGCCGT	TCAAGAAGAT	CACGTCACCG	ATTCAAAATA	CCTAGAACAT	1200
AAAGTGCATT	TAATGGAAGA	TAGCGCTAAG	CATGTCAAAG	AAAATATTGA	TAAGATGTTT	1260
TATGAAAAAC	AAGATGAACT	CAATAAAATC	ATTGAAAAAA	TTCAAAAAGG	CGAA	1314

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330

GAGTGGTTAA	TGCTAAAAAA	GATTTTTTAT	GGTTTTATCG	TTTTATTTTT	GATTATCGTA	60
GGGTTGTTGG	CCGTTCTTGT	CGCTCAAGTT	TGGGTAACCTA	CGGATAAGGA	TATTGCTAAA	120
ATTAAAGATT	ATCGCCCCAG	TGTCGCTTCA	CAGATTTTAG	ACAGAAAAGG	GCGTTTGATC	180
GCTAATATTT	ATGATAAGGA	ATTTGCTTTT	TATGCGCGTT	TTGAAGAAAT	CCCCCCACGA	240
TTTGTTGAAA	GCTTCTAGC	GGTAGAAGAC	ACCCTCTTTT	TTGAGCATGG	GGGGATCAAT	300
TTAGACGCTG	TCATGCGCGC	TATGATTAAA	AACGCTAAAA	GTGGTCGTTA	CACTGAAGGG	360
GGTAGCACTC	TAACCCAACA	ACTCGTTAAA	AACATGGTGC	TCACACGGGA	AAAAACCCTA	420
ACCAGAAAAC	TCAAAGAAGC	TATCATCTCC	ATACGCATTG	AAAAAGTCTT	AAGCAAAGAA	480
GAAATTTTAG	AGCGTTATTT	GAACCAAACCT	TTTTTTGGGC	ATGGGTATTA	TGGCGTGAAA	540
ACCGCAAGTT	TAGGGTATTT	TAAAAAACCC	CTTGACAAAC	TCACGCTTAA	AGAAATCACC	600
ATGTTAGTCG	CCTTACCTAG	GGCTCCAAGT	TTTTATGACC	CTACCAAAAA	TTTAGAATTT	660
TCACTCTCTA	GGGCTAATGA	TATTTTAAGG	CGGTTGTATT	CTTTAGGCTG	GATTTCTTCT	720
AACGAGCTCA	AATCCGCTCT	CAATGAAGTG	CCAATCGTCT	ATAACCAAAC	TTCCACGCAA	780
AATATCGCTC	CCTATGTCGT	GGATGAAGTG	TTGAAGCAAT	TGGATCAATT	AGACGGGTTA	840
AAAAGCTAAG	GCTATACCAT	AAAACCTACG	ATAGATTTGG	ATTACCAACG	CTTAGCGTTG	900
GAGTCTTTGC	GTTTTGGGCA	TCAAAAAATC	TTAGAAAAAA	TCGCTAAAGA	GAAGCCAAAA	960
ACTAACGCTT	CTAATGATAA	AGATGAAGAC	AACTTAAACG	CCCAGCATGA	TAGTTACAGA	1020
AACGAGCACC	GG					1032

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

943

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331

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ATACGAACAC CAATGGATAC CATAAAAAGC ATTCCCATAA GAACTTTTAT TTTACTCTAT      60
AAAAGCTCAC CAAAATGTGT TGTGTTGGCA TCAATTACAG TGCTATTTGT CGGCATTCTT      120
CCATCTCTGA ATATTCTTGT TATGATAAAA TTGATTGATA TTGTGGTGAA TCTATTACAA      180
AAGCATACGC ATTTTGAATA CAGCTTGCTG TTACCAACTT TACTACTATG GGGAGCCTTG      240
CTGTTTTTAA CGCATGTGTT CTCAGGAATT TTATCAAGCT TGCAAACCAT TATTGCCGAA      300
CAATTTTCTA TAAATATCAT CACTCAGCTT GCTAATAAAC TCACACAAGT TAAAAATCTA      360
AATTTTTTTG AGAATAAAGA CCATACTATC AAGCTTAACA CTATCCATAA CGGACTGCAC      420
ATCGCCCCC TAAATTATGT CAGTAATCTT TTTTCAATC TACAACGCAT TATAGGGCTT      480
ATCAGTCTGT TTGGGATATT ATTTTCCATT AGTATTTATC TACCCTTTAT AATGATTTTT      540
GCAACAGTGC CTTGTATTCT CATTTCACAC CATATAGCAA AAAAACATAG TGCTTCCATA      600
GATAAACTTC AAGACCAAAA AGAAAGCATG CAAATTACT TATACTCTGG ACTAGATAAC      660
CAAAAGAACA AGGACAACCT ATTATTTAAC TTCATGCTAA ATTTTCACCA TAAATTTATT      720
GAAACAAAAG AATTGTATCT CAATAATTTT GTGAAAGTAG CCCAAAAAAA CTTAATATTT      780
ACCATATATG CTGATGTTTT AATCACCCTT CTAAGTATTG CACTATTTTT TCTAATGGTT      840
TTTATTATCC TTTCAAAATT AATTGGTGTG GGAGCAATTG CTGGGTATAT CCAAGCATTT      900
AGCTCTACCC AACAACAAC TACAAGATTA TCATTTTATG GAAAGTGGTT TTTTGCTATC      960
AATAAATACT TTGAAAATTA TTTCTGTATT TTAGATTACA AAATACCGAA ACCAGAAACA     1020
CAATCAAAAT TAGAAGAAA AATCCATAGC ATTACATTTG AAAATATTAG TTTCTCTTAT     1080
CCTAATTCAA AACTTATTTT TGAAAACCTT AATCTCTCTT TACACTCTAA TAAAAATTAT     1140
GCATTAGTCG GCAAGAATGC TAGCGGAAAA AGCAGCTGTA TTAATTTTAT ATTAGGTTTT     1200
TATACCCCAA ATTCAGGTCA AATTATCATT AATAACAAAT ACCCATTACA AGACTTGGA      1260
CTAAATAGCT ACCATCAACA AATGAGTGCC ATATTTCAG ATTTTCTCT TTAGCTGGG      1320
TATAGCATTG ATGATAATCT TTTTATGCAA AACAATATCA CTAAAGAGCA ATTGAAGCAA      1380
AAAAGAGAAA TACTAAAATC TTTTGATGAG AATTTTCAAA ATTGTCTTAA TGATTGCAAC      1440
AACACACTAT TTGGAGCGCA ATATAATGGG GTAGATTTTT CTTTAGGTCA AAAGCAACGC      1500
ATAGCTACCA TGAGAGCCTT TTTAAAACCA AGTAATTGCA TGTGTTTGA TGAGCCAAGC      1560
AGCGCCATCG ATCCCATTAT GGAAAAAGAG TTTTATGATT TTATTTTTAA AAAATCGCAA      1620
TCTAAGATGG CTTTAATTAT TACACACCGC ATGAATAGTG TCAAGCAAGC TAATGAAATT      1680
ATCGTGTTAG ATCAAGGCAA ACTAATAGAA CAGGGCAACT TTGAAACCC TATGAAAAAA      1740
CAGGGATTAT TTTGCGAATT GTTTTTGAAA CAACAATAC      1779

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(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332

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ACGCCCAGCA TGATAGTTAC AGAAACGAGC ACCGGTAAGA TTTTAGCCTT AGTGGGGGGG      60
ATTGATTATA AAAAAAGCGC TTTCATCGC GCCACGCAAG CCAAACGGCA GTTTGGGAGC      120
GCGATCAAGC CTTTGTGTA TCAATCGCT TTTGATAATG GCTATTCCAC CACTTCCAAA      180

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944

ATCCCTGATA	CCGCGCGAAA	TTTTGAAAAT	GGCAATTATA	GTAAAAACAG	CGTGCAAAAC	240
CACGCATGGC	ACCCTAGCAA	TTATACTCGC	AAATTTTITAG	GGCTTGTAAC	CTTGCAAGAA	300
GCCTTGAGCC	ATTCGTTAAA	TCTGGCTACG	ATTAATTTAG	CGATCGCTTG	G	351

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333

CAAGGAGTTA	CAACAATGGC	TTTTCAGGTC	AATACAAATA	TCAATGCGAT	GAATGCGCAT	60
GTGCAATCCG	CACTCACTCA	AAACGCACTT	AAAAC TTCAT	TGGAGCGATT	GAGTTCAGGT	120
TTAAGGATCA	ATAAAGCGGC	TGATGACGCA	TCAGGCATGA	CGGTGGCGGA	TTCTTTGCGT	180
TCGCAAGCGA	GCAGTTTGGG	TCAAGCGATT	CCCAACACGA	ATGACGGCAT	GGGGATTATC	240
CAGGTTGCGG	ATAAGGCTAT	GGATGAGCAA	TTAAAAATCT	TAGACACCGT	TAAGGTTAAA	300
GCGACTCAAG	CGGCTCAAGA	TGGGCAAACT	ACGGAATCTC	GTAAAGCGAT	TCAATCTGAC	360
ATCGTTTCGT	TGATTCAAGG	TTTGATAAT	ATCGGTAACA	CAACGACTTA	TAACGGGCCA	420
AGCGTTATTG	TCTGGTCAAT	TCAC				444

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334

TTCAAGGTTT	GGATAATATC	GGTAACACAA	CGACTTATAA	CGGGCCAAGC	GTTATTGTCT	60
GGTCAATTCA	CTAACAAAGA	ATTCCAAGTA	GGGGCTTATT	CTAACCAAAG	CATTAAGGCT	120
TCTATCGGCT	CTACCACTTC	CGATAAAATC	GGTCAGGTTT	GTATCGCTAC	AGGCGCGTTA	180
ATCACGGCTT	CTGGGGATAT	TAGCTTGACT	TTTAAACAAG	TGGATGGCGT	GAATGATGTA	240

945

ACTTTAGAGA	GCGTAAAAGT	TTCTAGTTCA	GCAGGCACAG	GGATCGGCGT	GTTAGCAGAA	300
GTGATCAATA	AAAACCTCTAA	CCGAACAGGG	GTTAAAGCTT	ATGCGAGCGT	TATCACCACG	360
AGCGATGTGG	CGGTCCAGTC	AGGAAGTTTG	AGTAATTTAA	CCTTAAATGG	GATTCATTTG	420
GGTAATATCG	CAGATATTAA	AAAAACGAC	TCAGACGGAA	GGTTAGTCAC	AGCGATCAAT	480
GCGGTCACTT	CAGAAACCGG	TGTGGAAGCT	TATACGGATC	AAAAAGGGCG	CTTGAATTTG	540
CGCAGTATAG	ATGGTCGTGG	GATTGAAATC	AAAATTGACA	GCGTCAGTAA	CGGGCCTAGT	600
GCTTTAACTA	AACGATGGTC	AAAGAGCGGT	CAAGATGAAA	CGAAGGGATC	TACTAACTAC	660
GGAAGGTATT	CTCGGACACG	CCTAGACGTA	AGAGCATCAA	TGTCGATTTCG	GTATTTAAAT	720
CACGCTTGCT	TGCTTCAGAG	CTAT				744

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335

TCACCTCTTT	GGTTAAAAAC	ACGATTCCCA	AATATTTGGC	TCGCTAAAAT	CCTTTATATG	60
GCTATCTTGC	TTTGCGCGAT	CGCTCATTCT	GTGGGGCTAA	TCTTGCGCTG	GTATGTGAGT	120
GGGCATTGCG	CTTGGAGTAA	CGCTTATGAG	TCCATGCTCT	ATATCGCATG	GGCTTCTGTT	180
ATCGCAGGGT	TTGTTTTACG	ATCCAAACTC	GCGCTATCGG	CTTCTAGCTT	TTTGGCCGGT	240
ATCGCGCTCT	TTGTGGCTCA	TTTAGGCTTT	ATGGACCCTC	AAATTGGCCC	TTTAGTGCCG	300
GTGTTAAAAAT	CCTATTGGCT	CAATATCCAT	GTCTCTGTCA	TCACCGCTAG	TTATGGCTTT	360
TTGGGCTTGT	GTTTTGTGCT	AGGGATTTTA				390

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336

946

AAAAGGCTTG	AAATGGGCTT	GTCTGTAGGC	ATTGTGGGTT	TGCCTAATGT	GGGCAAATCC	60
AGCACCTTTA	ACGCGCTCAC	CAAAACCCAA	AACGCCCAAA	GTGCGAATTA	CCCTTTTTCG	120
ACCATTGAAC	CCAATAAAGC	CATTGTGAAT	GTGCCTGACA	GGCGGCTTGA	TGCGTTGGCT	180
CAAATCGTAA	AGCCTGAACG	AATCTTGCAT	TCTGTGGTGG	AATTTGTGGA	TATTGCCGGA	240
TTGATTAAAG	GGGCGAGCAA	GGGGGAGGCT	TTAGGCAATC	AGTTTTTAGC	CAATATCAAG	300
GAATGCGAAG	TGATCTTGCA	AGTGTGCGC	TGTTTTGAAG	ATGACAATAT	CACGCATGTG	360
AACGATAAAA	TTGACCCCTT	AAATGATATA	GAAACCATTG	AATTGGAATT	GATTTTGGCG	420
GATATTGCCA	CTTTAGACAA	AAGGATCGAT	CGCTTGCAAA	AAGCCCTAAA	AAGCTCAAAA	480
GACGCTAAAA	ATCTTTTAGA	ATGCGCTTTG	AGTTTAAAAA	CGCATTTAGA	AGAATTGAAG	540
CCGGCGAAAA	CTTTCCCTTT	AAACACGAGC	GAGGCTTTTT	TGGAATTAGA	CAAGGAATTG	600
CGTTTTTTAT	CCCATAAAAA	AATGATCTAT	GTGCTAATG	TGGGCGAAGA	AGATTTAAAT	660
ATTCTCAACG	AGCATGCCAA	AAAAGTTGAA	AACCATGCGA	AAGTCCAAAA	TAGCGAGTTT	720
GTGCGCTTGT	CGCTAAAT	GGAAGAAGAA	ATGTTTCTA	TGAGTGGAGA	TGAAGTCAAA	780
GAATTTTTTC	AAAGTTTGGG	CGTAGAAGAA	AGCGGGCTAG	AAAAAACCAT	TCGTTTGAGT	840
TTTAAGGAAT	TAGGCTTGAT	CAATTATTTT	ACCGCTGGAG	TCAAGGAAGT	GCGATCATGG	900
ACGATTAAAA	AAGGTTCTAG	TGCGCCTGTG	GCTGCTGGGG	TGATCCATAA	GGATTITGAA	960
AAAGGCTTTA	TTAGAGCTGA	AACCATCAGT	TATGACGATT	TTATCGCTTA	TAAGGGCGAA	1020
GCCGGGGCGA	AAGAAAAGGG	AGCGTTACGC	ATTGAAGGTA	AGGATTATAT	CGTTCAAGAT	1080
GGCGATGTGT	TGCATTTTCG	CTTCAATGTC				1110

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337

AGGAATAAAA	CCATGCAAGC	GTTAAATCA	TTGCTTGAAG	TGATTACAAA	ACTCCAGAAT	60
CTAGGCGGCT	ATTTGATGCA	TATAGCTATT	TTCATCATTT	TTATTTGGAT	TGGAGGGCTT	120
AAGTTTGTGC	CTTACGAAGC	TGAAGGGATC	GCCCTTTTGG	TGGCCAACTC	CCCTTTCTTT	180
TCTTTCATGT	ATAAATTGGA	AAAACCTGCA	TACAAACAAC	ACAAAATGTC	TGAATCCCAA	240
TCCATGCAAG	AAGAAATGCA	AGATAACCCT	AAAATCGTTG	AAAACAAAGA	ATGGCATAAA	300
GAAAACCGCA	CTTATTTAGT	GGCTGAAGGT	TTAGGGATTA	CGATCATGAT	CCTAGGCATT	360
TTGGTGCTTT	TGGGGCTTTG	GATGCCTTTA	ATGGGCGTAG	TTGGGGGCTT	CTTGTGCTG	420
GAA						423

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

947

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338

CGATCACCAC	CCTATTCTTT	TTTATTCACA	ACGCCAGAAG	TGTTTGTCAA	TCAGCATTTT	60
CCATGGCTTT	CTGGGGCTGG	AAGGCTAGTG	GTTAAAGACT	TGGCGTTATT	TGCTGGAGGC	120
TTGTTTGTTG	CCGGATTTGA	TGCGAAACGC	TATTTGGAGG	GTAAAGGGTT	TTGCTTGATG	180
GACCGCTCAT	CGGTAGGGAT	TAAAACTAA	TGCTCTAGCG	GGTGTGCTC	T	231

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339

TGGTGTTTTA	CAAATATTCA	GGAAATCGGG	AATGATTTTT	TAATCCCTCA	AAGTTTCAAA	60
AAAAAAGATT	TTTCCAATTT	AGCCCAACAG	GTGTGCCATA	GGCATGAGGG	TTTTGGGGCA	120
GATGGGCTTG	TGGTCGTCTT	ACCGAGTAAA	GATTATGACT	ACGAATGGGA	TTTTTACAAT	180
TCAGACGGCT	CTAAAGCCGG	CATGTGTGGG	AATGCCAGCC	GTTGCGTGGG	GTTATTTGCC	240
TACCAACATG	CTATAGCCCC	TAAAGAGCAT	GTTTTTTTAG	CCGGAAAAAG	AGAGATTTCT	300
ATCCGCATAG	AAGAGCCCAA	CATCGTAGAG	AGCAATCTCG	GTAATTATCA	AATCCTAGAC	360
ACCATACCCA	ATTTAAGATG	CAAAAAATTT	TTTACTAATA	ACAGCGTTTT	AGAAAAATATC	420
CCTATGTTCT	ATCTTATCAA	TACAGGAGTG	CCTCATTTAG	TGGGATTTGT	GAAAAATAAA	480
GGGTTATTAA	ATTCTCTTAA	CACACTGGAA	TTAAGGGCTT	TAAGGCATGA	ATTTAACGCT	540
AATATTAAAC	TCGCTTTTAT	AGAAAAATAA	GAGACGATTT	TTTTACAAAC	TTATGAGAGA	600
GGGGTTGAAG	ATTTACGCT	AGCTTGCGGG	ACAGGCATGG	CAGCGGTTTT	TATCGCCGCG	660
CGCCTTTTTT	ATAACACCCC	TAAAAAGCC	ACTCTCATCC	CTAAAAGCAA	CGAATTTTTTA	720
GAGCTTTCTT	TAAAAATGA	TGGAATTTTT	TATAAAGGAG	TGCGCGGTTA	TATCGGCATG	780
AGCGTTTTAG	GCATGGGTGT	TTTTAAAAAT	GGGTGTTTTT			819

(2) INFORMATION FOR SEQ ID NO:1340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1077 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

948

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1077
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340

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TTTTTGGTTC AGTTTAAATGG GGATAATTGC ATGAAAGCTC AGTATTTCTT TTGGATTCTT      60
TTTTTGATTG GTTTTTATATG GATGCTTTAT CTGTATCAAG ATTTTTTAAT GGACGCACTG      120
ATCGCTGGGC TTTTGTGTGT GGGGCTTTTT CAAGTGAAAG TTTTTTTGAA TAAACGCTTT      180
TCTAATGTTA TCAGTTTCGTT TTTATGCGTT TTGGTTTTAG CGAGCGTTGT GATCGTGCCG      240
TTGTATTTTA TTGTTTATAA GGGTCTAAT GTCATTTTTG AAATCAATT TGAAAAACTT      300
TCAGCCTTAA TCAATGGCT TAAAGGGACA ATCACCAGAA ATTTGTCCGA TTTTCCTGCC      360
ATTCATGATG GGGTTAGCAA GTTTTTAGAA AATTTAGCG CCGCTTCCAT CACGGGCTAT      420
TTGTTGAAAG TGAGCAGTTA TATTGGGAAA TACAGCTTGA AACTCGTTAC AGACGCTTTA      480
TTTATCTTGG GGTATTGTT TTTCTTTTTT TACTATGGGG AGAAATTTA TCGTTATTTT      540
TTAGGGGTCT TGCCTCTTGA AATGAATCAA AGTAAAAAAA TTTTGAAGA AGTGGCTGGG      600
ATTTTACGAA TCGTGCCTTT AACTTCTCTC ATCACGGTTA TTTTAGAGGG CGTGGCGTTT      660
GGGACGATGA TAATATGGTT TGGGCATGAT GGCTGGTCTT TAGGGATTTT ATACGGCCTA      720
GCGTCTTTGG TGCCGGCTGT TGGGGGGGCT TTGATTTGGA TCCCTATAGC GATTTATGAG      780
CTTTATCATG GGCATGTGAA TGAGGCTATT TTTATCGTTT TGTATTCCAT TTTGTTAATT      840
GGTGTGTTGA TTGATAGCGT GATCAAGCCA ATTTTAATCG TTTTATCAA AAAAGAATC      900
TTTAAACCA CCCTTAAAT CAATGAAATA TTGATTTTCT TTTCTATGAT TGCTGGGATT      960
TCTCAATTTG CTTTTTGGGG GATTATCGTA GGGCCTACCA TCACGGCGTT TTTTATCGCG      1020
TTACTGCGAT TGTATGAAAA TTACTTTATT CAAAAGGAGC AAAAAACATG CGAATGT      1077

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(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 645 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341

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AGGTAAACA TGAACACAA AGTTGCATCT GCTAGAAATA TCGCAACGCT TCTTTTCTTA      60
TTCTTTTCTC AAAGTGAAGC TTTTGATTTC GGTAAAATCG CTAATATCAA AGCGGGTGCT      120
GAAAGTTTCT CTAAAGTCGG TTTCAATAAC AAACCTATCA AACTAATAA AGGGATTTAC      180
CCTACCGAAA CCTTTATGAC GATTATGGCT TACATGCAGG TGGATTTTAC GGAGCTCTTG      240
CCCAAAAGCG CTACGGCTAA CGGGCACCAT TTAGACGGGA GCCTTGGGGG TTGGGGGGGT      300
GCTGTGATTT ATGATAGCAC TAAGGATTTT ATTAACGAAG TTACAGGAAA ACCCTATGGG      360

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949

GCTATGACGT	GGAACACGT	GGGCTATTGG	GGCGGTCTTG	TAGGGCAAAA	ACCATGGGCT	420
AGTTGCGGGT	TAGCCACAGG	GAATTTGACC	CAAGGCCAAT	ACGATAAGAT	GACTCAAGCT	480
GAAATGACGC	AGTTGTCTAA	TCAAGAAGCT	TTAGCGGCTT	CCACTTGCGC	AAAAACCTAT	540
GCCGATCACA	CGAGAACTA	TGTGATTTAT	AACGCTTACT	TGCGCTACAA	CTACAAAGAT	600
ATTTTTGAAA	TTAGGGGCGG	AAGGTACGAA	TCCCAGCGGA	TTATA		645

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342

ATTTTCTATC	CAAATGGGTA	TAATAATCGC	ATGGGTTTTT	TAAAAGTTTT	AAAACATGAC	60
GCTTTAGGGC	AAGTAGGGAA	TATTGTTATA	GGGAATTTC	TAATAACGCT	CACTGTTTTA	120
GCGGTTTGTT	TTTCCTCTCA	AAGCGCTGAA	GAAACGACCA	TGCTCACCC	AAGCTACACG	180
CTCTTTTTTA	TTTTAGGGGC	GTTTTTATTA	GTCGCAATCA	GCGTGGGAGC	GATCAAAAAC	240
CTCAACGCGC	TTTTTTCTAA	AAGAGGGGTT	TAAAGCTTTT	CCTTACCCAT	TAGTTTGGAA	300
TCTTTATTGC	TCCCTAAAAT	CTTGCTCCCC	ATGGTGTGTT	TTATCTTCAG	TTTGTTCTGG	360
TTTGTGGCGA	GCGTGCGTTT	GGGCTATTAC	CTTTTTAACG	CGCAATCCAG	CGTGCTGTTT	420
ATCTTGACAC	CCGCTTTAAA	AACCTTTGCG	TTAAAACCCA	CTAAAACCTAT	AGGCGTTGCG	480
CTGTTTTTAG	GGCTTGTTTT	AATGAAATTT	TTATTTGTTT	TGAGCGTTTT	AAACGCTACT	540
AGGATCAAAA	AAGCGCGTTT	TTTACTCGGG	GGGTTGTGTT	TCATTCTGGT	GGGGGTTGTT	600
TTGGAATTGG	CTTTCAATTC	GTTACTGCCC	TTAATGAGTT	CTAGTTTGAG	CATCAATGAG	660
GGGTTTTATT	ATTTCTTGCA	ACAACAAGAA	TTACAAGAAA	ATAAATACTA	TCTTTTATGG	720
GGGGTGGATT	TTTTAAAAAT	CCTTTTATTG	TATGGGGTGA	TCCGTTACTT	GCTCACGCAT	780
AAATTAGAAT	TGGAT					795

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

950

(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343

CACATGAAAG	GCTTATGGCT	TGTAATCTCT	TTAGTTTTTG	TTGGTTTTTT	GTGGGCTAAT	60
GAATCTTATG	TTTTTAACAA	TTCTAAGGGG	CGTTTAACAG	AAAAAAGCGT	TGCGTTTATA	120
GAGGGCGTTT	CTAAAGAGCT	TTATCTTAAA	ACCGGCGTGC	GTTTTGCGAT	TGATATGACG	180
GATTTTGAAA	AAAATCCTAT	CGCTCTAGCG	AATAAAAAAG	AGCGCCAAAG	CTATCAAGAG	240
GGCTTTTTTA	AGCAGCTCAA	ACCCCTTTT	GTGGTATTCT	TTTTCTACCA	TGACGCTCAA	300
AAAATAGAAAT	TAGTGGCTAA	CCCTAAAGAT	TTGCTAGACA	CTGATAAAAT	CTTTTTTGAA	360
AAAATCGCTC	CCTTACTCCC	CACAAACGCT	AAAGAATACA	CGCCCCAAAG	AATTCAGCC	420
ATGCTCATT	ACGGCTATTC	GGTCGCAGTA	GATGCTTTAG	CGGAAAAATA	TCATGTGAAT	480
ATCACGCAAA	ATTTTAGCGC	TCCTAAGGGA	GTAACCTTTG	TAAAGGTGGT	TATTTATATT	540
TTGTTATTGA	CGCTTTTGGG	CGCGTTTTTG	GGGCTTTATT	TTTTTAAAA	ATCT	594

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344

GAGGGAAAAT	CAATGAAAGA	AAAAAACTTT	TGGCCTTTAG	GAATCATGAG	CGTGCTTATT	60
TTTGGGCTTG	GGATCGTGCT	GTTTTTAGTG	GTGTTGCCC	TAAAAAATTC	GCCTAAAAAT	120
GATTTAGTGT	ATTTCAAGGG	TCATAACGAA	GTGGATTTAA	ACTTTAACGC	CATGCTTAAA	180
ACTTATGAAA	ACTTTAAATC	CAATTATCGT	TTTTCAGTGG	GTTTAAAGCC	TCTTACCGAA	240
AGCCCTAAAA	CCCCCATTTT	GCCCTATTTT	TCTAAAGGCA	CGCATGGGGA	TAAAAAAATC	300
CAAGAAAACC	TTTTAAACAA	CGCTTTGATT	TTAGAAAAGT	CCAACACGCT	TTATGCACAA	360
TTGCAACCGC	TCAAACCCGC	TTTAGATTTC	CCAAATATTC	AAGTGTATTT	AGCGTTCTAT	420
CCCAGCCAAT	CCCAGCCCAG	ATTATTAGGA	ACGCTTGATT	GTAAAAACGC	ATGCGAACCT	480
TTAAAATTTG	ATTTGTTAGA	GGGCGATAAA	GTGGGGCGCT	ATAAGATCCT	TTTTAAATTT	540
GTTTTTAAAA	ATAAGAAGA	ATTGATTTTG	GAGCAACTGG	CTTTTTTTAA	G	591

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

951

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345

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GCAAATCAAT TTGCGCTACA ATTTTCCTTT TCTAATTTCA AGCATGGCGA TTTTACCACA      60
AGGGATTTTA TGCTCTATTC TTTATTATAT GGCTATTTTA ATATCAATCT TTTCCAGTAT      120
TTGACCTTTA GAGCAGGGTT AGGGTTTTTC ATAGCCTTTT TTCTCACGCT TTTTTTAATG      180
CCTAAATTTA TTCTATGGGC CAAGGCTAAA AAGGCTAACC AGCCCATTTT TAGCTTCGTG      240
CCAAGCCACC AGAATAAAAA GGATACCCCT ACGATGGGGG GCATTGTGTT TGTTTTGTGA      300
ACCATTTGTT CGAGCGTGTG GTGCGCGTCT TTGAGCAATC TTTATGTGTT GTTAGGGATA      360
ATCGTGTTAG TGGGCTTAG TTTTGTGGGT TTTAGAGACG ATTACACTAA AATCAACCAG      420
CAAAATAACG CCGGGATGAG TCGGAAAATG AAATTTGGCA TGCTGTTTAT CCTTTCGCTT      480
ATAGTGTCTG TTTTATTGAG CCTTAAGGGG TTGGACACTT TTTTATACGC GCCGTTTTTG      540
AAAAACCCCT TGTTTGAAAT GCCCAGCATG TTAGCGGTTG GTTTTTGGGT GTTGGTTTTT      600
TTATCCACGA GCAATGCGGT GAATTTAACC GACGGGTTAG ACGGATTAGC GAGTGTGCCT      660
AGCATTTTCA CCCTCTTAAG CCTTCTATC TTTGTGTATG TGGCAGGGAA TGCAGGAATTT      720
TCTAAATACT TGCTCTATCC TAAAGTCATA GATGTGGGGG AATTGTTTGT GATTTCGCTA      780
GCATTAGTGG GATCGCTCTT TGGCTTTTTG TGGTATAACT GCAACCCGGC AAGCGTGTTT      840
ATGGGCGATA GCGGGAGTTT GGCAATAGGA GGGTTTATCG CTTATAACGC TATTGTTTCG      900
CATAATGAAA TCTTGTCTGT TTTAATGGGG TCTATTTTTG TAATAGAAAC TCTGTCTGTG      960
ATCTTGCAAG TAGGGAGCTA TAAACCCGT AAAAAACGCC TTTTTTTAAT GGCACCCATC     1020
CATCATCATT TTGAACAAA GGGTTGGGCA GAAAATAAGG TGATCGTGCG TTTTGTGGATC     1080
ATTCTATATC TGAGTAATTT AGTCGCTCTT TTGAGCTTGA AGGTGTGT      1128

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(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346

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GCAAGATTTA TTAAATATT TGGCATGGGA AAATTTTCTA AATTAGGCTT TATTTTAGCC      60
ACTTTGGGTA GCTCTATCGG TTTAGGGCAT ATTTGGCGCT TTCCTTATAT GGTAGGTCAT      120
AATGGGGGGA GCGCGTTTGT GCTTTTATAC CTAGCACTAA CCTTGAGTTT AGGCATGTCT      180
ATGCTTTTAG TGGAAATGCT GATTGGAAAT TTGGGTAAAA AAGACGTTGT TTCCAATTAT      240
CAAATCTTAG ATCCTAAAAG GAAAAATAT TACCCTTTCA CTTCTTTTTT TATTTTAGGC      300
GGCCCTCTCA TTCTATCTTT TTATGCGGTG GTGTTAGGCT GGGTGCTTTA CTATCTTTTT      360
GTAGTAACCT TTGATTGGCC TAAAGATTTA GAGCAGGCTA AAATGCAATT CAGCATGCTT      420
CAAAATGGCA GTTTGATCTG GCCTGTATT GGCTTTAGCG CATGCTTGTT GCCGACAATA      480
TGGTTTGTTC CTAGGGGGAT TGAAGAGGGG ATTGAAAAAT TAAATGTCGT GCTGATGCCC      540
TTATTGTTTG TGATTTTCAT AGGGCTTTTA ATCTATGCGA TGACTTTAGA AAGCATGCCT      600
AAAGCTTTGC GTTTTTTATT TAATTTTGAG ATTCAAAAGA TTGATTTTAA GGTGTGTGATG      660
GACGCTTTAG GGCAGATGTT TTTTCTTTTG AGTTTAGGGG TAGGCACGAT CATTACTTAT      720

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SUBSTITUTE SHEET (RULE 26)

952

TCGGCTTTTA	CGCCTAAAAA	AGAAAACCTA	CTCAAAAGCT	CTCTGTTTAT	TGTTTACCG	780
GGTATTTTAA	TTTCTTTGAT	TGCCGGGGTG	ATGATTTTAA	CCTTTGTGTT	TGAATACCAT	840
GCAGACGTGT	CTCAAGGGCC	AGGGCTTGTT	TTTATTTTCT	TACCTTTAAC	TTTCGCTAAA	900
ATGGGATCA						909

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347

AGGTGTGTTA	AAATGAAAAT	TTCTTTATTG	GGGCATGGAA	AAACCACTCT	AGCCCTAGGG	60
CGTTTTTTTA	AAAAAAACCA	TAATGAAGTC	AAATTTTTTG	ATGATAAATT	CCCTGCATTT	120
TTTAAGGATA	GCGAGGGTTT	TCTTTGCTAC	CCTAGTAAGG	ATTTTAACCC	TAATGATTCC	180
CAACTAGAAA	TCGTCAGCCC	TGGCATTAGT	TTACGCGACC	CTTTAGTCAT	GAAAGCCAAG	240
CATTTAATGA	GCGAATACGA	TTATATTGAT	AGTTTGTGTT	ATCATTCTTT	CACGCCTACG	300
ATGATAAGTA	TTAGCGGCAC	TAACGGGAAA	ACCACCACGA	CCGAAATGCT	CACCACACTT	360
TTAGAAGATT	TTAAGGCTGT	GAGTGGGGGG	AATATCGGCA	CGCCCTTGAT	TGAATTGTTT	420
GAAAAACGAT	CGCCCTTGTT	GGTGCTAGAA	ACAAGCTCCT	TTTCTTTGCA	TTACACTAAT	480
AAGGCTTACC	CTTTAATCTA	CTTGCTCATC	AATGTGGAAG	CCGATCATT	GACTTGGCAT	540
TGCAATTTTG	AAAATTATTT	GAACGCTAAA	CTCAAGGTTT	TAACATTGAT	GCCTAAAAC	600
TCGCTCGCTA	TCCTCCCTTT	AAAATTCAAA	GAACACCCTA	TTGTTCAAAA	CTCGCAAGCG	660
CAAAAAATCT	TTTTTGACAA	AAGCGAAGAG	GTTTTAGAGT	GTTTAAAAAT	CCCTTCTAAC	720
GCCCTTTTTT	TTAAGGGAGC	GTTTTTATTA	GACGCGGCTT	TAGCCCTTTT	AGTTTATGAG	780
CAATTTTTTA	AAATAAGAA	TTTAAATG	CAAGATTATA	GAGAAAACGC	CCTTAAAGA	840
CTGAACGCTT	TTAAATCGG	CTCGCATAAA	ATGGAAGAAT	TTAGGGATAA	ACAAGGGCGT	900
TTGTGGGTAG	ATGACAGCAA	AGCCACGAAT	ATTGATGCCA	CCTTACAAGC	CCTAAAAACC	960
TTTAAAAACC	AAAAAATCCA	TTTGATTTTA	GGGGGCGATA	TTAAAGGGGT	CAATTTAACC	1020
CCCTTTTTTG	AAGAGTTTAA	AAACTATAAA	ATAAGCCCTT	ATGCCATAGG	ATCAAGCGCT	1080
TCTATCATA	AAGCCTTAGC	GTTAGAATTT	AATGTTTCTT	GTCAGGTTTG	TTTGAAGTTA	1140
GAAAAAGCGG	TTCAAGAAAT	TAAAAGCGTT	TTATTACAAA	ATGAAGTCGC	TTTGCTTTCA	1200
CCTAGCGCGG	CCAGTTTGGG	TCAATTTTCT	TCGTATAAAG	AAAGGGGTGA	AAAATTCAAA	1260
GCGTTTGT	TAAAAGAT					1278

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

953

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348

GATATGGGTA	ATCATTTTTTC	TAAATTAGGA	TTTGTTTTAG	CGGCTTTAGG	GAGCGCGATA	60
GGTTTAGGGC	ATATCTGGCG	CTTCCCCTAT	ATGACTGGGG	TGAGTGGTGG	GGGTGCTTTT	120
GTTTTATGT	TTTTATTTTT	ATCCTTAAGC	GTTGGTGCGG	CGATGTTTAT	CGCTGAAATG	180
CTATTAGGAC	AAAGCACGCA	AAAAAATGTA	ACAGAAGCTT	TTAAAGAGCT	TGACATTAAC	240
CCTAAAAAAC	GCTGAAATA	CGCAGGGATC	ATGCTTATTT	CTGGACCTTT	AATACTGACT	300
TTTTATGGCA	CTATTTTAGG	TTGGGTGCTT	TATTATTTGG	TGAGTATTAG	TTTTAATTTG	360
CCTAGCAGTA	TCCAAGAATC	TGAACAAATT	TTTACTCAAA	CTTTGCAGTC	TATAGGGTTA	420
CAATCCATAG	GGCTTTTTAG	CGTTTTATTC	ATAACCGGAT	GGATTGTTTC	TAGGGGGATT	480
AAAGAAGGCA	TTGAAAAACT	CAATTTGGTT	TTAATGCCCT	TACTCTTTGC	CACTTTTTTT	540
GGTTTGCTTT	TTTTATGCGAT	GAGCATGGAT	TCTTTTTCTA	AAGCTTTCCA	TTTCATGTTT	600
GATTTCAAGC	CAAAAGATTT	GACCTCTCAA	GTGTTCACTT	ATTCCTTGGG	GCAGGTTTTT	660
TTTTCTCTAA	GTATCGGTTT	AGGGATCAAT	ATCACTTATG	CTGCCGTTAC	GGATAAAACG	720
CAGAATTTGC	TTAAAAGCAC	GATTTGGGTG	GTTTTATCAG	GGATTTTAAT	TTCTCTTGTT	780
GGCAGGGCTT	ATGATTTTCA	CTTTTGTGTT				810

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349

TGCTCACA	GGCACAGGGT	TAATCTTCAC	TTCTTTACCG	GTGGTTTTTG	GCCAAATGGG	60
AGCGATAGGC	GTTCTTGTTT	CAATCTTTT	CTTGCTCGCG	CTCGCTTTTG	CTGGCATCAC	120
TTCTACGGTG	GCTTTATTAG	AGCCAAGCGT	GATGTATCTT	ACCGAAAAGT	ATCAATACTC	180
TCGTTT						186

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 561 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

954

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350

TTTCTCTTGT	GGGCAGGGCT	TATGATTTTC	ACTTTTGTGT	TTGAATATGG	GGCTAATGTC	60
TCACAAGGCA	CAGGGTTAAT	CTTCACTTCT	TTACCGGTGG	TTTTTGGCCA	AATGGGAGCG	120
ATAGGCGTTC	TGTTTCAAT	TCTTTTCTTG	CTCGCGCTCG	CTTTTGCTGG	CATCACTTCT	180
ACGGTGGCTT	TATTAGAGCC	AAGCGTGATG	TATCTTACCG	AAAAGTATCA	ATACTCTCGT	240
TTTAAGGTTA	CTTGGGGTCT	TGTAGCGTTA	ATCTTTGTGG	TAGGCGTGGT	GTTGATTTTC	300
TCGCTCCATA	AGGATTATAA	AGACTATCTC	ACTTTCTTTG	AAAAAAGTCT	TTTTGATTGG	360
TTGGATTTTG	CATCAAGCAC	CATTATCATG	CCTTTAGGCG	GGATGGCAAC	CTTTATTTTT	420
ATGGGCTGGG	TTTTGAAAAA	AGAAAAATTG	CGTCTTTTGA	GCGCGCACTT	TTTAGGCCCT	480
AAATTGTTTG	CAACTTGTA	TTTCTTGCTT	AAATACATCA	CCCCTTTAAT	TGTGTTTTCC	540
ATTGCGTTGA	GCAAGATTTA	T				561

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 855 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351

GAGTCTTTTA	TGGGGTGTTT	GTTTATCTTT	AAAAAAGTTA	GGGTTTATTC	TAAAATGTTG	60
GTTGCTTTGG	GGCTTTCAAG	CGTGTTGATC	GGTTGCGCGA	TGAATCCAAG	CGCTGAGACA	120
AAAAAACCAA	ATGACGCCAA	AAACCAACAA	CCAGTTCAAA	CTCATGAAAG	AATGACAACA	180
AGTTCTGAAC	ATGTTACGCC	ACTAGATTTT	AATTACCCGG	TGCATATTGT	TCAAGCCCCA	240
CAAAACCATC	ATGTTGTAGG	TATTTTAATG	CCACGCATTC	AAGTGAGCGA	TAATCTAAAA	300
CCCTATATTG	ATAAGTTTCA	AGACGCTTTA	ATTAATCAAA	TCCAAACTAT	TTTTGAAAAA	360
AGAGGCTATC	AAGTGTTGCG	TTTTCAAGAT	GAAAAAGCTT	TGAATGTGCA	AGATAAGAAA	420
AAGATTTTTT	CCGTTTTTGA	TTTGAAAGGG	TGGGTAGGAA	TCTTAGAAGA	TTTGAAAATG	480
AATTTAAAAG	ATCCCAATAG	TCCCAATTTA	GACACGCTAG	TGGATCAAAG	CTCAGGCTCT	540
GTATGTTTGA	ATTTTATGA	ACCAGAAAGC	AATCGTGTCG	TCCATGATTT	TGCTGTAGAA	600
GTAGGAACCT	TTCAGGCAAT	AACATACACA	TACACCTCTA	CTAATAACGC	TTCAGGAGGG	660
TTTAATTCTT	CAAAAAGCGT	TATCCATGAA	AATTTGGATA	AGAATAGAGA	AGACGCGATA	720
CACAAGATTT	TAAACAGAAT	GTATGCGGTT	GTCATGAAAA	AAGCTGTAAC	AGAACTTACA	780
AAAGAAAATA	TCGCCAAATA	CAGAGACGCT	ATTGATAGAA	TGAAAGGCTT	TAAAAGTTCT	840
ATGCCTCAAA	AAAAG					855

SUBSTITUTE SHEET (RULE 26)

955

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352

GAATTGGTTT	TGTTTGAAAA	GTTGAAATTT	TTTAAATCA	AAAAAGACGA	TGAAATCAG	60
CCAGAAGTCA	ATTTAAATTC	TGAAATCTAT	GAGCAATTTA	AGGTCCTTAG	ACTCCCGCTT	120
ATTTTAATCC	AATTGCTCGT	GCTTTTAGGC	ACTCTGGGAT	ACTTCGCCCT	AGAAAATTAT	180
AGCCTTATGC	AAGCTTTCTT	TCAAACGACT	TACACCATGA	CAGCTACAGG	GTTTGGCGCT	240
TTAAATGAAA	GCCAGTTTGG	GCCTATAAGT	ATTTTTTTAA	CTTCCATTTT	AATGTTTTGT	300
GGGACGGGAA	TTATTGCTTT	TAGCGTGGCT	ATTTTAGTTA	GCGTGGTCAA	TAAAGGCACG	360
CTTACCAGAT	TGATTAAGGA	GAAAGGTATG	ATTTATAAAA	TCGCGCGCCT	TAAGGATCAT	420
TATGTGATTT	GTTACCATAA	TGAATACACC	ATTGAGTTGA	GCAAGCAGTT	TCGCTCCGCT	480
CAAATCCCCT	TTGTGGTCGT	GGATAATGAT	CCTAATTTTG	AAGAAGAAGC	CATTAAGCAC	540
AAATACCCCT	ACTATATCAT	AGGCGATCCG	CACACCAATT	TAGCCATGCT	AAAAACCCAC	600
TTAAGCAGCG	CTAGGGGCGT	TGTGGCGTTG	TCTAAGATTT	TACCGGTGAA	CGTGGCGTTA	660
ATGGTGAGCG	TGCGCTTGTT	TGAAAAGGAA	TTAAAACGCA	AACCTTACTA	CATCATTGCG	720
AGCGCACACA	GCGATGAAGG	TTTAGAAAAA	TTAAAAAAT	TAGGGGCTGA	TATGGTGGTT	780
TCCCCTACAA	AACTCATGGC	GCAGAGAGTG	AGCGCGATGG	CGGTGCGTCC	GGATATGGAA	840
AATATCTTAG	AGCGTTTTAT	CAACAAAAAA	GACACGCTTT	TAGACTTAGA	GGAAGTGATT	900
GTCCCCAAAA	CCAGCTGGCT	TGTGTTAAGG	AAATTAAAAG	AAGCCCATTT	TAGAGAGATC	960
GCTAAAGCCT	TTGTGATTGG	TATCACTCAA	AAAGATGGCA	AATACATCCC	CATGCCTGAC	1020
GGGAAACGAT	TATTGCAAGC	GAATCCAAGC	TAT			1053

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353

ACCAAAAAGT TAAACAATAC TCTATTCAAT AAAGGATTAA TTATTTTAA AATGTTTAAA	60
AAAATCATTT TTTTGTGCGT TTTTGTGATA GGGGGATTG TCATTCCACC CCTTGAAGCC	120
ATGCCTATTT TCGCAATAA AACCCCAAA AAAAATTACC AAGAAGCCCA TGAAAAGCTC	180
TATAGAAGCA TCATTAAACG CAAAAGCTC ACGCGTAAAA AAAGCGGGTG GTATTTTAA	240
GGGGGGGTG GCGCTGTAGA AGCCATTAAG GACTATCAAG GCAAGGAAAT GAAAGATTGG	300
ATGCCACGCT CAATT	315

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354

ATCATGCGCT GTAAATTTTG CCCTAAGATC AGAAAAACAG ATTGGATTTT TATTTTAATC	60
GCCGCTTTAG GCTTTTATTC AGTTAATAAG CTAGGGTATG CGCCCAAATT CAATACCCCC	120
ACTCCAAAT CTTCACGCCC TCTTCACGC CCTATTGAAA AGCCTAACAA TATGACTGAA	180
GAAGAAAGGA AAAAGCGTTT TATAGAGTTG CAAAAGCAT GCTTACTTCA TAAAGACAAA	240
AAGGCATGCG AAGAGGTTTT T	261

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355

CGAGCTATCA CAACAAATCA ATTCTAGGA ACAAACATGT TTTTAAAC TTATCAAAAA	60
TTACTGGGCG CGAGCTGTTT GGCGCTGTAT TTAGTGGGCT GTGGGAATGG TGGTGGCGGT	120

957

GAATCGCCCGG	TTGAGATGAT	TGCAAATAGC	GAGGGTACGT	TTCAAATCGA	CTCCAAAGCA	180
GATAGCAATTA	CTATTCAAGG	CGTGAAGCTT	AATAGAGGTA	ATTGTGCTGT	CAATTTTGTT	240
CCAGTAAGTG	AGACGTTTCA	AATGGGTGTT	TAAAGTCAAG	TTACTCCAAT	CTCTATACAG	300
GATTTTAAAG	ATATGGCAAG	CACTTATAAG	ATATTTGATC	AAAAGAAAGG	GTTGGCAAAC	360
ATAGCAAATA	AAATTTCTCA	ATTAGAGCAA	AAGGGTGTGA	TGATGGAACC	TCAAACCCTT	420
AATTTTGGAG	AAAGTTTAAA	AGGCATTTCT	CAAGGGTGCA	ATATTATAGA	GGCAGAAATA	480
CAAACCGACA	AAGGCGCTTG	GACTTTTAAC	TTTGATAAA			519

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356

ATATCAAACA	TGGAATAAC	CCCGAAAGAC	AGAGCAAGAA	TCCTTATAGA	AGAGCTTAAA	60
ATCTTGCAAG	GCGTTATCAA	CAGAATGGCA	CAAAATTCTT	TAGAATGCAA	AAAATGGACT	120
CTCGCTCTCG	CTGTGGGTGT	CTTATCCCTC	AAAATAGAGG	CAATTCTTAA	TTTTTATGGG	180
TTATGCGTTT	TAGGGGTGTT	GTTAGCATGT	TTTTATCTTT	TAGACGCTTA	TTATCTCATG	240
CAAGAAAGGC	TGTTTAGGGA	GCAATACCAA	TGGCTAATAA	AAAACCGACT	TAAAACCGAT	300
GAAAGGCTGT	TTGAAGTCTT	CCCTATTTCAT	CAAACCTGCC	AATCAACGCA	ATTCTTATCC	360
GCCATGCGTT	CGTTTAGTCT	TTTCCCCTAT	TGGGCGTTAG	GTTTGTGTTT	GGTGGGCTAT	420
GGTTTTTGTT	GT					432

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357

958

CCCCTTAAAT	CAAAGGCAAG	CAAACCTTTA	GGCGCTAACA	TCGTGTATAA	AATCCATTGT	60
TTGGTTAAAG	GGGTAACTTT	AGAGCAGCAA	AACAAGCTTT	TAAAAACCAT	TGAGCCTTTT	120
AAAAAATTCG	CTTCATTAGA	GTTTATAGAC	ATCAATTCGC	TAGATTATTC	CATAGAAAGC	180
TATCTTAATG	AGTCTTGCTC	CAAGCGTTAT	GGCGGGCTTC	TTGTTTGTG	CCGGCTCTTG	240
CTCGCTTCGC	TCTTCCCTAA	TTATCTATAA	ATCATTTCCTA	TAGATGTGGA	TACGGTGTTC	300
TTAGGCGATG	TTGCAAGCGC	TTATTTTGCG	CTGATAATG	AACCCACTAA	ATTGCTTGCG	360
ATGGTGAGAG	ACACTTTTTC	CCACCTTCCT	TTTGAAGCCT	TTTGTGATTT	TTGCGAACGC	420
ACATGCAAGA	ATTTTAAAAAT	TGATCTTTTG	CGCTTTAGCC	AAAACGAATT	AAAACGCATC	480
CATCAGGGCT	TTAACATGGG	CTTTTGGTG	GCGAATTTAG	ATTTATGGCG	CGAAAATGGG	540
TTTGAAAAAA	TCGCTTTAGA	GTTTTTGAAA	ACTAGGGGAA	AGGATCTTTT	CTACCCTGAG	600
CAGTGTTTAA	TCAATATGGT	GTTTTTAGAG	CGTATTTTAG	AATTGCCTAT	TCATTATAAT	660
TGCTATTCTG	ATTTTTTCAA	AGAGCACTAC	CCTAAAAGTA	TCATCATGCT	CCATTTCATC	720
AAATACAAGC	CGTGGCGTTC	TGTCAGTTCT	TTGAACGGGC	GTTTGATTTC	CTATGAAGCT	780
GAAGCGAGTT	TTTGGCTCGC	CAACCTTTTT	TGCACCCCTT	TTAAAAACGA	TTTTTTTAAA	840
GAACGCCTTG	AAATGGCTAA	AGACCAACAA	ATGCAATCTT	TTAAAAACCA	CATCCGATCA	900
AAAACGATTA	GGGATTATTT	TTATTTTAGG	ATAAAAAATA	TTTTGAAAAA	AGTTTTCGAA	960
CTCTCT						966

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358

AAAAAGTTTT	CGAACTCTCT	TAAAGGACAA	AAAAAACGA	TGAAATTTTT	AAAAATCTTT	60
GCCAGTAGCG	TAACCTCTAGA	TGAAAAATTT	TAAATGTTCC	TTCTTTGCAA	CGCTCTTTCT	120
AACGCTTACA	AAAATAGCGA	TTTGTTTTCT	TTCTCTAAAG	GCTTTTTAGG	CGCTTTTTTTA	180
ATCGGGTTTG	TGGTGTATTA	TGGTTGCGCG	CTAATCCCTA	AAAAACGCTT	GAAATATTCA	240
TTAGAATGCG	TGTTTATAGG	AAGCGGTATT	ATTTTTAGCG	TGGCAGAAAT	TTTTACGCTG	300
TTTATGTTTA	AAATGCCTTT	TTCCAAAGGC	TTGATTGACA	CGCTTTTAGC	CACAAACAGC	360
TCTGAAACGA	TGGCGTTTAT	AAAAAGCTAT	AAAAATTATT	TGCTTTACTA	CGCTTTGATT	420
TTGATCGCTT	TGTTGATCGC	CATTAAAAATC	ATTCGCTTTA	GAGCGCTTGT	GCCTGGTGTG	480
ATAGCGAGCG	TTTTAGGGCT	TTCTATCCTT	ACAATAGGGA	GCGTTCGTAA	CATTAAACAC	540
CTTACAAAGA	ACGATGCGAT	TTTAAAAAGA	TCACTCTTTT	CTCTTTCTTT	AGCTAGGGGG	600
TTTTATTCCG	CTTATTGAG	TTTGTTTGAT	CGCCAACAAG	CCATAAAATT	TTATAGCTTT	660
TTAAATAATC	TTTATTTACC	AAGCGATTAT	CTTTCTAGCA	CGGGCGATAT	TTCAAATGTC	720
GTCTTAGTCA	TCGGCGAAAG	CGCGAGCAGA	AATTTTCATGC	AACTCTATGG	CTATAGCGTT	780
CCTAATAATC	CCTTATGCGA	GCGAACTCGC	CAAGCGAGAG	AGAGAGAGAG	AGAGAGTAAC	840
AACCTGTTTC	TGTTTTCTGA	CACGATAAGC	AAAGAAGCCC	ACACCTCTGA	TGCTTTTGAA	900
AGCCTGCTCA	ATTATAGCGA	TGCTGAAACG	ACTAAACCTT	GGTATCATTA	CCACAACATG	960
ATAGATATTT	TCAAGCGATC	CCATTATGAA	ACTTTTTGGT	TAGAAAAACA	AATCGTTCGAT	1020
GAATGGGGGA	TCACACAAAA	TCTAGTCTCT	AATCGTTCTA	AAAACCGCTA	CTATATTTTG	1080
GGAAACTATG	GTGCATACGA	TGAAGAGCTA	GTGAAATTTT	ATTCTAAAAA	TGTCCAACCC	1140
CAATTAATAA	GCAAGAATTT	TATCGTGTTT	CATTTGCTTG	GCTCTCATTG	TTGGTATGCC	1200
GATCGTTTTCC	CTAAAAGCTT	TGCCAAATTC	AAACCAAGCG	ATTTGCTTTT	TTCTAATTTG	1260
CATGCAAGCA	GCGATAGAGA	CAAGCAAATC	GTCGCTGATT	ATGTCAATTC	GCTTTATTAT	1320
AACGACTTTG	TTTTGAATGG	AATTTTTAAC	CTCTTTAAAG	ATAAAGACGC	TATTGTGTTT	1380

959

TATTTGAGCG	ACCATGCGCA	AGATATTTTT	GAAAGCGGCC	CTACTTATGG	GCATAGCTGT	1440
TCTAAAGCGG	GATTAGAAAT	CCCTTTTATG	ATTTATGTGA	GCGATATTTT	TAAAGAAAAA	1500
CACCCCGAGA	AAGTGAAGTT	GATTAAAAAC	GCTTTAAACA	AACCTTTCAT	GAGCGATGAT	1560
TTAATCCATT	CTCTTTTGCC	TTTGTTGGGC	ATTCACACTA	AAGATGAAAT	AGAGAGTAAA	1620
AACCTTTTTA	GCCCCCAATT	TGACGCCCAA	AGAAAAAGGG	CTGTTTGTTA	TGGCAGCATG	1680
AATTATGATA	GGACTAAA					1698

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359

AAATCTTTTA	TGCCACCCAC	ACGCCCCCAA	GCGAGTATTT	TAAGGCTAAC	CCTAAAAAAC	60
CCTTTGAGCA	TGCTATCTCG	TTATTCGCTC	TGTCTGTTGA	AAAAAACGCG	CTTGCAAACA	120
ACATCAAACA	GCGCACCAAA	AGCATGCTTG	ATTGCGGGCT	TATTGAAGAA	ATCAAAGCCC	180
TTTATATTAA	ATACCCTAAA	GATTGCGCAGC	CTTTTAAAGC	CA		222

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360

ACTTCCGCAT	CAAGGGTGGC	TAAAGACATC	ATCAGCGAGT	CTCAAACCT	TTGCGCAAGA	60
AAATTCGGCC	GTTTGTATGC	GTTATGAAA	GAAATGAAA	TGCTCATTCT	CATCGGATCT	120
TATCAAATGG	GGAACGATAA	AGAGCTTGAT	GAAGCGATTA	AGAAAAAGGC	TCTAATGGAG	180
CAATTTTATG	TGCAAGATGA	AAACGCTTTA	CAGCCTTTTG	AACAAAGCTT	TCAGCAATTA	240
GAAGAAATCT	TAAGA					255

(2) INFORMATION FOR SEQ ID NO:1361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361

GATAAAAGGA ATATCATGGA ATCACAACCTC ATGAAACTCG CCATTGAAAC TTATAAAATC	60
ACTTTGATGA TTTCTTTACC GGTATTATTA GCGGGCTTAG TGGTGGGGCT GTTAGTCAGT	120
ATTTTTCAAG CGACCACCA AATCAATGAA ATGACTTTGT CTTTGTGCC TAAGATTTTA	180
GCCGTGATG GGGTCTGAT TTTAACCATG CCGTGGATGA CGAACATGCT TTTAGATTAC	240
ACCAAAACCT TAATCAAGCT CATTCTTAA ATCATAGGC	279

(2) INFORMATION FOR SEQ ID NO:1362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362

AAAATGCTAG AAACCACTAT TGATTTTCT CGTTACAGCA GCGTGAAAAT CCGTGCGCCT	60
TTAAAGTGA GCGTTTGA AAACGATAAT GAAATCTCTC AAGAACACCA GATCATAGGA	120
TTAGCGAACA ACCTTTAAAT CGCTCCTGAC GTGAAAAATC TCGCTTTATT AGGAAAAAAC	180
TACGATTATA TTTGCGATAA GGGTGAGTGG GTGGAGGTAG GGGGAGCGGC CAATGCGTCT	240
AAAATTTTTA ATTATTTTAG GCGCAATGAT TTAGAGGGTT TAGAGTTTTT AGGGCAATTG	300
CCTGGCACTT TAGGGGCGTT AGTTAAAATG AATGCTGCA TGAAAGAATT TGAAATAAAA	360
AATGTTTLAG AAAGCGCTTG CGTTAATGGC GAATGGCTAG AAAAGAAGC TTTGGGGCTA	420
GATTATCGCA GCAGCGGTT TAATGGCGTT GTTTTGAGGG CTAGGTTTAA AAAGACGCAT	480
GGTTTTAGAG AAGGGTTTT AAAAGCGTGT AAAAGCATGC GCAAAGCCA CCCCAAATTG	540
CCTAATTTTG GGAGCTGTTT CAAAACCCG CTAACGATT ATGCGGGGCA GGCTTTTAGA	600

961

GGGCGTGGGC	TTAAGGGGTT	ATTGTCTAAA	AAGAGTGGGG	CTTTGCCAAA	GCAACATGCG	660
AAATTTTGGG	TGAATTTGGG	GGGCGCAGAA	TTTGAAGAAG	CCCTAGATCT	GATAGAACTC	720
GCCAAAACCA	GAGTGCTACA	AGAATATGGC	ATTCATTTAG	AAGAAGAAGT	GAAAATTTTA	780
AGG						783

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363

CTCAATAGCG	AACATCCCTT	GTTTGATTGG	GCTAGCAAGC	AGACTTATAT	CCAAATGGCG	60
AACATGATGA	TGGCAGCGGC	CATGTTAGGG	ATTGATTCTT	GCCCCATTGA	AGGGTATGAT	120
CAAGAAAAAG	TGGCGGCTTA	TTTAGAGGAA	AAAGGCTATC	TAAACACGGC	AGAATTTGGC	180
GTGTCGGTAA	TGGCTAGTTT	TGGTTATCGT	AACCAAGAGA	TTACCCCTAA	AACCCGCTGG	240
AAGACAGAAG	TTATTTATGA	AGTGATTGAA				270

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364

AAAGAGATAA	CCATGAGAAA	ACTATTCATC	CCACTTTTAT	TATTCAGCGC	TTTAGAAGCG	60
AACGAGAAAA	ACGGCTTTTT	CATAGAAGCC	GGCTTTGAAA	CTGGGCTATT	AGAAGGCACA	120
CAAACGCAAG	AAAAAAGACA	CACCACCACA	AAAAACACTT	ACGCAACTTA	CAATTATTTA	180
CCCACAGACA	CGATTTTAA	AAGAGCGGCT	AATTTATTCA	CCAATGCCGA	AGCGATTTCA	240
AAATTTAAAT	TCTCATCTTT	ATCCCCTGTT	AGAGTGTGTT	ATATGTATAA	TGCTCAATTA	300
ACTATAGAAA	ACTTCTTGCC	TTATAATTTA	AATAATGTTA	AGCTTAGTTT	TACAGACGCT	360

SUBSTITUTE SHEET (RULE 26)

962

CAAGGCAATG	TGATTGATCT	AGGCGTGATA	GAGACTATCC	CCAAACACTC	TAAGATTGTT	420
TTGCCCGGAG	AGGCATTTGA	TAGTCTAAAA	ATTGACCCAT	ATACTTTAAT	TCTTCCAAAA	480
ATTGAAGCCA	CTAGCACTTC	TATTTCTGAC	GCTAACACGC	AGAGGGTGTT	TGAAACGCTC	540
AATAAGATTA	AGACAAATTT	GGTCGTAAAT	TATAGGAATG	AAAACAAATT	TAAAGATCAC	600
GAAAATCATT	GGGAAGCCTT	TACCCACAAA	ACCGCAGAAG	AATTCACCAA	TTTAATGTTG	660
AACATGATCG	CTGTTTTAGA	CTCCCAATCT	TGGGGCGATG	CGATCTTAAA	CGCTCCTTTT	720
GAGTTCACTA	ACAGCCCAAC	AGATTGCGAT	AATGATCCTT	CAAAATGCGT	AAATCCTGGG	780
ACAAACGGGC	TTGTCAATTC	TAAAGTCGAT	CAAAAATATG	TGTTAAACAA	ACAAGACATT	840
GTCAATAAAT	TTAAAAACAA	AGCGGATCTT	GATGTAATTG	TTTTAAAGGA	TTCAGGGGTT	900
GTAGGGCTTG	GGAGTGATAT	TACCCCTAGC	AACAATGATG	ATGGCAAGCA	TTATGGCCAG	960
TTAGGGGTAG	TAGCTTCTGC	TTTAGATCCT	AAAAAATCT	TGGCAACGA	CCTTAAGACT	1020
ATCAATTTAG	AGGATTTAAG	AACCATCTTG	CATGAATTCA	GCCACACTAA	AGGCTATGGG	1080
CATAACGGGA	ATATGACCTA	TCAAAGAGTG	CCGGTAACGA	AAGATGTCAA	G	1131

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365

ATAATGGGCG	TTGGAGAGAA	AGAAGAGAAA	AAAGAAAGCC	AAAAGGTGGC	GGTTATCACT	60
GGGGCGAGTT	CTGGGATTGG	GTTAGAGTGC	GTGTTAATGC	TGTTAAATCA	AGGCTATAAG	120
GTCTATGCGC	TCTCTAGGCA	CGCGACTTTG	TGCGTAGCGT	TAAACCATGC	GTTATGCGAG	180
TGCGTTGATA	TTGATGTGAG	CGATTCTAAC	GCTTTAAAGG	AAGTGTTTTT	AAACATCAGC	240
GCTAAAGAAG	ATCATTGCGA	CGTTTGTATC	AATTCGCGCG	GTTATGGGGT	GTTTGGGAGC	300
GTGGAAGACA	CGCCCATTTA	AGAGGTTAAA	AAGCAATTTA	GCGTGAATTT	TTTCGCCCTT	360
TGTGAAGTGG	TGCAACTTTG	TTTGCCCTTA	TTAAAAAACA	AGCCTTATTC	TAAGATTTTC	420
AATCTTTCTT	CCATAGCGGG	GCGTGTGAGC	ATGCTCTTTT	TAGGCCATTA	CAGCGCGAGT	480
AAGCATGCCT	TAGAGGCTTA	TAGCGATGCC	TTGCGTTTAG	AGCTTAAGCC	CTTTAACGTT	540
CAAGTGTGTT	TGATTGAGCC	AGGCCCGGTG	AAAAGCAATT	GGGAAAAAAC	CGCTTTTGAA	600
AATGATGAGC	GGAAAGATAG	CGTTTATGCT	TTGGAAGTGA	ATGCGGCT		648

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

963

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*.

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366

GACTCAAATA	GAAGCGCTTT	TATATGCCAC	AATCTAGCGA	TGGTTTIGAT	GATTTTCACA	60
AGCATCTTGA	AGATAGCGTT	AAAAGTTTTA	TCAGAGCGAA	AAAAAATCG	TTATGGTTTT	120
CCTAGAATCT	TTGATGTTGC	AGACATAGAA	CAAGAAGAGA	GGGAAGTCAT	TGAATGGCGA	180
GAAAAAAGA	AAGCGTCAAA	ACAAAGCTAT	AAACAAAACC	TTCAAATCAA	TAAAATCGCT	240
AACGATTTAA	AGCGTGATAA	GATAGTGGAT	AAAAGAACGA	TTTTAAGCGT	GATAGACGCT	300
GATATAGAGC	GTGGTTTTAT	CCGCGCTAAA	GATTTGTTAA	AACAATTAGA	AAAAATTAGC	360
GCTTCTCTTT	CTAAAGACAT	CGTAATAACG	ATAAAGCAAG	TAGAAAAATT	AGAGCTTAAC	420
TATGCGCTAA	TAGACAATAT	CCAACATAAC	ACGCTTGATG	ACACGCTTGA	TTTTACCTTT	480
ATTGTTGGGG	ATTCTTTGAG	CGTTCAGTCG	CTTTATGTTA	CCTTTAATCT	TGTGATTGAT	540
ATTGATAGAC	CCATGAGCGA	GCAGTTTCTC	AACCATATTG	GGAAATTGGG	GAGTTTTGAA	600
TCTAGAGAGC	AAGCGTTAGA	GTGGGTGCGA	TTATCGCAAA	CTAAACTGAT	CATTGAAACG	660
CCTAAAGAAG	CGTTAAAAAA	TGCGGAATTA	TCACAAATTG	AAGAAATATT	GACCGGCTGT	720
ATTTTAAATG	GCGCTTACCG	CCTTCAAAAC	GATCTTAAGA	AAGGGCGA		768

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367

GGCAATGCTA	GGACTTGTAT	TGTTATATGT	TGGGATTGTC	TTAATCAGCA	ATGGGATTGC	60
GGATTAAACCA	AAGTCGATCC	TAAAAGCACC	GCGGTGATGA	ACTTTTTTGT	GGGCGGACTT	120
TCCATTGTTT	GTAATGTGGT	GGTCATCACT	TACTCCGCGC	TCCACCCTAC	AGCCCCTGTA	180
GAAGGTGCAG	AAGATATTGT	TCAAGTATCG	CACCATTTGA	CCAGTTTCTA	TGGGCCAGCG	240
ACTGGGTTAT	TGTTTGGTTT	TACCTACTTG	TATGCCGCTA	TCAACCACAC	TTTTGGTTTG	300
GATTGGAGAC	CCTATTCTTG	GTATAGCTTA	TTCGTAGCGA	TCAACACTGT	TCCTGCTGCG	360
ATTTTATCCC	ACTATAGCGA	TATGCTTGAT	GACCACAAAG	TGTTAGGCAT	CACTGAAGGC	420
GATTGGTGGG	CAATCATATG	GTGGGCTTGG	GGTGTTTGTG	GGCTTACCGC	TTTCATTGAA	480
AACATCTTGA	AAATCCCTTT	AGGGAAATTC	ACTCCATGGC	TTGCTATCAT	TGAGGGTATT	540
TTAACCGCTT	GGATCCCTGC	TGGTTACTC	TTTATCCAAC	ACTGGGTG		588

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1920 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

964

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368

AGCATTTGCC	ATGAATATTT	AAAGGTTAAT	TGCAAGAAA	AATTAGCCGG	TTTGTAGAGAT	60
TTTGTGCATT	ATAATGAAAA	CGCCAAAGAC	TCCTTGCCCT	TAAAAGCGCT	TTTTTTAAGC	120
GGGGTGGATG	CTTTGAGTAA	AGACGCGCTT	TATTATCTAG	AAAAGATCAT	GCGTTTTGGC	180
TCTAAAAATG	GGGTTTTGAG	CTTTGTCAAT	TGGGAGAGCG	AAAAAAACAA	TCAATCCGCA	240
GAAGATTTGA	AACGCTATGC	GGAGTTTTTT	AAAGACAGGA	CAAGTTTTGA	GGGGTTAAAA	300
TACCTTAAATG	TAGAAATCAT	CAGCGATCAA	GGTATTAAAT	CCCAACACAT	GCAAGACTTC	360
GCTGATAAAA	TTAAAGCGTA	TTACAAGCAA	AAAAAAGAAG	TTAAAAGGGA	GTTGAAGGAC	420
TTACAAAGAG	ACAAAGAATT	TTGGACTAAA	AGCTCTCAGC	ATGAAGTAAG	CGTGCCGGTG	480
GGGTGGGATA	TTAACCATAA	GGAAGTGTGT	TTTAAATCG	GTAACGAACA	AAACCACACG	540
CTCATTTGCG	ACCACAGCGG	GAGTGGGAAA	TCCAATTTCT	TGCATGTGTT	GATTCAAAAAT	600
CTAGCTTTTCT	ACTACGATCC	CGATGAAGTC	CAACTCTTTT	TGTTAGACTA	TAAAGAGGGG	660
GTGGAATTTA	ACGCGTATGT	AGCAGATCCC	GCTTTAGAGC	ATGCGAGGTT	GGTGAGCGTG	720
GCGAGTTCAA	TCTCTTATGG	CATCACTTTC	TTGAAATGGC	TTTGTGATGA	AATGCAAAAA	780
AGAGCCGATC	GGTTCAAGCA	GTTTAAATGTG	AAAGATTTAA	GCGATTACCG	CAACATGAA	840
AAAATGCCCA	GACTGATCGT	GGTGATTGAT	GAATTTTCAGG	TGCTTTTTAG	CGATAATAAA	900
TCCACTAAAG	CGGTGGAGGG	GCATTAAAC	ACCCTGCTTA	AAAAGGGCCG	TAGCTATGGG	960
GTGCATTTGG	TTTTGGCCAC	TCAAACCATG	CGCGGCACTG	ACATTAATCC	AAGCTTTAAG	1020
GCTCAAATCG	CCAACCGCAT	CGCTTGCCT	ATGGATGCAG	AAGACAGCAG	TAGTGTTTTG	1080
GGCGATGATG	CGGCTTGTTGA	GATTCAAAAC	CCAGAAGGCA	TTTTCAACAA	CAACGGAGGG	1140
AATAGAAAAT	ACCACACCAA	GATGAGTGTC	CCTAAAGCCC	CTGATGATTT	CAATCTTTT	1200
CTCACAAAAA	TACACGCTGA	ATTTAACCBA	AGAAATCTCG	CACCCATAGA	TCGTAAAAATC	1260
TATAATGGCG	AGACACCTTT	AAAAATGCCC	GACACCCTTA	AGGCTAATGA	AATGCGTTTG	1320
CATCTGGGCA	AAAAAGTGA	TTATGAGCAA	AAGGACCTGA	TAGTGGAGTT	TGAAAGTAAC	1380
GAATCGCAIT	TGTTGGTGGT	GATCCAAGAT	TTAAACGCTC	GCATCGCTTT	AATGAAACTC	1440
TTATTCCAA	ACGTTAAGAG	CGCGAACAAA	GAATTGGTTT	TTTGCAATAA	AGAAAAACGC	1500
TTGATAAGGT	CTTTTGATGC	ACAAAAAGAA	TACGGCATCA	CGCCTGTAGA	AAATATTTTA	1560
AGCGTTTTAG	ACACCGCTAT	GAATCCTAAC	AGCGCGCTTG	TGATAGACAA	TCTCAACGAA	1620
GCGAAAGAAT	TGCACGACAA	AGTAGGGGCG	GAAAAGTTAA	AATCGTTTTT	AGAAAAAGCC	1680
ATAGACAACG	AGCAGTATTG	CGTCATTTTT	GCGCATGACT	TTAGGCAAAT	TAAACTAAT	1740
TACCATTTTG	ACAAGTTAAA	AGAATTGTTA	AACAACCACT	TCAAGCAATG	CCTAGCCTTT	1800
AGGTGCAATG	GGGAAAACTT	GAACGCTATC	AAAAGCGATT	TGCCTCCACC	AAGCAAACTT	1860
AACGTGCTAT	TGATAGAGCT	TTCCAAAGAC	AGCGTTACTG	AATTCAGGCC	TTTCAGCTTA	1920

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

965

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369

AGGCCCAATC TCTCTAGCCA GTTCCTTTTAC ACGGAAATGC TGAGCTTAAA ACTAACCTAT	60
GAAAGCACCC TCCAACAGGA TTTAAAAAAA ATCTTAGGGA TTGAAGAAGT CATAATGCTA	120
TCCACAAGCC CCATGGAATT ACGATTGGCC AATCAAAAGC TAGGCAATCG TTTCATTAAA	180
ACCTTACAAG CCATGAACGA ATTAGACATG GGTGCATTTT TTAACGCTTA CGCTCAAACA	240
ACCCAAAGAT CCCACCCATG CCAC	264

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370

GAAAAATCAA CGAGCAACTT GAAGAAGCCA AGCGTTTGGA GAAGCAAGTT GATATGCAAG	60
ATCGCCACTC ACAAGCGAG ATCGATAGGC TTATGCGTGA AGCCAAAGAG CATGAAAGAG	120
AAGCTAAGAG GCGCTATGGT GAATATCTTA AGGATAAAAA TGATTGAAAT AAGCGAATGG	180
TTGCAAAAAC TAGACGATGC CTTAGATAAA GTTGTGCTA AAAAAGAGCC AGAGAGTTTT	240
CTCAAGCCGA TCATTTTACC AATAGAGGAC TACCAAAAGA GTGTCAGGCA AATTCAGCG	300
CAATTCACAG ACGCGCCGAA GTTCAATGAA GAGGGTGCTT ACCCTCAATT TTTAAGCTGT	360
GGTTTATTGC AAGTTAGGGG CAAAAATGGT GCTAACATGG AATTTTATT GCCTAAAGTT	420
TATCCTTTCC CCCCTAAAAG CTTGTATATA GAGCATGAAA AAGACGGGCA GTTTTGTAGA	480
GAAATGCTCA TGCCTTACT CTCCAGCGCG CTTTGTAGTC AATTGGAAGT GATCTTAATT	540
GATGCGTTGA GCTTGGGGGG CATTTTCAAT CTGGCCAGAA GGCTTTTGA TAAAAACAAT	600
GACTTTATTT ACCAGCAAAG GATTTTGACC GAAAGCAAGG AAATAGAAGA AGCCCTAAAG	660
CATTGCCA	669

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

966

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371

ACATGGGTGC	ATTTTTTAAC	GCTTACGCTC	AAACAACCCA	AAGATCCCAC	CCATGCCACT	60
AGCTATGGCG	TTTTTGCGGC	GAGTTTGAAT	ATGGAATTGA	AAAAGGCTTT	AAGGCATTAT	120
CTTTATGCGC	AAACTTCTAA	CATGGTGATC	AACTGCGTTA	AAAGCGTCCC	CTTATCCCAA	180
AACGACGGGC	AAAAAATCTT	ATTGAGCTTG	CAAAGCCCTT	TTAACCAGCT	CATAGAAAAA	240
ACCCTAGAAC	TAGACGAAAG	CCACTTGTGC	GCAGCAAGCG	TTCAAAACGA	CATTAAGGCG	300
ATGCAGCATG	AGAGTTTATA	CTCGCGCCTT	TATATGTCT			339

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372

CGAGCTTCAA	TGAAAACTT	TTCCCCACTC	TATTGTCTTA	AAAAGCTCAA	AAAACGCCAT	60
TTAATCGCTC	TGAGTCTGCC	CTTGCTTTCT	TATGCGAATG	GCTTTAAAAT	CCAAGAGCAA	120
AGCTTGAATG	GCACGGCTTT	AGGCTCGGCG	TATGTCGCTG	GGGCTAGGGG	TGCTGACGCT	180
TCTTTTACAA	ACCCGGCTAA	CATGGGCTTT	ACTAACGATT	GGGGCGAAAA	CAGAAGCGAA	240
TTTGAAATGA	CCACCACCGT	GATCAATATC	CCGGCCTTTA	GCTTTAAAAGT	CCCTACGACC	300
AATCAAGGCT	TATATTCGGT	AACAAGTTTA	GAAATTGATA	AAAGCCAACA	AAATATTTTA	360
GGCATCATCA	ACACTATAGG	GTTAGGCAAT	ATCCTTAAAG	CGCTTGCCAA	TACGGCCGCT	420
ACCAATGGCT	TATCACAAGG	TATCAATCGT	GTTCAAGGGG	TTATGAAC		468

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

967

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373

GCGGATCGAG	AGGATAAACT	CTCTCACTCT	ATAATCATGC	GGTATTTTAG	AAGCGCTTTT	60
TTATTATTTT	TCATGACGCT	TTTTTTTGTT	TCTTGCTCTA	AGCACCCCTT	TTCTAAGCAA	120
ACCCCTAAGA	CTAAGGAGCG	GATCCGACAA	GAAGAAGCCA	ATAAAAAAAG	AGAAGAGACT	180
TTGAATGCCT	TGCGCCAATT	CAGACTCATT	TACATTAACA	CGCCGGTTTT	TCGCTTTTAT	240
GATTACGGCA	CGATCAAAAC	CGATAAAGAC	CACAATACTG	AAGTAACCTT	TTATAAGCTC	300
AGCCAAAAAG	TGGGCGATAT	TTACATGACT	AAACGGAGCA	TTTGTTTTAG	CCAAAAATGT	360
TCGGCCAAAT	GGATTGCTGC	AAGGGATTTC	TTTGGCAAGG	TGAGCTATGG	GGATTTGTTT	420
GATGATATTG	TTTTAGGGAG	GGATATTTTT	AAAGGTTTAG	GGAAACGCCA	CCTAACCCCT	480
GAATATGTGA	TCCAAAGGTT	TCAAAAAAGC	GGGGAAATTA	TCCTTTATGA	AAGAAAAAAT	540
GGCCTGATTT	CTTTCCAAA	CTTGACTCAA	AAAATTGCTA	TTAGGATTGA	ACCCTATGAG	600
CCTTCTTTGC	AAGATTTAGA	AGACAATGAA	AACGCTGATA	GCGAGCTTCA	A	651

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374

GAAATCGCTG	AGATCGTGAG	CCAATGGACG	CACATCCCGT	TCCAAAAAAT	GTTCCAAAGC	60
GAAAAAATA	GGGTTTTTAA	CATTGAAAGC	GAATTGCAAA	AAAGGGTGGT	GGGGCAAGAA	120
AAAGCGCTCA	AAGCGATCGC	TAAAGCGATT	AAAAGGAATA	AGGCTGGGCT	TAGCGATAGC	180
AACAAGCCCA	TAGGGAGTTT	CCTCTTTTAA	GGGCCAACAG	GCGTGGGTAA	AACCGAGAGC	240
GCTAAAGCTT	TGGCGCAATT	CTTGTTTGAT	AGCGATAAAA	ATCTTATACG	AATTGACATG	300
AGCGAATACA	TGGAAGCA	CGCTATCAGC	CGTCTTATTG	GGGCCGCTCC	TGGGTATGTG	360
GGCTATGAAG	AAGGCGGGCA	ATTGACCGAA	GCGGTGCGCA	GAAAACCTTA	TAGCGTAGTG	420
TTATTAGATG	AAGTGGAAAA	AGCCCATCCG	GATGTGTTTA	ACTTCTTGTT	ACAGGTTTTT	480
GATGAGGGGC	ATTTAACCGA	TAGTAAGGGC	GTGAGGGTGG	ATTTCAAAAA	CACGATTTTG	540
ATTTTAACCA	GCAATGTGTC	TAGCGGCGCG	CTTTTAGAAG	AGGATTTGAG	TGAAGCCGAT	600
AAACAAAAAG	CGATCAAGA	GAGCCTGAGA	CAATTCTTCA	AGCCGGAATT	TTTAAACCGC	660
TTAGATGAAA	TCATCTCCTT	TAACGCCCTA	GATAGTCATG	CTATCATC		708

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

968

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375

GTGAGGTTTT	GTTATTCTAA	AAAATATAAA	AAAACGATTA	TTTTAAAAAA	GGATTGGATG	60
ATGTTTGATA	ACACGCTTAT	CAATTTATTT	GAGACAGCGC	CTCTTTTAAC	TTCGCTTTTA	120
GCTGGGATTT	TAACTTTTTT	AAGCCCTTGC	GTGTTGCCTT	TGATCCCGGC	GTATATGTCT	180
TATATTCGCG	AAATTTCTTT	AGAGGATATT	AAAGATGGTA	AGGCTAAAAG	GGTTTCGGTT	240
TTTTTAAAT	CCITGATGTT	TGTGGTGGGG	TTTTCGCTCG	TGTTTTTGGG	CGTGGGCATG	300
TCTATGGCCA	AGCTTATCCA	TAGCTTTTCG	TTTTCTGGG	TGAATTATAT	CGCTGGGGGG	360
ATTGTGATCC	TTTTTGTTTT	GCATTTTTTA	GGCGTGTTTC	GTTTTCGCT	TTTGTATAAA	420
ACCCAAAGCG	CTGTTTAGC	GAGCAAATCT	AACAGCATGC	AGCGCTTTTA	CCCCTTTCTT	480
TTGGGCATGA	GTTTCGCTTT	GGGTTGGACG	CCATGCATCG	GGCCGATATT	CACTTCTATA	540
GTGATCATGA	GTGCGAGTAA	GGACGCTTAT	GGCTTAATGC	TTATGGTGGT	GTTTGTATAG	600
GGCTTGGCGA	TCCTTTTGT	ATTGGTGGCT	TTAATGCTAG	AAAGAGCGCT	TTTGTTTTAA	660
AAATCCTTAA	GAAATACAA	CCGCGCGATT	GAAATTGTTT	CAGGTTGGT	GCTTATTTTA	720
ATGGGAATAT	TGATCATGAC	AAATTCCTTA	GAAAGCTTAA	CTAACTTTTT	ACAAAAT	777

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376

ATAGGAGGTG	CGCATGCGTT	TTTATATTAT	CTTACATTTT	TGTTTATTGT	GGGTTTTGGC	60
GTGTTTGTTT	ATAGTATTGA	TCCGCAAGCT	TACGCTTTCA	ATTTAGGGAG	CTATAGCTTT	120
AACCTCCCA	TTGCCGTATG	GCTTATGGGC	GTTTTGGGCA	TGTTTCGCTT	TTTTTCATGG	180
GTTTTTTTAT	TCAAGCACAA	TCTCAGCCAT	AAAATCCGCT	TATACCATGA	AAAAAAGGAT	240
TTTGACAAAT	TGCTCAAACA	AATCCTATCC	CAAGACACCC	AAAAGACTTT	TTTAAAAACA	300
AAATTTAAAA	GCGATCTCGC	TAAAAACCTC	TCTCAAATCT	TAGCCCGCTA	TGATTTAAAA	360
GCTGATTTAA	ACACGCCAAA	TAGCGGGTGC	GAAAAAGTGG	ATAACCTTTT	TAAACATTAC	420
CACAATATAG	AAAATAACAC	CCTTGAGCCT	AAAGATCAGC	CTAAACATTC	CCTAGCTTAT	480
GAGCATGCTT	ATTTTCTTAA	ACGCTTGAAG	GCTTTCATTC	ATAACGATTT	GAAAAACGCC	540

SUBSTITUTE SHEET (RULE 26)

TTTGAAGTTT TAACAAACGC GCAAATCCCT TTGGAATTAC GCCGCTACGC CTTA

594

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377

CAAGATAAGG	GTTATTATT	GAGTGTAGCA	CTACCTAACT	CAAACAACGC	CTCTCAAAAC	60
AACATTTTAA	GCCTTTCTGT	CCTTCACAAC	CAGATTAAAA	TGTCTTATGG	TAATAAAGTG	120
ATGGACTTTA	CCCTCCAC	CTTACAGGAT	TACATTGTGG	GCATTCAAGG	ACAAAGCGCA	180
CTCAATCAAA	TTGAAGCTGT	TGGGGGGAAT	AACGCTATCA	AGTGGCTTTC	AACATTGATG	240
ATGGAGACTA	AAGAAAACCC	GCTTTTTCG	CCGATTATT	TAGAAAACCA	CTCTTTAAAT	300
GAAATCTTAG	GCGTAACAAA	AGATCTTCAA	AACACCGCAA	GCTTGATTTC	TAACCCTAAT	360
TTTAGAAATA	ACGCTACCAG	CCTTTTAGAA	ATGGCGAGTT	ACACCCAACA	AACCAGCCGT	420
TTGACAAAAC	TCTCTGATTT	TAGGGCTAGA	GAGGGAGAGT	CCAATTTTTC	AGAGCGCTTG	480
TTAGAGCTTA	AAAACAAGCG	TTTTAGCGAT	CCTAACCTTA	GTGAGGTTTT	TGTCAAATAC	540
TCTCAACTCA	GCAAACACCC	CAATAACCTT	TGGAFTCAAG	GGGTGGGAGG	AGCGAGCTTT	600
ATTTCTGGGG	GCAATGGCAC	GCTTTATGCG	TTGAATGTGG	GCTATGACCG	ATTGGTTAAA	660
AGCGTGATCC	TTGGGGGTTA	TGTGGCTTAT	GGCTATAGCG	GTTTTAACGG	GAACATCATG	720
CATTCTTTGG	CTAATAATGT	GGATGTGGGG	ATGTATGCCA	GGGCTTTTTT	GAAAAGAAAC	780
GAATTCACTT	TGAGCGCGAA	TGAAACTTAT	GGAGGCAATG	CGAGTCATAT	CAATTCTTCT	840
AATTCCTTGC	TCTCTGTGTT	GAACCAACGC	TACAACCTACA	ACACCTGGAC	AACGAGCGTG	900
AATGGGAATT	ACGCTATGA	TTTCATGTTT	AAACAAAAAA	GCGTGGTGCT	AAAACCTCAA	960
GTGGGCTTGA	GCTATCATTT	CATAGGCTTG	AGCGGGATGA	AAGGTAAAAT	GCAAATCCA	1020
GCTTACCAAC	AATTCGTGAT	GCATTCAAAC	CCTTCTAACG	AATCGGTTTT	AACGCTCAAC	1080
ATGGGGTTAG	AGAGCCGTAA	ATATTTTGGT	AAAAATTCCT	ATTATTTTGT	AACGGCGAGG	1140
TTGGGTAGGG	ATCTTTTGAT	CAAAGCTAAA	GGCGACAATG	TGGTGCGTTT	TGTGGGTGAA	1200
AACACTTTAT	TGTACCGCAA	GGGGGAAATT	TTTAACACTT	TTGCGAGCGT	GATCACAGGA	1260
GGCGAAATGC	ATTGTGGCG	TTTGATGTAT	GTGAATGCCG	GGGTGGGGCT	TAAAATGGGC	1320
TTGCAATACC	AAGATCTTAA	TATCACTGGG	AATGTGGGCA	TGCGAGTGGC	GTTT	1374

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

970

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378

ACGATACTAT	GCCCAGGGGC	TAAAAGCTAT	AAGTATTGGG	AAGGCATGGG	CATGTCTCAT	60
ATTATTAAGA	GCATTGAAGC	TTTAGATGAC	TATACCATTA	GATTCACGCT	TAATGGGCCA	120
GAAGCCCCGT	TTTATAGCGAA	TTTGGGCATG	GACTTTMTAA	GCATTTTGAG	TAAGGATTAC	180
GCTGATTACT	TGGCTCAAAA	TAATAAAAAA	GACGAGTTGG	CTAAAAAACC	TGTTGGGACA	240
GGGCCTTTCA	AATTCTTTTT	GTGGAATAAA	GATGAGAAAA	TCATTCTGGT	TAAAAACCAG	300
GATTATTGGG	GCCTTAAAGC	GTATTTGGAT	AAGGTGGTGG	TGCGCACCAT	TCATAATTTT	360
TCCACTCGCG	CCTTAGCGTT	AAGAACCGGT	GAAATCATGC	TCATGACCGG	GCATAATCTC	420
AATGAAGTGG	AGCAATTAGA	AAAACCTCAT	AATATCGTGG	TGGATAGAAG	CCCTGGGTTG	480
ATCGCCAAC	GGCTTTTCATT	GAACACGCAA	AAAAAGTATT	TPAATAACCC	TTTGGTGCCT	540
TTGGCTATCA	ATCATGCCAT	CAATGTTGAT	GATTACATCA	AGGTGATTTA	TGAAGGTTTT	600
GCTCAAAAAA	TGGTCAATCC	CTTCCCGCCC	ACCATATGGG	GTTATAACTA	TAATATCAAA	660
CCCTACGAAT	ACGATTGTAA	AAAGGCTAAG	GAGTTGTTGA	AACAAGCGGG	CTATCCTAAC	720
GGCTTTAAAA	CCAATATTTG	TACATCTTTA	CTC			753

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379

ATTTCATATTA	AACGAATTTT	TTTACTTAAA	AACACCCCAT	TTAACCCGCC	ATTATTCCCTC	60
CACATTGCCC	CACTCAAACC	ATTTCATGATT	ATTATTAAC	TGTTTTGGAA	TACTTTTAGC	120
TTGTTTGTTA	AAAAAACCAA	TAAGGATTTG	ATCATGCGCG	TTACCTTTGG	CTCCAAATAC	180
AACCAAATGA	ATCACTACCA	AAACGCTTTA	CAAAATAAAA	TCAACGACGC	TAACACGCAG	240
ATCGCTTCAG	GGCTAAAAAT	CCGTTATGGT	TATCAAAACA	GCGACATTAA	CAACCAGAAT	300
TTAAAAATTC	AATACGAAGA	AAACACCTTA	GATCAAGGCA	TTGATGTGGC	TCAAAACGCT	360
TACACTTCAA	CGCTCAATAC	CGACAAAGCC	TTGCAAGAAT	TTTCTAAAAC	GATGGAGGCG	420
TTTAAACCA	AACTCATCCA	ATCCGCTAAC	GATGTGCATT	CAGAGACTTC	TCGCGCCGCT	480
ATCGCTAACG	ATTTAGAACG	CTTAAAAGAG	CATATGATAA	ATGTCGCTAA	TACCTCCATA	540
GGGGGGGAAT	TTTTATTGG	AGGCAGTAAG	GTGGATAGAC	CCCCCATTGA	TAGTAATGGG	600
AAATACCATG	GCAATGCGCA	AGATTAAAC	GCGCTTATTA	GCTCTGATAA	CCTTGTGCCT	660
TATAATATCA	GCGGGCAAGA	TTTGTTTTTA	GGCACCGATA	AAGACAAACA	CAAACTCATT	720
ACCACCAACA	TTAAATTACT	CAATCAAAAC	AAGCTCCACC	CTGATGTGAT	GGACGCTTTA	780
GAGCATTCTT	CATTGCCTGA	AGAAGTTTTT	ATTAAACCCA	GCGATACCTT	GCGAGAAGTC	840
ATCGGCGATA	ACGATAAAAA	CCCCACCAAT	GACCCTAAAG	AGTTTTTTTA	TTTGCAAGGC	900
TTTAGGCCTG	ATGGCTCTAG	TTTTAAAGAA	AAATTGCGGT	TGGATAAAGC	CTATCAAAAC	960
CAAGAAAGCG	CGACTAAAGT	GAGCGATTTG	TTGGATAAAA	TCGGGCATGC	TTACGGGAAC	1020
ACTTCGCAAA	ATAAAGTCGT	GGATGTGAGT	TTGAACAATT	GGGGGCAAT	TGAGATTAAA	1080

SUBSTITUTE SHEET (RULE 26)

971

AACCTAACCC	CCGGCAGTGA	AAATTGGAAT	TTTCATTGTA	TTTCTAGCGA	TGGGGATTTT	1140
GACGATTTAG	ACGCCTTGCG	TTCGAGCGGT	AAAAGGGTTA	CTGAATATGT	CAAAAGCGCG	1200
TTTGTAACGG	ATAGGAGTTT	GAGCCAAGTT	AAAGCGGTGC	CTAACATGTA	TAACCCATAA	1260
GTGCTTGAAA	TCCCTAGCGT	GTTTGCTGACT	AAAGACAATG	TTTTAGCTAA	CAAAAACACC	1320
AAGTTGAGCG	AGATTTTTGG	CGATAAGGTG	GAAACTTTAA	AAATCAACGC	CAGCCGTTTG	1380
GGCGATGAAA	GCGCTATTAA	AATCCCAAAC	CTCCCTATTA	ATTTGGATAT	TCCCATTCTT	1440
TTAGATGTGA	AAAACCTCTAC	GATTAAAGAT	TTGAAAGACG	CGATTAAAGA	ACGCTTCAAT	1500
AATGAAGTGG	ATGTGGAAAT	TGAAACGAAC	GGGCGTTTGA	GGATCATTGA	CAATTCCTCT	1560
AAAGAATCGC	CTATTTCTTT	TGCCTTAAGC	ACCCTGGATC	AAAAAGGGCT	AGAAGTGGCC	1620
GGTATCCCCA	CTAATAACGC	GAGCGAATAC	CAAAAAACCT	ATTTCAATAA	AGAAGGGGCC	1680
AAATTAGAAA	GCAATGTTGC	CCAAACCGCT	CAAAATGATG	CGGCTAATGG	CTCTACTAAA	1740
CTGAGTGAAG	TCTCTAAGGG	GAGTTTGGAA	AATAGCGTTT	TAAACATGAA	ATTAAACGAT	1800
GTGAATGGTT	CGTTTTTAGA	AGCGCAAATA	AACCTGGATA	ATAATGGGGC	TTTTTTGAGT	1860
TTGCCTAATG	GCGTTAAAT	CCCGCTTTAT	GACCCACAA	CCGCTGATAT	TCAAGCGTCT	1920
AAACCCAATG	AAGTCACCTA	CAGGCAGCTC	ATGGATGCGA	TGAGTATCGC	GCTCAATTAC	1980
AGCAACACTG	ATCCTGCAAT	CTACCAACAA	ATCAGCGATA	ACCCTACTTC	AAAAGAAAGC	2040
AAGGAGCGAT	TCATTGAATT	GTTAAAACAA	GCTAAAGACA	ACCTTTCTAT	TAATTTGAAT	2100
GAAGAGGGTA	AAGTCATTAT	CCAAGACAAC	ATGCATTCAA	ACACCAAAAT	GCAGTTCATG	2160
CTTTTTGATA	AAGACGCGAA	TGATTTTTCT	CAAAACGCCT	TACACAGCGA	CAAACCAAGC	2220
CTTAAATTAA	ACGCTAATAA	CGCCCTAATT	ATTGACAAGC	CAAGCGTGAA	TTTTTTTGAT	2280
CAATTAGAAA	ATATTATCAC	TTCTGTAAGA	AAAGGGATTT	ATCGCCCGA	CGCTTTAGGG	2340
GATACTTATT	CTAGCGACAT	GCGTAATTTA	GGCATTCAAA	ACGGCATCAC	CCTTATAGAT	2400
CACCTGAGCG	ATCACATAGA	AAAAATGATC	GCTAAAAACG	GCGCTCATGG	TAAGGCATTT	2460
GAAAACATCA	TCAGGCGTAA	TGAAGTTTAA	AAAACACAAG	TTCAAAGCAT	TCGTGGGGAA	2520
ACGACCGGCA	CGGATATGGC	AGAACTTAT	AACAAGTTTT	CCAATCTCAC	TAACAACTAT	2580
AACGCCGTTT	TGGCTTCCAC	GAACAAAATC	AATAATCTGT	CTTTAACGAA	GTATTTA	2637

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380

AGGATTGATC	AAATTAAAAT	TATGAAATTG	GTGAGTCTTA	TTGTAGCGTT	AGTTTTTTGT	60
TGTTTTTTAG	GGGCTGTAGA	GTTGCCTGGA	GTTTATCAAA	CTCAAGAATT	TTTATACATG	120
AAAAGCTCTT	TTGTGGAGTT	TTTTGAGCAT	AACGGGAAGT	TCTATGCCTA	TGGTATTTCT	180
GATGTGGATG	GCTCTAAAGC	CAAAAAGAC	AAACTCAATC	CTAACCCAAA	GCTAAGGAAT	240
CGCAGCGATA	AAGGCGTGGT	TTTTTAAAGC	GATTTGATTA	AGGTTGGGGA	ACAATCTTAT	300
AAAGGCCGTA	AGGCGTATAA	TTTTTATGAC	GGCAAGACCT	ACCATGTGAG	AGTCACTCAA	360
AATTCAAACG	GGGATTTTGA	ATTCACCTCA	AGCTATGACA	AATGGGGGTA	TGTGGGCAAT	420
ACCTTCACCT	TGAAACGCGT	GAGGGGTGCC	GAAATCAGTA	TTTTAAAGCT	CAAGCGTTTT	480
AATCTCATGC	GCTCTTTTAA	CAGGCAGACC	CACCTTTTTT	CTATTGGTAA	GGCCTACGCG	540
ACA						543

(2) INFORMATION FOR SEQ ID NO:1381:

SUBSTITUTE SHEET (RULE 26)

972

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381

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AAGGATTAA GCAAGATGTT TGTGGTTTT ATAGAAGGTT TTGGTTTAGC GATTTCCTTG      60
TGC GCGCGCGG TGGGGGCGCA ATCCFTGTTT ATTGTGAAA GGGGATGGC TAGGAATTAT      120
GTGTTTTTGA TTTGCGCCTT GTGTTTTATG TCGGATATTG TCTTAATGAG CATGGGCGTG      180
TTTGGCGTGG GGGCTTATTT CGCTAAAAAC CTTTATTTGA GCTTGTTTTT GAATTTATTT      240
GGGGCAGTTT TTACCGGATT TTACGCTTTT TTGGCTTTAA AAACCCTTTT TCAAACCTTT      300
AAAAAAAAGC AAGTCCAAAC CCTAAAAAA TTATCCTTAA AAAAGACCTT ATTATTCACT      360
TTAGGCGTTA CCTTACTCAA TCCTCAAGTG TATTTGAAA TGGTGTTTTT AATTGGCGCG      420
AGCGCTATGT CTTTAAACCT AGTGCAAAA TTCGTCCTTC TAGCTGGCAC TTTATCGGCT      480
GCCTTTTCTT GGCTTTTATT GTTATGCACC ATGTCCTTAC GCTATGGCTC TAAACTTTTG      540
AACAAACCAA AAATCTTTAT GGGCGTGAAT CTCCTTGTA CCGCTATCAT GGAACGCTC      600
AGCGTTACTT TATTCAGGA TTTTITAGCG TTATTGAGCA AAACC                        645

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(2) INFORMATION FOR SEQ ID NO:1382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382

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ATGGATATTT TAAAAGCAGA GCATTAAAC AAACAGATTA AAAAAACCA AATCGTTTCA      60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGC TTTTAGGGCC TAATGGGCG      120
GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCTAGTGG GGGGAGCGTT      180
TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA      240
GGCTACTTGC CCCAAGAATC CAGTATTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC      300
CTAGCAGGGG AGAGCACTTT TAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG      360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA      420
GAAAGRAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAA ACCCTAAATT CGTGCTGTTA      480

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973

GATGAGCCTT	TTGCGGGCGT	GGATCCGATT	GCGGTGATTG	ACATTCAAAG	AATCATTGAA	540
AGCTTGATTG	GATTAAACAT	TGGCGTGTG	ATTACTGATC	ACAATGTGCG	AGAGACCTTG	600
AGCGTGTGCC	ATAGGGCGTA	TGTGATCAAA	AGCGGCACGC	TTTTAGCGAG	CGGGAACGCT	660
AATGAAATTT	ATGAAAACGC	TTTGGTGCCT	AAGTATTATT	TAGGGGAAAA	TTTAAAGGTA	720

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383

AACACTGGTT	TGTGGCACTC	TTGGGGTTTG	GCTCCAGCGC	TTTTGGAAAC	GCAACTGCCC	60
AAACATGCTC	ACCAATTTTT	TCAAATCTTC	TTTTTCCCCA	AAAAGCCCTT	CAACAAATG	120
ATCGTTATTG	TGGAGTTGCT	TGTCAATTTT	ATCTTTAATC	TCCTTCACGC	CATACATGTT	180
GGGGTTAAAA	TGATAGATAA	TATCAAACCTC	CCACTTAGAC	GCATAAAAT	GCGCGCTCTC	240

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384

ATTGATCTAG	GCGTGATAGA	GACCATCCCC	AAACACTCTA	AGATTGTTTT	ACCCGGGGAG	60
GCGTTTGATA	GTTTAAAAGA	GGCGTTTGAT	AAAATTGACC	CCTATACTTT	CTTTTTTCCA	120
AAATTGGAAG	CCACTAGCAC	TTCTATTTCT	GATACTAACA	CGCAGAGGGT	GTTTGAAACG	180
CTCAATAACA	TTAAAACAAA	TCCTTATAATG	AAATATAGTA	ATGAAAATCC	AAACAATTTC	240
AACACTTGTC	CTTACAATAA	TAATGGTAAT	ACAAAAAATG	ATTGTTGGCA	AAATTTACCC	300
CCACAAACCG	CAGAAGAATT	CACCAATTTA	ATGTTGAACA	TGATCGCTGT	TTTAGACTCC	360
CAATCTTGGG	GCGATGCGAT	CTTAAACGCT	CCTTTTGAAT	TCACTAACAG	CTCAACAGAT	420

974

TGCGATAGCG	ATCCTTCAAA	ATGCGTAAAT	CCCGGAGTAA	ATGGGCGTGT	TGATACTAAA	480
GTCGATCAAC	AATATATACT	CAACAAACAA	GGTATTATTA	ATAATTTTAG	AAAAAAAATA	540
GAAATTGATG	CGGTTGTTTT	AAAAAATTCA	GGGGTTGTAG	GGTTAGCCAA	TGGATATGGC	600
AATGATGGTG	AATATGGCAC	ATTAGGGGTA	GAAGCCTATG	CTTTAGATCC	TAAAAAATC	660
TTTGGCAACG	ACCTTAAGAC	TATCAATTTA	GAAGATTTAA	GAACCATCTT	GCATGAATTC	720
AGCCACACTA	AAGGCTATGG	GCATAACGGG	AATATGACCT	ATCAAAGAGT	GCCGGTAACG	780
AAAGATGGTC	AAGTGGAAAA	GGATAGTAAT	GGCAAGCCAA	AAGATTCTGA	TGGCCTTCCC	840
TATAATGTGT	GTTTCGCTTTA	TGGGGGATTC	AATCAGCCCG	CTTTCCCTAG	CACTACCCT	900
AATTCCATCT	ATCACAATTG	TGCGGATGTC	CCGGCTGGCT	TTTTAGGGGT	AACAGCAGCG	960
GTTTGGCAGC	AGCTCATCAA	TCAAAACGCC	TTGCCGATCA	ACTACGCTAA	CTTGGGGAGT	1020
CAACAAACT	ACAACCTAAA	CGCTAGTTTA	AACACGCAAG	ATTTAGCCAA	TTCCATGCTC	1080
AGCACCATCC	AAAAAACCTT	TGTAACCTTCT	AGCGTTACCA	ACCACATTTT	TTCAAACGCA	1140
TCGCAAGTTT	TTAGAAGCCC	TATTTTAGGG	GTAAACGCTA	AAATAGGCTA	TCAAAACTAC	1200
TTTAATGATT	TCATAGGGTT	GGCTTATTAT	GGCATCATCA	AATACAATTA	CGCTAAAGCT	1260
GTTAATCAAA	AAGTCCAGCA	ATTGAGCTAT	GGTGGGGGGA	TAGATTGTGT	ATTGGATTTC	1320
ATCACCCTT	ACTCCAATAA	AAATAGCCCT	ACAGGCATTC	AAACCAAAG	GAATTTTCT	1380
TCATCTTTTG	GTATCTTTGG	GGGGTTAAGG	GGCTTGTTATA	ACAGCTATTA	TGTGTTGAAC	1440
AAAGTCAAAG	GAAGCGGCAA	TTTAGATGTG	GCTACCGGGT	TGAACCTACG	CTATAAGCAT	1500
TCTAAATATT	CTGTAGGGAT	TAGCATCCCT	TTAATCCAAA	GAAAAGCTAG	CGTCGTTTCT	1560
AGCGGTGCGG	ATTATACGAA	CTCTTTTGTT	TTCAATGAAG	GGGCTAGCCA	CTTTAAGGTG	1620
TTTTTCAATT	ACGGGTGGGT	GTTT				1644

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385

GATCATAGCT	TTAATATTCA	AAATAGTATA	AAAAGGAAAG	TCATGTATGC	GGCTCATCCT	60
ATTAAACCCA	TAAAGCCCC	TAAACTCAA	TCTCAATTTT	TAAGGCGTGT	GTTTGTGGGC	120
GCGTCCATTA	GGCGCTGGAA	TGACCAAGCA	TGCCCTTTGG	AATTTGTGGA	ATTAGACAAG	180
CAAGCCCATA	AAGCGATGAT	TGCGTATCTG	CTCGCTAAAG	ATTTAAAGA	TAGGGGTAAA	240
GATTTAGATT	TAGATCTTTT	AATCAAATAT	TTTTGCTTTG	AGTTTTTGGA	GCGCTTGGTT	300
TTAACCGATA	TTAAACCCCT	TATTTTTTAC	GCCCTCCAAC	AAACGCATAG	TAAAGAGTTA	360
GCTTCTATG	TTGCGCAAAG	TTTGCAAGAT	GAAATCAGTG	CGTATTTTTT	TTTAGAGGAA	420
CTCAAAGAGT	ATTTAAGCCA	CAGGCCTCAA	ATTTTAGAAA	CTCAAATTTT	AGAGAGCGCG	480
CATTTTATG	CGTCTAAGTG	GGAGTTTGAT	ATTATCTATC	ATTTTAACCC	CAACATGTAT	540
GGCGTGAAAG	AGATTAAAGA	TAAATTGAC	AAGCAACTCC	ACAATAACGA	TCATTTGTTT	600
GAAGGGCTTT	TTGGGGAAAA	AGAAGATTG	AAAAAATTGG	TGAGCATGTT	TGGGCAGTTG	660
CGTTTCCAAA	AGCGCTGGAG	CCAAACCCCA	AGAGTGCCAC	AAACCAAGTG	TCTAGGGCAT	720
ACTTTATGCG	TGGCGATTAT	GGGGTATTTA	TTGAGTTTGT	ACTTGAAAGC	TTGTAAAGC	780
ATGCGGATCA	ATCATTTTTT	GGGCGGGCTT	TTCCATGATT	TACCCGAAAT	TTTAACCCGA	840
GACATTATCA	CGCCCATCAA	ACAAAGCGTT	GCAGGGCTTG	ATCATTGCAT	TAAAGAGATT	900
GAAAAAAGG	AAATGCAAAA	CAAAGTCTAT	TCCTTTGTGT	CTTTGGGCGT	TCAAGAAGAT	960
TTGAAATATT	TACCCGAAAA	CGAGTTTAAA	AACCGCTACA	AAGACAAGTC	TCATCAAATC	1020
GTTTTCACTA	AAGACGCTGA	AGAATTATTC	ACGCTTTATA	ATAGCGATGA	ATATCTTGGG	1080
GTTTTCGGGG	AGCTTTTGAA	GGTGTGCGAT	CATTTGAGCG	CGTTTTTAGA	AGCCCAAATC	1140

SUBSTITUTE SHEET (RULE 26)

975

TCTCTTTTCTC ATGGCATTTC TAGCTACGAT TTAATCCAAG GAGCTAAAAA CCTTTTAGAA 1200
 TTGCGATCCC AAACGGAACT GCTTGATTG GATTAGGGA AATTGTTTAG AGATTTTAAG 1260

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386

AATATTACAA	TCAAGGATAG	AACGATGAAA	ACAAATGGTC	ATTTTAAGGA	TTTTGCATGG	60
AAAAAATGCT	TTTtagggcgc	GAGCGTGGTG	GCTTTATTAG	TGGGGTGTAG	CCCGCATATT	120
ATTGAAACCA	ATGAAGTTGC	TTTGAAATTG	AATTACCATC	CAGCTAGCGA	GAAAGTTCAA	180
GCGTTAGATG	AAAAGATTTT	ACTTTTAAGG	CCAGCTTTCC	AATACAGCGA	TAATATTGCT	240
AAAGAGTATG	AAAACAAATT	CAAGAATCAA	ACCACGCTTA	AAGTTGAAGA	GATCTTGCAA	300
AATCAGGGCT	ATAAGGTTAT	TAATGTGGAT	AGCAGCGATA	AAGACGATTT	TTCTTTTGCG	360
CAAAAAAAG	AAGGGTATTT	GGCTGTGCGT	ATGAATGGCG	AAATTGTTTT	ACGCCCCGAT	420
CCTAAAAGGA	CCATACAGAA	AAAATCAGAA	CCCGGGTTAT	TATTCCTCCAC	TGGTTTGGAT	480
AAAATGGAAA	GGGTTTTAAT	CCCGGCTGGG	TTTGTCGAAGG	TTACCATACT	AAAGCCTATG	540
AGTGGGGAAT	CTTTGGATTTC	TTTTACGATG	GATTTGAGCG	AGTTGGACAT	CCAAGAAAAA	600
TTCTTAAAAA	CCACCCATTTC	AAGCCATAGC	GGAGGGTTAG	TTAGCACTAT	GGTTAAGGGG	660
ACGGATAATT	CTAATGACGC	AATTAAGAGC	GCTTTGAATA	AGATTTTTCG	AAGTATCATG	720
CAAGAAATGG	ATAAGAAACT	CACTCAAAGG	AATTTAGAAT	CTTATCAAAA	AGACGCCAAG	780
GAATTAAAAA	ACAAGAGAAA	CCGA				804

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387

SUBSTITUTE SHEET (RULE 26)

976

TCAAATTTTA	AAAAAGGATT	TTTTATGTTT	AAAAGCAGAT	TAAATTCATG	GATTTTATTA	60
GGGATTTTAG	GGGTTTTAGT	GGTGGTTTTT	TGGGATGTCA	TAAAATACAA	AATAGAAGAT	120
TTGCAACATG	ATCATTATCT	ATCACAAGTG	AAAGAAAGGG	AAGAATATTA	TAAAAACCAC	180
ATAGAAGAAG	CTTTGAAAAA	GGATAGCGAA	TGCTTTGAAA	AAGGAGGCGA	TAAAGTGGAT	240
TGCTCGGCTG	CTATGAGAAT	AGCTGCTGGT	GAAAGAAATA	GAAGAATGTT	AGAGATTAAA	300

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388

AAATTATTTT	TAGTTATAAT	TTTTCAAAAA	ACCTTAAGAG	AAATCATGCA	AGATTTACAA	60
CATTTCAAAA	ATGATATTAC	GCTCATTCTA	TCTAAAGACA	GATTAGATAC	TTATGACAGC	120
CTAGAGCAAT	ACAAAGAAAA	TTTAAAACTC	ATTGCTTTCA	TCACGCCTAA	AATTTCTAAC	180
TTAGAAATTT	ATTTACGCAA	CGCTTTAGAC	TATTGCCTGA	CTCAAATGAA	AGGGAGTGAA	240
TGGGTGTTTA	ACGAAAGCGT	TTTAACCCCT	TTAATCAAAG	AATTAAAAGA	AAAGAAAAAA	300
GAAATCACGC	ATTCCTTAAT	CTTATCTAAA	ATGTCCTTAG	GGGCAGTGAT	CAGGCTTATT	360
TTTTGTTATA	AGTTAGAGGG	GGTAATATTA	GATTTAAAGC	GCATCAATTT	CAAATCCTAT	420
TACCCCAATA	ATAAAAATGC	ATTATTTATC	AACAATAAGA	AAAATCCATT	ATCTAGTGCT	480
TCAAAGGTTT	ATATTGCTTT	AAACTTGCTA	TGGACAATTA	GAAATCGTGC	GTATCATTTG	540
GAAAATTTAC	TCAAATCCCA	ACCGAACAAG	CGCCACGCA	TTACGACTTA	TTTCATTGGG	600
TTAAAGACA	ATGATAGGGC	AAGAATTCCT	ATGAATATCA	GTGTAGAACC	AAGTAAAATC	660
GTCTTGTTTT	TAGATGATTT	AATTAAAAGC	ATCGGAAATA	AAGACTTGGA	AGATTTAAGT	720
AGTTTG						726

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

977

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389

GGCATGAAAG	CGTTGAAGAC	TTTTTTTAAA	AAATCCCTTA	TTCTGTTACT	AGCAATTGCC	60
TTAAACCACT	TAAACGCTGT	GGCTATGATT	GTGGATAATC	CTACGCAGAA	CGCTTGGAA	120
GGTGCTAAAA	GAGCATGGGA	TGAAAGCAAG	TGGGCTAAAC	ATTTAGCCAC	TATTACTGAA	180
AGGATCAAGC	TCGCTCAAGA	CACATTAGAT	AGGGCTAATC	AGACGCTTAA	TTCCATCAAC	240
AAAGTGAATG	ATGTTTTGAA	CAAAACCAAT	CAATTTCTAA	CAGGCAGTAT	TTTAAGCATC	300
CCCAATCCCA	TGCAGTATGT	AGAAAAATC	CAAAGTTTGT	CCAAGCAAGT	TCAAGCCAAT	360
ACTGAAAGGA	TCAAAGAAAA	TGCACAAAAC	TATGATATAC	GCAATCAAAT	TGCAGCCAAA	420
CGCATCTCTG	AAAAATGCC	TGAACCTCAAT	TGGGATGTCA	GTCAAGACGC	GAGCCCTACA	480
GAGAAAAACT	TACACCAATT	TTTCACGAGC	AAGGGGAAAG	AAAGCGCTAA	CACAAAGGCT	540
CTAAGGATT	TTGCTAACGC	CATAGGTAAC	ACTCAAATCA	GCACGGCGAA	CGATTTAGGA	600
GCTGGACTTA	GAGGCAGAGC	CTTATTAGAA	TACATTTGCA	TTCAAAAAGG	CAATTTAGAA	660
GCGGCTAAAA	AAATCCAATT	ATTAGACAGC	CAATGACTT	TAGCTCTACT	CAATAACGAC	720
TATACGGCTT	ATGAAAAACT	TAGAGCTGAA	AAAGAAGAAT	TAAAAAGACA	AATCGCTTCA	780
AATGTGTATG	CGAAAGTCAA	ACAGCTTGTT	GTAGCTTCCC	AAGATAGAGC	GTTTAGTCAA	840
ATGATAATG	AGTTGGGCGT	TAAACTTTT	GGGTCAACG	ATGAGAATGT	TAAAAAAGGT	900
TATTCGAAGA	AAGAAAACAG	AAATGGCAAA	AGCGAGTGCA	TCCCTAACAT	GCTCAATGTT	960
AATCGCTTAA	AAGCGCAATT	TGATGAGCTT	AATTTAGATT	ATAGTAGGGA	TATTGCTGGT	1020
AAAAAAGGTT	AAGCAGCCGC	TAAAGTGTTT	AATGACTACA	AACACCGATT	CCAACAATTA	1080
AGCGTAGAAA	CTGCTTTAGA	AATCGCTCAA	AATTTAAGTT	TTATGAATAA	GACGCTAGGT	1140
TTAATGGTGC	AAATGCAAAG	CTATGCATTC	AAGCAACAAA	TGGGCTATTT	TGAAGATATT	1200
ATTCTGCTG	ACGCCCTAAA	AGATGACAAA	GAGCATCAAG	AAAATCTTGA	ACAAAAACAA	1260
CAAGAAATAG	AGAAAGTCTA	TAGGGCTAAA	TTAGACGCTT	ATGGTTTCCC	TAATGGTAGT	1320
GTAGGAAAGG	CAAGTGGCGT	GAATTCAAAT	AGTAATAATG	AAGCCCCAAG	CTCTGATAAT	1380
ATCCAGTCGT	TTAATCCGTA	T				1401

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390

AGATTAAATA	ACATGGCCGC	TCCACTACTT	GCTCTGCCCT	TTCTTTCTAA	CCCTTTAGTG	60
CTTGGTGCTT	TAGCTGTCTAT	AGGAGTGGGT	GCTTACTTGT	ATCCCAATAA	GCAAGATTCT	120
TTAGTTGTGC	AAGCAGATGG	GCTTTATAGT	GAAATTCCTG	GGTTTTCTAT	TTCTGTTTTCT	180
AGCAAGATCT	TGAAAGGAAT	TGGTGAGCCT	TTAGCCAATG	TTATCCAACC	TTTTGGTATG	240
GTTTTTAGGAA	TGCTTTTAAT	CCTTTTGTAT	TCCTTTAAAC	GCTATCAAAA	CAATGATTTA	300
TTTGAAATCA	AAACCTTTTT	AATGCTTTTT	GTGTTTGTAG	GATACCTTTC	TTTGTACCAT	360
TATGCTTTTA	AATCTGATGG	TTCTAGTAGC	GGTAATGGTC	GCTCCAGTTT	TGCCTTTCAA	420
AATCATGTAA	CAGAAATTTT	TGACACGCCCT	GCTAACTTGC	TAAATGCTGG	GATTCTTAAT	480
GTGGTTAAGG	AATATCAAAC	AAATAGTGCA	AGAGAACACA	AGAATATAGA	CACGCACCAC	540
AGTATCACTA	ACGCTAATAT	TTCAATCCAT	GTCAGACAAA	TTTAAACGAG	TTTGAATAAA	600
CTATATGAAG	ACTTCAAAAT	TAATAATGGA	CTATCGCTAA	AAACCCCTTAT	TGCAGCTGTT	660
TTGTTATTAG	TTATTTTAGG	ATTAGAATTG	TTTTTATTGT	TCAAAGTTTT	CTGTTATGTT	720

SUBSTITUTE SHEET (RULE 26)

978

TTTATGACTT	ATTTAGAAAA	AATTATTTAC	TTGTCTTTGG	TTATTTTCAT	GCTACTGCTA	780
GGGTTTTTTC	AGCAGACTAG	AGGTTTTTTA	GTGTCTTATG	TGAAAAAAT	TATTTTCATTG	840
ACTTTTTTACA	TGCCTTTGTT	GTTGCTATTA	GTGTTATTCA	ACTCTTTTGC	ATTACAATAC	900
GCAATCAAAG	TGGGAGGGAG	CAATGAAATA	GTGGCTAAAT	TTGGCATTAT	TGTAGCAATA	960
GGAATTTTAC	TGACATTTAT	TCAAAAAGTC	CCCGAAATGA	TTAACGCTAT	CTTTGGCACA	1020
CAAGGTGGTC	TAACGGATGC	TAAAAGCTTC	ATATATCAAG	GTGTGCAAAT	GGCTAGTGCCT	1080
GGAGCTGGAG	CCATAGCTGG	AAGTCTTAAG	AGTGTGGGTC	GTTTCAGATT	TGGTAGAACG	1140
CTAGAAGCTT	ATAAAGACGC	AAAATCTACG	ATAAACAGCA	CTACGGCTAA	CATGAGAGAC	1200
ATGCCAGGAC	ATCCTGGTGT	TAGAGTGGGT	GTGGAGACGA	TTGAACTTCC	CAAGTCTCAT	1260
AGAGCTAGCA	AA					1272

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391

AAAAATCGCT	ATCTTAAGAG	GGGGCGAAAC	GCTATCTTGG	AACCTTCAAG	AAATCGCCTA	60
AAACATGCCG	CCTTTTTTGT	GGGGCTTTTT	ATCGTTTTGT	TTTTAATTAT	AATGAAGCAC	120
CAAACCTCCC	CCTATGCTTT	CACGCATAAT	CAAGCCCTTG	TCACTCAAAC	CCCCCCTAT	180
TTCACGCAAC	TCACTATCCC	TAAACCAAAT	GACGCTTTAA	GCGCGCATGC	GAGCTCTTTA	240
ATCAGCTTGC	CTAACGACAA	TCTTTTGAGC	GCTTATTTTA	GCGGCACTAA	AGAAGGGGCA	300
AGGGATGTGA	AAATCAGCGC	GAATCTTTTT	GACAGCAAGA	CTAATCGCTG	GAGCGAAGCC	360
TTCATCTCTT	TAACCAAAGA	AGAGCTTTCT	CATCATTCGC	ATGAATACAT	CAAAAAATTA	420
GGTAACCCCT	TGCTTTTTTT	GCATGATAAT	AAAATTTTGT	TGTTTGTCGT	AGGGGTGAGC	480
ATGGGCGGGT	GGGCCACTTC	TAAAATCTAT	CAATTTGAAA	GCGCTTTAGA	GCCGATTCAT	540
TTTAAGTTTG	CGCGAAACT	CTCTTTAAGC	CCTTTTTTAA	ATTGAGCCA	TTTAGTAAGG	600
AATAAGCCTT	TAAACACCAC	TGATGGCGGG	TTTATGCTAC	CACTCTATCA	CGAATTAGCC	660
ACCCAATACC	CCTTGTGTGT	GAAATTTGAC	CAACAAAATA	ACCCAAGAGA	GCTTTTAAGG	720
CCTAATACCT	TAAACCACCA	GCTCCAACCA	AGCTTAACCC	CCTTTAAAGA	CTGCGCTGTC	780
ATGGCGTTTA	GAAACCATTC	TTTTAAAGAT	AGCCTCATGC	TAGAAACCTG	TAAAACCCCC	840
ACTGATTGGC	AAAAACCCAT	TTCTACAAAT	CTTAAAAACT	TAGATGATTC	TTTAAATTTA	900
CTCAATTTAA	ATGGAATATT	GTATTTGATC	CACAACCTTA	GCGATTTATC	ACTGCGTCGT	960
AAAGAACTTT	GGCTTTCTAA	ATTAGAAAAC	TCCAATCGT	TTAAAACCTT	AAAAGTTTGT	1020
GATAAAGCGA	ATGAAGTGAG	TTACCCAAGC	TATAGCCTTA	ATCCGCATT	TATAGATATT	1080
GTCTATACTT	ACAACCGCTC	TCATATCAAA	CACATCCGTT	TCAATATGGC	TTATTTAAAT	1140
TCCCTTCTCA	AG					1152

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

979

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...555
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392

TTAGTCATGT	TTATATCTTC	TTCTTACACG	CTGAGTTTTG	TATGGCTTTT	TTTAATTTTC	60
TTTTTTTTCA	AAAATAAGCC	ATTGGGTTTG	AGGTTTTCGC	TCTCTTTGAT	AAGCGTGATT	120
TTAAGCAATA	TCGCTTTGAA	AGACTCCCTA	TCGCTCAATG	AATTTTTAAG	CAGTTTTTACA	180
GCCCCCTTAA	GCCCCCTTAG	CTGTCTTTTG	ATCCTTGCTT	ATGCAAGCTT	TTCTTGCCAT	240
ATACTCAAAA	AGCCCCCTTT	AGAAACCTTG	CAATCTTATA	GCGTCATGCT	GTTTTTCAAT	300
CTGTTGCTTT	TGACAGATAT	TTTAGGGTTT	TTGCCTTTTT	CAATCTACCA	TCATTTTCATG	360
GCTTCTCTGA	TTTTTAGCGC	GCTTTTTTGC	AGCAGTTTGT	TTTTGAGTAG	CCCCTTATTA	420
GGCGTGATCG	CTTTAGTGGC	TTTATCCAGT	TCGCTTTTGA	TGCGTTCTAA	TTTTCAAATC	480
TTAGATTCTT	TATTGGATTT	CCCATTATTT	CTTTTTGTCT	TTTTTAAGAC	TTTATATCTT	540
GCTAAAAAAA	GGTTA					555

(2) INFORMATION FOR SEQ ID NO:1393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393

AAAAGAATAC	TGATGAAGAA	AAGAAAACAT	GTATCCAAGA	AAGTGTTTAA	TGTCATTATC	60
TTGTTTGTGG	CAGTATTCAC	TCTTTTAGTC	GTCAATTCACA	AAACCCTTTC	AAACGGCATT	120
CACATACAAA	ATTTAAAAAT	TGGAAACTTT	GGCATTTCTG	AATTATACIT	AAAACCTAAT	180
AACAAGCTTT	CTTTGGAAGT	TGAGCGGGTT	GATCTCTCTT	CTTCTCTCCA	TCAAAAACCC	240
ACTAAAAAGC	GTTTAGAAGT	TTCTGATTTG	ATTAAAAATA	TCCGTTATGG	CATTTGGGCG	300
GTGTCTTATT	TTGAAAAACT	TAAAGTCAAA	GAATCATTTT	TAGACGATAA	AAATAAAGCC	360
AATATCTTTT	TTGATGGGAA	TAAATACGAG	TTAGAATTTT	CAGGAATCAA	AGGGGAATTT	420
TCCCTAGAAG	ACGATAAAAA	TATCAAGCTT	AAATCATCA	ATTTGCTTTT	TAAAGATGTT	480
AAAGTCCAAG	TGGATGGCAA	CGCCCACTAT	TCACCCAAAG	CCAGGAAAAT	GGCGTTCAAT	540
TTGATTGTCA	AGCCCTTAGT	TGAACCCAGC	GCTGCAATTT	ATTTGCAAGG	GCTAACCAGT	600
TTAAAAACCA	TAGAATTAAA	AATTAACACT	TCTCCAATGA	AAAGCCTAGC	GTTTTTAAAG	660
CCTCTTTTCC	AACGCCAATC	GCAAAAAAAT	TTAAAAACGT	GGATTTTTGA	CAAGATCCAA	720
TTTGCCAGCT	TTAAGATTGA	TAACGCTTTA	ATCAAGGCTA	ATTTCACTCC	TAGCGAGTTT	780
ATCCCATCGC	TTTTGGAAAA	TTCTGTAGTT	AAAGCCACTT	TGATTAAGCC	TTCAAGTCGT	840
TTTAATGATG	GCTTATCGCC	CATTAAAAATG	GATAAAACCG	AATTGATTTT	CAAAAACAAA	900

SUBSTITUTE SHEET (RULE 26)

980

CAGCTCCTCA	TACAGCCCCA	AAAAATCACT	TATGAAACCA	TGGAATTAAC	CGGCTCTTAC	960
GCCACTTTTT	CCAATTIGTT	AGAAGCCCCT	AAGTTGGAGG	TTTTTTTAAA	AACGACCCCCT	1020
AATTATTATG	GCGATAGCAT	TAAGGATTTA	TTGAGCGCTT	ATAAAGTCGT	TTTACCTTTG	1080
GATAAAATCA	GCATGCCATC	TAGCGCGGAT	TTGAAGCTCA	CTTTGCAATT	CTTAAAAAAC	1140
ACCGCCCCCT	TATTTAGCGT	TCAAGGCAGC	GTTAATTTGC	AAGAAGGCAC	TTTCTCGCTC	1200
TATAATATCC	CCCTTTACAC	GCAAAGCGCT	CAAATCAATT	TGGACATCGC	CCAAGAATAC	1260
CAATACATCT	ACATAGACAC	GATCCACACG	CGCTATGCAA	ACATGCTGGA	TTTAGACGCT	1320
AAAATCGCTT	TAGATTTAGG	TCAAAAAAAC	CTTTCTTTGG	ATTCTTTAGT	CCATAAAATC	1380
CAAGTCAATA	CCAATAACAA	TATCAACATG	CGCTCTTATG	ATCCCAATAA	CACTCAAGAA	1440
GATCCGCAAA	CTAACTTTAC	TTTGGATCTA	AAAAGCTTGC	ATTCTATCAT	TCAAGAGGGT	1500
GAAAATTCAG	AAGTTTTTAG	AAGAAAAATC	ATAGACACCA	TTAAAGCCCA	AAGCGAAGAT	1560
AAATTCTACT	AAGATGTTTT	TTACGCCACA	GGAGACACTC	TCAAAAGCCT	GTCGTTGAGT	1620
TTTGATTTTT	CCAACCCCGA	TCACATACAA	TGGAGCGTGC	CACAACCTCT	ATTAGAAGGC	1680
GAATTTAAAG	ATAACGCCTA	TACTTTTAAAG	ATCAAAGATT	TGAAAAAGAT	CAAGCCCTAT	1740
TCCCCCATTA	TGGACTATAT	TGCCCTAAAA	GACGGCTCTT	TAGAGGTTTC	TACGAGCGAT	1800
TTTGTCAATA	TTGATTTTTT	TGCTAAAGAT	TTGAAATCA	ACCTCCCCAT	TTATAGGAGC	1860
GATGGATCGC	ATTTTGATTG	TTTTTCTTTA	TTTGGCTCTA	TCAATAAAGA	TGAAATTTCT	1920
GTCTATACTC	CAAGCAAAAG	CATATCCATA	AAAGTTAAGG	GGGATCAAAA	GGATATTACC	1980
CTTAATAACA	TTGATTTGAG	TATTGATGAT	TTCTTGAGTA	GTAAATGCC	AGCTATTGCG	2040
GGATTATTCT	CAAAAGAACG	AAAAGAAAAG	CCTAGCTCTA	AAGAAATCCA	AGATGAAGAT	2100
GTTTTTCATTA	GCGCCAAACA	ACGCTATGAA	AAAGCCCA	AAATTATCCC	CATCTCTACA	2160
CGCATCCATG	CTAAAGATGT	CGTGCTGATC	TATAAAAAAA	TGCCTTTTCC	TTTAGAAAAAT	2220
CTTGATATTG	TCGCTCAAGA	CGATAGGGTG	AAAATTGATG	GCAATTATAA	AAACGCCATG	2280
ATCATGGCGG	ATTTAGTGCA	TGGGGCTTTG	TATCTTAAGG	CTCATAATTT	TAGCGGGGAT	2340
TATATCAACA	CCATTCTTCA	AAAAGATTTC	GTAGAAGGAG	GCATTATTCAC	GCTTATTGGG	2400
GCTCTTGAAG	ATCAGGTTTT	CAATGGCGAA	TTGAAATTCC	AAAACACAAG	CTTAAAGAAT	2460
TTCCGCCCTCA	TGCAAAACAT	GGTCAATCTC	ATCAACACCA	TTCCCTCCCT	TATTGCTTTT	2520
AGAAACCCCTC	ATTTAGGGGC	TAATGGCTAT	CAAATCAAAA	CCGGCTCCGT	TGTGTTTGGG	2580
ATCACTAAAG	AATATTTAGG	GTTAGAAAAA	ATTGATCTTG	TCGGCAAAAC	GCTTGATATT	2640
GCTGGCAATG	GAATCATTGA	ATTAGACAAA	AACAAATTAG	ATTTAAACTT	AGAAGTTTCC	2700
ACTATCAAGG	CTTTGAGTAA	TGTCTTAAAT	AAAATCCCTA	TCGTGGGCTA	TCTCGTTTTA	2760
GGAAAGGAG	GTAATAATCAC	CACTAACGTG	AATGTCAAAG	GCACGTTGGA	TAAGCCTAAA	2820
ACCCAAGTAA	CTTTAGCGTC	AGATATTATC	CAAGCGCCTT	TTAAATCTT	ACGCCGTATT	2880
TTACAGCCTA	TTGACATCAT	CGTGGATGAA	GTCAAGAAAA	ACATTGATTG	AAAAAGGAAA	2940
TTAAAA						2946

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394

AGACCATTCA	GATCGCTTAT	AAGGATTACC	CACGCCCCAA	AACTAAACC	CTCATTGCGA	60
TTAGAGTGCG	TTATTACTTG	GGAGGCAATT	AACAGCATGG	AAATCACGCT	TTTTGACCCC	120
ATAGACGCCC	ACTTGCAATG	GCGAGAAAC	GCGCTTTTAA	AAGCGGTGTT	GGAATATTCT	180
AGCGAACCTT	TTAGCGCCGC	AGTGATCATG	CCCAATCTCA	GTAAGCCTTT	GATTGACACT	240
CCAATCACCC	TAGAATATGA	AGAAGAAATT	TTAAAAAATT	CTTCAAACTT	CAAGCCTTTA	300

SUBSTITUTE SHEET (RULE 26)

981

ATGAGTTTGT	ATTTTAACGA	TGGTTTGA	TTAGAAGAAT	TGCAACGAGC	TAAAAACAAA	360
GGCATTAAAT	TTTTAAACT	CTACCCCAA	GGCATGACCA	CAAACGCGCA	AAATGGCACT	420
TCGGATTGT	TGGGTGAAAA	GACTTTGGAG	GTTTTAGAAA	ACGCCCAAAA	ATTAGGCTTT	480
ATTTTATGCG	TCCATGCAGA	ACAAGCTGGG	TTTTGTGTGG	ATAAAGAATT	TTTATGCCAT	540
AGCGTTTATG	AAACTTTCGC	CCTTTCATTC	CCTAAACTCA	AAATCATTAT	AGAGCATTTG	600
AGCGATTGGC	GCAGTATCGC	TTTGATTGAA	AAGCATGACA	ACCTCTATGC	GACTTTGACC	660
TTACACCATA	TCAGCATGAC	TTTAGATGAC	TTATTAGGGG	GGAGTTTGGG	CCCGCATTGT	720
TTTTGCAAAAC	CCTTAATCAA	AACCAAAAAA	GACCAAGAAA	GGCTCTTATC	CCTTGCTTTA	780
AAAGCCCAAC	CTAAAATCTC	TTTTGGATCG	GACAGTGCCC	CGCATTTCAT	TTCTAAAAAG	840
CATAGCGCTA	ACATCCCGGC	GGGCATCTTT	TCTGCCCTTA	TTTTGTGCCC	TGCGTTGTGC	900
GAACTTTGTG	AAAAACACAA	CGCTTTAGAA	AATTTGCAAG	CCTTTATCAG	TGATAACGCT	960
AAAAAAATCT	ACCGCTAGA	CAATTTACCC	AGTAAAAAAG	CGCATTGTGC	TAAAAAACCC	1020
TTTATAGTCC	CTACGCACAC	GCTTTGCTTG	AATGAAAAAA	TCGCTATCTT	AAGAGGGGGC	1080
GAAACGCTAT	CTTGAACCT	TCAAGAAATC	GCC			1113

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395

GAAATTTATA	TGCCGAAAA	TTCTAAACTA	CAACCTGCTA	AGTTAGGGAA	AAATTTTGAC	60
CCTGTGGATC	ATTCTAACAG	GAATTTTTC	TTTCTCTCA	TTCTGTCTGT	ATTGTTACAC	120
TGGTTGATTT	ATTTTITATT	TGAACACAGA	GAAGATTTTT	TTCTTCAAA	ACCCAAGCTC	180
GTTAAATTAA	ATCCTGAAAA	TTTATTGGTT	TTAAAAAGAG	GCCATTACAC	AGATCCCACT	240
AAAAACAACC	CAGGCGCTCC	TAAACCCACG	CTAGCTGGCC	CTCAAAAACC	CCCCACACCC	300
CCCACACCCC	CCACTCCGCC	AACCCACCA	AAACCTATAG	AAAAGCCAAA	GCCTGAGCCT	360
AAACCAAAGC	CCAAACCAGA	ACCAAAAAG	CCCAACCACA	AACATAAGGC	GCTCAAAAAA	420
GTGGAAAAAG	TGGAAGAGAA	AAAAGTAGTA	GAGGAGAAAA	AAGAAGAGAA	AAAAGTAGTA	480
GAACAAAAAG	TAGAGCAGAA	AAAAATAGAA	GAGAAAAAAC	CTGTCAAAAA	AGAAATTTGAC	540
CCTAACCAGC	TTTCTTTCTT	GCCTAAAGAA	GTTGCGCCAC	CCAGACAGGA	AAACAATAAA	600
GGCTTGGATA	ACCAGACTAG	AAGGGATATT	GATGAATTGT	ATGGCGAAGA	ATTTGGAGAT	660
TTAGGCACAG	CCCGAAAAAG	ATTTCATCAG	GAA			693

(2) INFORMATION FOR SEQ ID NO:1396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

982

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396

AGTCGTTATC	ACCCAAGAGG	TTTGTAGCCAA	TTGCCTAAAC	TCAAATCAT	TTGCATCACC	60
GCTACAGGCA	CGGATAATGT	GGATATAAAA	AGCGCGAAAG	CTTTAGGCAT	AGAAGTCAAA	120
AACGTGAGCG	CTTATCTAC	CGAATCTGTA	GCCCAGCACA	CTTTAGCGTG	CGCGTTGTCT	180
TTGTTGGGGA	GGATCAATGA	TTACGATCGT	TATTGCAAAA	GCGGGGAATA	TAGTCAAAGC	240
GATATTTTTA	CGCACATTAG	CGATATTAAA	ATGGGGCTTA	TTAAAGGAGG	TCAATGGGGG	300
GTTATTGGTT	TAGGCAATAT	CGGTAAAAGA	GTCCGCAAGC	TCGCTCAAGC	TTTCGGGGCA	360
AAGGTGGTGT	ATTTTTCCTC	TAAAGATAAA	AAAGAAGAAT	ACGAGCGCTT	GAGTTTAGAG	420
GAATTGCTTA	AAACAAGCGG	TATTATCAGC	ATTCATGCCC	CCTTAAATGA	AAGCACGCGC	480
GATTTAATCG	CTCTGAAAGA	ATTGCAAAGC	TTAAAAGATG	GGGCGATTTT	AATCAATGTG	540
GGGCGTGGGG	GCAITGTGAA	TGAAAAGGAT	TTGGCTTTAA	TTTTAGAAAC	CAAAGATTTC	600
TATTACGCGA	GCGATGTC					618

(2) INFORMATION FOR SEQ ID NO:1397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397

ATATTAGAGA	ATTGAGGAT	TTACGCCAGG	CTTTTGAAAA	TGATACTAAA	AAATTGATT	60
TTGTTATTTT	TAGCAAAGAG	AAAACCTATT	TTCATAGAAG	CTAATTTTTA	TACCATTAGT	120
GGGAGCAAGC	TTAATGAAGT	CGCAAGATCC	TATCAAGACT	TAGCTTTAAA	ATTTGAAGCA	180
TTTCCTAATT	ACGAATTTAT	TTGGATAACT	GATGGCATAG	GTTGGCTAGA	CGCTAAAAGC	240
AAGCTCCAAG	AAGCTTACAA	ATCTGTAGAA	ATCTATAACT	TAAGCTATGT	GAATGATTTT	300
ATATCAAAGG	TGCAAAAA					318

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

983

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398

TGCGTGATGC	TAATGGCAAT	TTTTACCCCT	TATATTCTTA	TTTGAAAAT	GATGAAAAAG	60
TCTATGAGTT	TATTCGCCAA	TATGGGGTTG	GAGCAAATTT	TTTGCAACAG	AGACATTAAA	120
GATTTAAATG	ATTTTGTTTT	TGGTATAGAA	GTGGGGCTTG	ATAGCAATGC	GAGAAAAAAT	180
CGTAGCAGAA	AGGCTATGGA	AAATCATCTT	ATCGGTCTTT	TTGTCCAAGC	TCAATTAAAT	240
TTTAAAGAAC	AAGTAGATAT	TAGAGAATTT	GAGGATTTAC	GCCAGGCTTT	TGGAAATGAT	300
ACTAAAAAAT	TTGATTTTGT	TATTTTATAG	AAAGAGAAAA	CTTATTTTCA	TAGAAGC	357

(2) INFORMATION FOR SEQ ID NO:1399:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 912 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...912
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399

CTTGATGATCA	ATTCTAAAC	CGGACTGCTC	ACCATTAAAG	GCGAGGACGC	TTTAGGCAAG	60
GCTAGTTTGA	AGGATTGGG	TTTGAGCGCT	GGCATGGTGC	AATCTTATGA	AGCTTCGCAA	120
GACACGCTTT	TTATGTCTAA	GAATTTGCAA	AAAGCGAGCG	ATTGCAATT	CACTTACAAT	180
GGGGTGAGCA	TCACGCGCCC	CACTAATGAG	GTCAATGATG	TGATCAGCGG	GGTTAATATC	240
ACTTTAGAGC	AAACCACAGA	GCCTAATAAG	CCTGCCATTA	TCAGCGTGAG	CAGAGACAAT	300
CAAGCCATTA	TAGACAGCCT	TAAAGAATTT	GTCAAAGCCT	ATAATGAGCT	TATCCCTAAA	360
CTAGACGAAG	ACACGCGCTA	TGACGCTGAC	ACTAAAATCG	CCGGGATTTT	TAACGGCGTG	420
GGCGATATTC	GTGCCATTAG	ATCCTCTCTT	AATAATGTGT	TTTCTTATAG	CGTGCATACG	480
GATAATGGGG	TAGAAAGCTT	GATGAAATAC	GGGCTTAGTT	TAGACGATAA	GGGCGTGATG	540
AGTTTGGATG	AAGCTAAATT	ATCAAGTGCA	TTAAATTCTA	ACCCTAAAGC	GACTCAAGAT	600
TTTTTCTATG	GGAGCGATAG	CAAGGATATG	GGGGGCAGAG	AAATCCACCA	AGAGGGCATT	660
TTTTCTAAAT	TCAATCAAGT	CATCGCTAAC	CTCATAGATG	GAGGGAACGC	TAAATTAAG	720
ATTTATGAAG	ATTCCCTAGA	CAGAGACGCT	AAAAGCCTGA	CCAAAGACAA	AGAAAACGCT	780
CAAGAGCTTT	TAAAAACCCG	CTATAACATC	ATGGCGGAGC	GCTTTGCCGC	TTATGATAGT	840
CAAACTCTTA	AAGCCAATCA	AAAATTCAAT	TCCGTGCAAA	TGATGATCGA	TCAAGCAGCG	900
GCTAAAAAGA	AT					912

(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

984

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400

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AGGAACATTA TGCAATACGC TAACGCTTAT CAAGCCTACC AGCATAACCG AGTGAGTGTG      60
GAATCCCCGG CAAAACTCAT TGAATGCTT TATGAAGGGA TTTTAAGATT TTCTTCGCAA      120
GCCAAACGCT GTATTGAGAA TGAAGACATT GAAAAGAAGA TCTATTATAT TAATAGGGTT      180
ACGGATATTT TCACGGAGTT GTTGAATATT TTAGACTATG AAAAAGGGGG GAAAGTGGCG      240
GTGTATCTTA CAGGCTTATA CACCCATCAA ATCAAAGTTT TAACGCAAGC CAATGTGGAA      300
AATGACGCGA GTAAGATTGA TTTGGTGTG AATGTGGCTA GGGGGTTGTT AGAGGCATGG      360
AGGGAAATCC ATTCAGATGA ACTCGCC                                     387

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(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401

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TTTGATGATC TTTATGGATC AAACCTCACTT CCATTTTATC CACGGGTAAC CCCGGTAAAA      60
TTCCCCACTT TCAAATGGGC GTTACTCAAA GCGTTGATTA AGGACGATTT CCCCACATTA      120
GGCTGGCCCA CAAGGGCGAC AATGATTTC TTCATGGGT TGAATGCTC CGCATTAAAA      180
GTTTTTTTAA TTTTGGTTA TATAGTTTT AAAAGTTGGC ACTATAGCGC TATAAGACTA      240
ATTGTTATA                                     249

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(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

985

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402

AAGCGAGACA	AGAATGTTAA	AATGCGAAAG	GGGCGTGTGA	TGTTATGCGT	GTTTGATATA	60
GAAACCATTC	CTAATATAAG	CTTGTGTAAA	GAGCATTTTC	AATTAAAAGA	AGACGATGCG	120
CTAAAAATCT	GTGAATGGAG	TTTGTAAAAG	CAAAAAGAAA	AAAGCGGGAG	CGAGTTTTTG	180
CCCCTTTATT	TGCATGAAAT	CATCTCTATT	GCAGCAGTCA	TTGGCGATGA	TTACGGGCAA	240
TTTATCAAAG	TAGGGAATTT	TGGTCAAAAA	CACGAGAATA	AAGAGGATTT	TGCGAGCGAA	300
AAAGAGCTTT	TAGAGGACTT	TTTCAAATAC	TTTAACGAAA	AGCAACCGCG	CCTAATAAGC	360
TTTAATGSCA	GAGGTTTTGA	TATTCCCCTA	CTCACGCTCA	AAGCCCTTAA	ATACAATTTA	420
ACCTTAGACG	CTTTTACAG	CCAAGAAAAC	AAATGGGAAA	ATTACCGCGC	GCGTTATAGC	480
GAGCAGTTTC	ATTTTGATTT	GATGGATAGC	TIGAGCCATT	ATGGATCCGT	TAGGGGGTTG	540
AATCTAAATG	GCGTTTGCTC	TATGACGAAT	ATTCCTGGTA	AATTTGATGT	GAGCGGGGAC	600
TTAGTGCATG	CGATTTATTA	CAACCCCAT	TTAAGGCCAA	AAGGAGGAAA	AAGGCATTAT	660

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403

AGATTTAAGG	CTAGAAATGT	GCGTTTTTTC	ATTTTTTTAA	TTCTCATTTG	CCCTTTAATA	60
TGCCCCTTAA	TGAGCGCGGA	TAGCGCTTTA	CCTAGCGTCA	ATCTCTCTTT	AAACGCTCCT	120
AGTGATCCTA	AACAATCGT	AACCACCCCT	AATGTCATCG	CCTTACTCAC	GCTTTTGTTT	180
TTAGCCCCAT	CGTTGATTTT	AGTGATGACG	AGTTTCACCC	GTTTGATCGT	GGTGTTTTCT	240
TTTTTAAGGA	CCGCTTTAGG	CACGCAACAA	ACCCACCCA	CTCAAATCT	AGTCTCGCTC	300
TCTTTGATAT	TGACTTTTTT	TATCATGGAA	CCTAGCTTGA	AAAAGGCTTA	TGATACAGGG	360
ATTAAGCCTT	ATATGGATAA	AAAGATTTCT	TACACCGAAG	CGTTTGAAAA	AAGCACTCTG	420
CCTTTCAAGG	AATTCATGCT	TAAAACACAA	CGAGAAAAAG	ATCTAGCCCT	TTTTTTTAGG	480
ATTAGGAATT	TGCCTAACCC	TAAAACCCCT	GATGATGTGA	GCTTGAGCGT	TTTAATCCCG	540
GCATTTATGA	TAAAGCGAGT	GAAAACAGCG	TTTCAAATCG	GCTTTTACT	CTACTTGCTT	600
TTTTTGTTGA	TTGATATGGT	TATCAGCTCT	ATTTTAAATG	CGATGGGTAT	GATGATGCTC	660
CCGCCTGTAA	TGATTTCTCT	GCCTTTTAAA	ATTTTGTTGT	TTATTCTGGT	GGATGGGTTT	720

SUBSTITUTE SHEET (RULE 26)

986

AATTTATTGA CCGAAAATTT AGTGGCGAGT TTTAAATGG TT

762

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404

AAGTGGGGAA	TTTTACCGGG	GTTACCCGTG	GATAAAATGG	AAGTGAGTTT	GATCCATAAA	60
GATCATCAAA	TCACATCAT	TGATTTACCG	GGCACTTACG	CGCTCAATGA	CTTCACCACT	120
GAAGAAAAGG	TGACTAAAGA	TTTTTTAGAA	AAAGGGCAAT	ACAATCTCAT	TCTCAATGTG	180
GTGGATTCCA	CCAAATTTAGA	GCGTAATTTA	GCCTTAAGCG	CGCAGTTATT	AGACACAAAT	240
AAAAAAATGC	TGCTTGCGCT	CAACATGTGG	GATGAAGCCA	AGAAAGAAGG	GATCAACATC	300
AATACAGAAA	AGCTCTCTCA	AGAATTGGGG	GTTGTGTGCG	TGCCAACAAG	CGCGAGATCC	360
AAAGAAGATC	GCTTGAACAC	AGAGCTTTTA	TTAGACGAAA	TTGTCAGGCT	TTATTCTCAA	420
AACACTACAA	ACAACGAAAA	CATCAAAGTC	CCATCTCAAA	GTTTTAAAGA	GTCTTTAAAA	480
TACAGCCAGA	GCGCCCAAAG	AATCGCTAAA	TCAGTGATCA	GTGAAAACAA	ACAAAATGCG	540
AGTTTTGAAC	ACACTTATAA	GATTGATAAG	ATTTTAATGC	ACCAGCGTTA	TGGGATTTTC	600
ATTTTTTTAG	GGTTTATGTT	TATCATCTTT	TCTTTGAGCT	TTTTAATAGG	AGGGGGAGTG	660
CAAAAAGCCC	TTGAAGAAGG	GTTFAAAATT	TTGAGCGATA	GTATTAAAGA	AAATGTGGCT	720
AATGAAGATT	TAGCGTCTTT	GGTGGGCGAT	GGCATTATTG	GGGGAGTGGG	AGCGACGGTT	780
TCATTCCTGC	CTTTAATTGT	GGTGTGTGAT	TTTGGGATTT	CTTTACTAGA	GACGACAGGC	840
TATATGAGTA	GGGTAGCGTT	TTTACTAGAC	GGGATCTTGC	ATAAATTGCG	TTTGCATGGG	900
AAGAGTTTTA	TCCCTTTAAT	CACCGGTTTT	GGTTGCTCAG	TGCCTGCTTA	CATGGCGACA	960
AGAACCTTAC	AAAACATATA	CGAACGATTG	ATCACGCTTT	TTGTGATCGG	CTTTATGAGT	1020
TGCTCGGCAA	GACTGCCTAT	TTATGTGCTG	TTTGTAGGCT	CGTTTTTCCC	CTCTTCAAGT	1080
GCTGGGTTTG	TGCTGTTTTG	CATTTATATT	TTGGGGGCGG	TTGTGGCGTT	AGTGATGGCC	1140
AAATTACTCA	AATTAAGCGT	GTTTAAAGGA	CAGACTGAAT	CCTTTATCAT	GGAAATGCCC	1200
AAATACCGCT	TTCCCAAGTG	GAGAATGGTC	TATTTCAAGT	TTTACACCAA	ATCGCTTTCT	1260
TACCTCAAAA	AAGCCGGGAC	TTATATTTTA	GTGGGAGCGA	TTTTGATCTG	GTTTATGTCC	1320
CAATACCCTA	AAAATGATGC	GGCTATGAAG	ACTTATAAAC	AAGAAAGCTT	GTTAGTCCAA	1380
AAAAACGCTA	ATCTTTCAAG	CGAAGCTAAA	GAAGAAAAAT	TAAAAGAATT	AAAAACCGAA	1440
TTGGATAAAA	AGAAATTTAA	AAATAGCGTT	GTAGGAAGAG	GCGGGGCGTA	TTTAGAAAAA	1500
GCTTTTAACC	CTATGGATTT	TGATTGGCGT	TTGAGCGTCT	CGCTTGTAAC	CGGTTTTATG	1560
GCTAAAGAGG	TGGTGGTTTT	TACTTTGGGG	GTGTTGTTTT	CTTTAGGGGA	TCAAACGAA	1620
AAATCTGATG	CTTTTAGAGA	GATAATCAGA	AAAGAAAGTCA	GCGTGCCTAG	CGGGATCGCT	1680
TTTATCGTGT	TTGTGATGTT	TTATATCCCT	TGTTTTGCAG	CGACCATTAC	TTTTGGTAGG	1740
GAAGCTGGGG	GGATCAAGTT	TGTAGCGTAT	TTATTCATCT	TCACAACCGT	TGTAGCGTAT	1800
GCGTTTTTCT	TGATAGCTTT	TTATGCGACT	CAAATTTTGG	TT		1842

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

987

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405

ATGAAAAGAA	TTTTAGTTTC	TTTGGCTGTT	TTGAGTCATA	GCGCGCATGC	TGTCAAAACT	60
CATAATTTGG	AAAGGGTGGA	AGCTTCAGGG	GTGGCTAACG	ATAAAGAAGC	GCCTTTAAGC	120
TGGAGGAGCA	AGGAAGTTAG	AAATTATATG	GGTTCTCGCA	CGGTGATTTC	TAACAAGCAA	180
CTCACTAAAA	GCGCCAATCA	AAGCATTGAA	GAAGCTTTGC	AAAATGTGCC	AGGCGTGCAT	240
ATTAGAAACT	CTACCGGTAT	TGGAGCTGTG	CCTAGCATTT	CCATTAGGGG	GTTTGGTGCT	300
GGAGGCCCAG	GGCATTCTAA	TACGGGAATG	ATTCTAGTCA	ATGGGATTCC	TATTTATGTC	360
GCGCCCTATG	TTGAAATTGG	CACGGTTATT	TTTCCTGTAA	CCTTTCAGTC	TGTGGATAGA	420
ATCAGCGTAA	CTAAGGGTGG	GGAGAGCGTG	CGTTATGGCC	CTAACGCTTT	TGGCGGTGTG	480
ATCAACATCA	TCACCAAAGG	CATTCCCTACC	AATTGGGAAA	GTCAGGTGAG	CGAGAGGACC	540
ACTTTTGGGG	GCAAGTCTGA	AAACGGGGGC	TTTTTCAATC	AAAATTCTAA	AAACATTGAT	600
AAAAGCTTAG	TTAATAACAT	GCTTTTTTAA	ACCTATTTAA	GAACGGGGGG	TATGATGAAT	660
AAGCATTTTG	GAATCCAAGC	TCAAGTCAAT	TGGCTCAAAG	GGCAAGGGTT	TAGATACAAC	720
AGCCCTACGG	ATATTCAAAA	TTACATGTTA	GATTCATTGT	ATCAAATCAA	TGATAGCAAT	780
AAAATCACCG	CTTTTTTTCA	ATATTATAGT	TATTTCTTGA	CAGACCCCTG	ATCTTTAGGC	840
ATAGCCGCTT	ACAATCAAAA	TCGTTTTCAA	AACAACCGCC	CCAATAACGA	TAAAAGCGGG	900
AGAGCGAAGC	GATGGGGAGC	TGTGTATCAA	AACTTTTTTG	GGGACACGGA	TAGGGTAGGG	960
GGGGGATTTC	ACTTTT					975

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2391 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406

AGACTAAAC	CAAATGTTAT	AGAGCGTAGG	ATGTTAGAAA	AGCTTTTAAG	CGCTATCAAA	60
CAAAAAGTTT	CAAACTATTT	TTAGGGGTTT	TTGCCTAAAA	GCTATTCTAT	GAGCGAAGAA	120
AACAACATTT	TAGGCTTGTA	TGATGAGCAT	TTTTTGCTCA	CTAAAAACGA	AAACTTAGTG	180
GGCATCTCTC	GTTTAGAGGG	GTTTAGCTAC	ACCCATTTAA	GCACAGAGCA	ATTGCAAGAT	240
CTTTTCACTG	AGCGCCAAAT	GGCGTTAGAT	TCTTTAGAAA	AAGTCGTGGC	GCGTCTTGTG	300
GTAAAAGGC	GTAATTTGA	TTATAACAA	AGCATTCAAT	CTGACTCTCA	ATACTTGCAA	360

SUBSTITUTE SHEET (RULE 26)

988

CGGATCTTGA	ATCAGTTTGA	AAATAAAGAA	GTGTATGAGA	ATCAGTATTT	TTTAGTTTTA	420
GAAAGCACTC	ACTCTTTGCA	TGGCGTTTTG	GAGCATAAGA	AAAAATCTTT	CATGCACGCT	480
AATAGAGAAA	ATTTTAAGGA	TATTCTCTCT	TATAAAGCGC	ATTTTTTGCA	AGAACTTTA	540
AAAAGCTTAG	AAATCCAGCT	CAAAAACATAT	GCCCCCAAAC	TCTTAAACTC	TAAAGAGGTT	600
TTGAATTTTT	ATGCAGAATA	TATTAATGGG	TTTGAACTCC	CTTTAAACC	CCTAGTAGGG	660
GGGTATTTGA	GCGATAGCTA	TATCGCTAGT	TCTATCACTT	TTGAAAAAGA	TTATTTCATT	720
CAAGAAAGCT	TTAATCAAAA	AACCTATAAC	CGCTTGATTG	GCATTAAAGC	TTATGAGAGC	780
GAAAGGATCA	CTTCTATAGC	GGTGGGAGCG	CTTTTATACC	AAGAGACGCC	TTTGGATATT	840
ATCTTTTCCA	TAGAGCCTAT	GAGCGTCAAT	AAAACGCTGA	GTTTTTTAAA	AGAGAGGGCC	900
AAGTTTAGCA	TGTCTAATCT	TGTTAAAAAC	GAGCTATTAG	AATACCAAGA	ATTAGTCAAA	960
ACCAAACGAT	TATCCATGCA	AAAATTCGCC	CTAAACGTTT	TTATCAAAGC	CCCCAGTTTG	1020
GAGGATTTAG	ACGCTCAAAC	CAGCTTAATT	TTAGGGCTTT	TATTTAAAGA	AAACTTAGTG	1080
GGCGTTATAG	AAACTTTTGG	CTTGAAAGGG	GGGTATTTTT	CCTTTTTCCC	TGAACGCATC	1140
CATTTAAACC	ACCGCTTGCG	TTTTTTAACC	TCTAAAGCCC	TAGCGTGTTT	GATGGTGTTT	1200
GAAAGGCAAA	ATTTAGGTTT	TAAGGCTAAT	TCATGGGGGA	ATAGCCCTTT	GAGCGTGTTT	1260
AAAAATTTGG	ATTATTCCCC	TTTTTTATTC	AAATTCACCA	ACCAAGAAGT	GAGCCATAAT	1320
AACGCTAAAG	AAATTGCCAG	AGTGAATGGG	CATACTTTAG	TTATAGGGGC	AACCGGAAGC	1380
GGTAAAAGCA	CGCTGATTAG	CTATTTAATG	ATGAGCGCTT	TAAAATACCA	AAACATGCGC	1440
CTTTTAGCTT	TTGACAGGAT	GCAAGGGTTG	TATTCCTTCA	CCGAATTTTT	TAAAGGGCAT	1500
TACCATGACG	GCCAATCTTT	TAGTATCAAC	CCCTTTTGTT	TAGAGCCTAA	TTTGCAGAAT	1560
TTAGAATTTT	TGCAATCCTT	TTTTTTGAGC	ATGTTGGATC	TTGCCCTTTC	AAGGGATAAA	1620
GAAGCCTTAG	AAGACATGAA	TGCGATTTC	GGCGCGATTA	AGAGCCTTTA	TGAGACCTTA	1680
TACCCCAAAG	ATTTTAGTTT	GCTGGATTTT	AAAGAAACGC	TTAAAAGAAC	CTCATCTAAC	1740
CAATTGGGCT	TGAGTTTAGA	GCCGTATTTG	AATAACCCCC	TTTTTAACGC	TTTGAATGAC	1800
GCGTTCAACT	CCAACGCTTT	TTTAAATGTG	ATAAACCTAG	ATGCGATCAC	CCAAAACCCCT	1860
AAAGACTTAG	GGCTTTTAGC	CTATTACTTG	TTTTATAAGA	TCTTAGAAGA	GTCTAGGAAA	1920
AACGACAGCG	GCTTTTGGT	TTTTTTAGAC	GAATTTAAAT	CCTATGTGGA	AAACGATTTG	1980
TTAAACACTA	AAATCAACGC	TTTAATCAGC	CAAGCCAGGA	AAGCTAATGG	CGTGGTGGTG	2040
TTGGCCTTGC	AAGACATTTA	CCAACCTAGC	GGGGTTAAAA	ACGCCCATAG	TTTTTTAAGC	2100
AACATGGGGA	CTCTCATTTT	GTATCCGCAA	AAAAACGCTA	GGGAATTGAA	ACACAATTTT	2160
AATGTGCCTT	TGAGCGAAAC	TGAAATTTCT	TTTTTAGAAA	ACACCCCTCT	GTATGCCAGG	2220
CAGGTTTTAG	TCAAAAATCT	GGGTAACGGG	AGTTCCAACA	TGATTGATGT	GAGTTTGAGG	2280
GGCTTGGGGT	GTTATTTGAA	AATCTTTAAT	TCAGATTCCA	GTCATGTCAA	TAAAGTGAAA	2340
GCGTTACAAA	AAGACTACCC	TACAGAGTGG	CGTGAGAAAC	TTTTGAAGAG	T	2391

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407

AAAATGATTC	TTAAAAGTTC	CATTGATCGC	CTTTTACAAA	CGATAGATAT	TGTAGAAGTC	60
ATTAGCTCTT	ATGTGGATT	GAGGAAATCA	GTTTCGAATT	ACATGGCTTG	TTGCCCTTTT	120
CATGAAGAAA	GGAGCGCGAG	TTTTAGCGTC	AATCAAGTTA	AAGGGTTTTA	CTATTGCTTT	180
GGGTGTGGGG	CGAGCGGGGA	TAGCATTAAG	TTTGTGATGG	CGTTTGAAAA	ACTTTCGTTT	240
GTGGAAGCGC	TTGAGAAATT	AGCCCAACCG	TTCAATATAG	CTTTAGAGTA	TGACAAAAGGC	300
GTTTATTACG	ATCATAAAGA	AGATTACCAC	CTTTTAGAAA	TGGTGAGTTC	GTTGTATCAA	360

989

GAAGAGCTTT	TTAACGCCCC	GTTTTTTTTG	AATTATTTGC	AAAAAAGAGG	GCTTAGCATG	420
GAGAGCATCA	AAGCGTTTAA	GTTAGGCTTA	TGCACGAATA	AAATTGATTA	CGGCATTGAA	480
AATAAAGGCT	TGAATAAGGA	CAAATTGATT	GAATTGGGCG	TGCTAGGCAA	GAGCGATAAA	540
GAGGATAAAA	CCTATTTGCG	CTTTTTGGAT	CGCATCATGT	TCCCTATTTA	TAGCCCTAGT	600
GCTCAAGTGG	TGGGTTTTGG	AGGGCGCACC	TTAAAAGAAA	AAGCGGCCAA	GTATATCAAT	660
TCGCCCCAAA	ATAAGCTTTT	TGATAAATCC	AGCTTGCTCT	ATGGCTATCA	TTTGCTTAAA	720
GAACACATTT	ATAAACAAAA	GCAGGTCATT	GTAACAGAAG	GGTATTGGGA	TGTGATTTTA	780
TTGCACCAGG	CGGGTTTTAA	AAACGCCATA	GCCACGCTTG	GGACAGCTTT	AACGCCATCG	840
CATTTGCCCT	TGCTTAAAAA	AGGCGATCCA	GAAATCCTTT	TGAGCTATGA	TGGGGATAAG	900
GCAGGCGGGA	ATGCGGCTTA	TAAAGCGAGC	TTGATGTTAG	CTAAAGAGCA	AAGGAAAGGG	960
GGGGTGATTT	TGTTTGAAAA	CAACCTAGAC	CCAGCGGATA	TGATCGCTAA	TCATCAGATT	1020
GAAACTTTAA	AAAATTGGCT	ATCGCGCCCC	ATAGCTTTCA	TTGAATTGT	TTTAAGGCAC	1080
ATGGCCGGTT	CTTATCTTTT	AGACGATCCT	TTAGAAAAAG	ATAAGGCCCT	TAAAGAAATG	1140
TTAGGGTTTT	TGAAAAACTT	TTCCTTGCTT	TTACAAAAATG	AATACAAGCC	CTTAATCGCT	1200
ACGCTTTTGC	AAGCGCCTTT	GCATGTTTTA	GGGATTAGAG	AGCCAGTTTC	TTTTCAGCCT	1260
TTTTACCCCA	AAACAGAAAA	GCCTAATCGC	CCTCAAAAGT	TCGCGCATGT	TTCTAGCATG	1320
CCCAGTTTGG	AATTTTGA	AAAATTGGTG	ATCCGCTACC	TTTTAGAAGA	CAGAAGCCTA	1380
TTGGATTAG	CGGTGGGTTA	TATCCATAGT	GGGGTATTCT	TGCATAAAAA	ACAAGAATTT	1440
GACGCTTTAT	GTCAAGAAAA	ATTGGACGAC	CCTAAATTAG	TTGCGTTATT	ATTAGATGCG	1500
AATTTACCCC	TAAAAAAGG	GGGTTTTGAA	AAGGAATTGC	GTTTGTGAT	TTTGGCGTAC	1560
TTTGAGCCGC	CAACTCAAAG	AAATCCC				1587

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408

CTAAGAGGGC	ACAGGCGTAC	TTATATAGGC	TCCATGCCCG	GGCGTATTGT	CCAAGGGCTT	60
ATTGAAGCTA	AAAAGATGAA	TCCGGTCATG	GTTTTAGATG	AAATTGATAA	GGTGGATCGA	120
AGCGTTAGGG	GCGATCCAGC	GAGTGCCTTA	TTAGAGATCT	TAGACCCTGA	GCAAAATATC	180
GCCTTTAGGG	ATCATTACGC	GAATTTGAGC	ATTGATTTGT	CGCAAGTGAT	TTTTATCGCT	240
ACCGCTAATA	ATATTGACAG	GATCCCAGCT	CCTTTAAGAG	ACAGAATGGA	ATTTATCAGC	300
GTGTCCAGCT	ACACGCCCTAG	CGAAAAAGAA	GAGATCGCTA	AAACTACCT	CATCCCCCAA	360
GAATTAGAAA	AGCAGCCCTT	AAAGCCTAGC	GAAGTGGATA	TTAGCCATGA	ATGTTTGAAA	420
CTCATTATTG	AAAAATACAC	CAGAGAAGCG	GGCGTTAGGG	ATTTACGAAG	ACAGATCGCA	480
ACGATTATGC	GTAAGCGGCG	TTTAAAAATAC	CTAGAAGATA	ACCCGCACAA	AAAAGGGCGG	540
ACCAAAAAAA	GCGAAGACAA	AGATAAAAAA	GGCGGAAATG	AAGAAAACGA	AAAAGAGGTT	600
GAGAGTAAAG	ATTTTTCGCT	CTCTATCAGC	CCTGATAACC	TTAAAGAGTA	TTTAGAACGC	660
ATGGTGTTTG	AAATTGACCC	CATAGATGAA	GAAAAATAAA	TCGGTATCGT	CAATGGCTTG	720
GCATGGACTC	CAGTGGGCGG	TGATGTGCTT	AAAATTGAAG	CGGTTAAGAT	TAGAGGCAAG	780
GGGGAATTGA	AACTCACCGG	GAGTTTGGGC	GACGTGATGA	AAGAATCCGC	CATTATTGCC	840
TTTTCTGTTG	TCAAAGTCTT	GTTGGATAAC	GAAACCTTAA	AAGTGCCTAA	AATCCCTAGC	900
GAGACCGATG	CAGAGAATAA	GAAAAAGAAA	AAAGTGCCTGA	AAGTTTATAA	CGCTTACGAT	960
TTGCACTTGC	ATGTCCCTGA	GGGGGCTACG	CCTAAGACGC	GCCCGAGCGC	TGGGATCGCT	1020
ATGGCGAGCG	TGATGGCGAG	CATTTTGTGC	GATAGGGCTA	TAAGAAGCGA	AGTGGCGATG	1080
ACGGGCGAAT	TGACTTTGAG	CGGGGAAGTT	TTACCCATAG	GGGGGTTGAA	AGAAAAATTG	1140

SUBSTITUTE SHEET (RULE 26)

990

ATCGCTGCTT	TTAAAGCCGG	CATCAAAACC	GCTCTCATTC	CTGTCAAAAA	TTACGAAAGG	1200
GATTTAGACG	AGATCCCTAC	TGAAGTGC GA	GAGAATTTAA	ACATCGTTGC	GGTGAAAAAC	1260
ATCGCTGAAG	TGTTAGAAAA	AACCTTGCTT				1290

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409

AAAAGATATA	GAAAAACTGC	TCTCTTACGG	CTTGACAATG	GCGACAAGCT	GTCATTAATG	60
AGGGAATTTT	TTAAAGCGT	TAGAGGGTTT	TTGAACCTTC	TTAGAATGAT	TTTCCCCGAG	120
CGCTTTCAAA	ACGCCTTTTT	AGGGTTAAGC	GAATTGTTTT	ACTACGCTTC	CAGCTTGAGT	180
TTTTATACGA	TTTTGTCTTT	ATCGCCTATT	TTGTTGTTTG	TGTTTCAGTCT	TTTGTGTCT	240
CATTACTTGC	AAGCGCACAG	CGGTGAAATG	GAAGCCTTGA	TTTTCCCTAA	CGCTCCTAAA	300
CTCATTGGCG	CGATTAAAGGA	TTTTTTAGAA	AATTTTAAAA	AAACAGACAT	GACCTTAGGC	360
ACGCTTGAAG	AGGTGCTTAT	TGTGGTGGCG	TTGGTGCTTT	TTTGTGAAAA	CTACCGCTCC	420
ATCGCGTCAA	AAATTTTGA	CGCAAAGCCC	AGAGATTATG	CGCATTTTAA	GGGTAAAGAA	480
ATCTTTTTAT	TTTGGGGGTT	TGGCAGCACT	TTAGTGTTTT	TATTCGCTTT	GCCTTTGGTG	540
GTGTTTTTTG	ATATTAAAGAT	CCAAGTGTTT	TTGAAGATA	AAGATTCAAG	CTGTGTGCAT	600
GTTTTAAGAT	GGATAGGCAC	TTACGCGTTT	TTTTTGATCC	TTTTTACCAT	TCCCACGAAT	660
AAGGTGTTTA	AACATTATTT	TTGGGTGTTT	TTATGGGTGT	TTTTTACGAG	CGTTTCTTGG	720
CATGTGCTGA	AATGGGCTTC	CACCTTATTT	ATGTGTTATA	CCAATCCGCA	CTTACTCATG	780
AGCCTGTATG	GGAGCCGTTT	CCCATTTTGT	GTTTTT			816

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...747

991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410

GTAGGTGTTG	TTATGATAAA	AAAGACCCTT	GCATCGGTTT	TATTAGGATT	GAGTTTGATG	60
AGTGTGTTAA	ATGCCAAAGA	ATGCGTTTCG	CCCATAACAA	GAAGCGTTAA	GTATCATCAG	120
CAAAGTGCTG	AGATCAGAGC	CTTGCAATTA	CAAAGTTACA	AAATGGCGAA	AATGGCGCTA	180
GACAATAACC	TTAAGCTCGT	TAAAGACAAA	AAGCCAGCCG	TCATCTTGGA	TTTAGATGAA	240
ACCGTTTTGA	ACACTTTTGA	TTATGCGGGC	TATTTAGTCA	AAAACATGCAT	TAAATACACC	300
CCAGAACTT	GGGATAAATT	TGAAAAAGAA	GGCTCTCTTA	CGCTCATTCC	TGGAGCGCTA	360
GACTTTTTAG	AATACGCTAA	TTCTAAGGGC	GTTAAGATTT	TTTACATTTC	TAACCGCACC	420
CAAAAAATA	AGGCATTAC	TTTAAAAACG	CTCAAAAGCT	TTAAGCTCCC	CCAAGTGAGT	480
GAAGAATCCG	TTTTGTATAA	GGAAAAAGGC	AAGCCTAAAG	CCGTTAGGCG	GGAGTTAGTC	540
GCTAAGGATT	ATGCGATTGT	TTTACAAGTG	GGCGACACTT	TGCATGATTT	TGACGCCATT	600
TTTGCTAAAG	ACGCTAAAAA	CAGCCAAGAA	CAACAAGCCA	AAGTCTTGCA	AAACGCTCAA	660
AAATTCCGCA	CAGAATGGAT	TATTTTACCC	AACTCTCTTT	ATGGCACATG	GGAAGATGGG	720
CCTATAAAG	CATGGCAAAA	TAAAAA				747

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411

CATGACAAAA	AATTTGATCT	CTTAGGCGGA	GTCATGGATT	TCGTAGGGTT	TGAAGATTTA	60
AAATGCAAG	ACAAAGAAAA	CTCTCAAAAA	GTTTTTGTGA	TCCGTAACGA	TAAGTTAGGC	120
GATTTTATTT	TAGTGATTCC	CGCTTTAATC	GCTCTCAAGC	ATGCTTTTTT	AGAAAAAGGC	180
GTAGAAGTGT	ATTGGGCGT	GGTTGTGCCT	AGCTATACCA	CCCCAATCGC	TTTAGAATTC	240
CCTTTCATTG	ATGAAGTTAT	CATAGAAGAC	AACCATTTAG	CCACCACCCC	CAAAAACCGC	300
TCCACCGACG	CCCTTATCTT	TTTATTTTCT	AATTTTAAAA	ACGCCAAACT	TGCTTTTCAGT	360
TTGAGAAAA	CCATCCCTTA	TATCCTAGCC	CCAAAGACCA	AAATCTATTC	TTGGCTTTAT	420
CAAAAGAGAG	TGCGCCAAAA	CCGCTCTTTA	TGCTTAAAAA	CCGAATACGA	ATACAATTIG	480
GACTTAATCC	ATGCGTTTTG	TAAAGACTAC	GATCTCCCTA	ACGCTCAACT	TAAAAAATC	540
GCATGGAAGC	TTAAAGACAA	ATCCAAAGAG	CGATCCATCA	TCGCTTCAAA	ACTCAACGCT	600
AATGTTGATC	TATTGTGGAT	TGGCGTGCAT	ATGCATAGCG	GAGGCAGTTC	GCCCGTATTG	660
CCCGCTTCGC	ATTTCATTGA	GTTGATTGCA	ATCTTGCATG	AAAAATTAAG	TTGTGAGATC	720
ATTCTTATTT	GCGGGCCAGG	CGAGAGAAAA	GCCACAGAAG	AACTCCTTAA	AGAAGTCCCT	780
TTGCTGCACC	TCTATGATAC	GAGCCATAGT	TTAGTGGAAT	TAGCCAAATT	GTGCGCGAAT	840
TTAAGCGTCT	GTATCGGGAA	CGCTTCAGGC	CCTTTGCATG	TGAACGCTTT	ATTTGACAAC	900
CAATCTATCG	GGTTTTACCC	TAACGAAGTC	ACCGCTCTTA	TGCCCAGATG	GCGGCCTTTC	960
AACGAACAAT	TTTAGGCAT	CACCCCGCCT	AATGGCTCAA	ACGATATGGG	TTTGATTGAC	1020
ATTCAAAAAG	AAAGCGAAAA	GATTATGGGA	TTTATCACAA	AAAATCTTTC	TCATCACATG	1080
CAAGAAAGA						1089

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1986 base pairs

SUBSTITUTE SHEET (RULE 26)

992

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412

GGTAACACGA	TTATAAAGAT	GCAAAAATCA	CTGATCACAA	CCCCCATTTA	TTATGTGAAT	60
GACATCCCTC	ATATTGGCCA	TGCTTATACG	ACTTTGATTG	CGGACACTTT	AAAGAAGTAT	120
TACACGCTTC	AAGGCGAAGA	AGTCTTTTTT	TTAACCGGCA	CCGACGAGCA	TGGGCAAAAG	180
ATCGAACAAA	GTGCGAGACT	GAGGAATCAA	AGCCCCAAAG	CTTACGCCGA	TAGCATTAGC	240
GCGATTTTAA	AAAACCAAGT	GGATTTTTTC	AATTTAGATT	ATGATGGTTT	TATCCGCACC	300
ACAGACAGCG	AGCATCAAAA	ATGCGTGCAA	AACGCCTTTG	AAATCATGTT	TGAAAAAGGG	360
GATATTTATA	AAGGCACTTA	TAGCGGGTAT	TATTGCGTGA	GCTGTGAGAG	TTATTGCGCG	420
GTCTCTAAAG	TGGATAATAC	AGATAGTAAA	GTCCTATGCC	CTGATTGCTT	GAGAGAGACC	480
ACGCTTTTAG	AAGAAGAGAG	TTATTTTTTC	AAATTGAGTG	CGTATGAAAA	GCCTTTATTG	540
GAGTTTTACG	CTAAAAACCC	TGAAGCGATT	TTGCCCATTT	ATCGTAAAAA	CGAGGTAAC	600
TCTTTTATTC	AGCAGGGTTT	ATTGGATCTG	TCTATCACGC	GCACGAGCTT	TGAATGGGGT	660
ATTCCTTTGC	CTAAAAAGAT	GAACGATCCT	AAGCATGTGG	TGTATGTTTG	GCTGGACGCT	720
TTATTGAAAT	ATGCGAGCGC	GTTAGGGTAT	TTGAACGGTT	TAGACAATAA	AATGGCGCAT	780
TTTGAACGCG	CTAGGCATAT	TGTGGGTAAG	GATATTTTAC	GCTTCCATGC	CATTATTGG	840
CCAGCCTTTT	TGATGAGTTT	GAATTTGCC	TTATTCAAAC	AGCTCTGTGT	GCATGGGTGG	900
TGGACGATAG	AGGGCGTGAA	AATGAGTAAG	AGCTTGGGTA	ATGTTTTAGA	CGCTCAAAAG	960
CTCGCCATGG	AGTATGGGAT	TGAAGAATTA	CGCTATTTTT	TATTGCGTGA	GGTGCCTTTT	1020
GGGCAAGATG	GGGATTTTTC	TAAAAAAGCG	TTAGTAGAAC	GGATTAATGC	GAATTTGAAT	1080
AACGATTTGG	GGAAATTTGT	GAATCGTTTG	CTAGGCATGG	CTAAAAAGTA	TTTCAATTAT	1140
TCTCTAAAAA	GCACCAAAAT	CACCTGCGTAT	TATCCTAAAG	AGCTAGAAAA	AGCACATCAA	1200
ATTTTAGATA	ACGCTAATTC	TTTTGTGCCT	AAAATGCAAT	TGCATAAGGC	TTTAGAGGAA	1260
TTGTTTAATA	TTTATGATTT	TTTGAATAAA	CTCATCGCTA	AAGAAGAGCC	GTGGGTCTTG	1320
CACAAAAACA	ACGAATCAGA	AAAATTAGAA	GCCTTATTGA	GTTTGATCGC	AAACACGCTA	1380
CTACAATCAA	GCTTCTTGCT	CTATGCGTTC	ATGCCAAAGA	GCGCTATGAA	ATTAGCGAGC	1440
GCTTTTCGTG	TAGAAATCAC	GCCCAATAAT	TACGAACGCT	TTTTTAAGGC	TAAAAAATTA	1500
CAGAGATATG	TTTTACAAGA	CACCGAGCCT	TTATTTTCCA	AAATTGAGAA	AATTGAAAAG	1560
ATTGAAAAGA	TTGAAAAGAT	TGAAAAGATT	GAAAAAGGGG	AGGAAGCCCT	AGCAGAAAAA	1620
GCAGAAAAAA	AAGAAAAAGA	AAAAGCCCCA	CCAACACAAG	AAAATTATAT	TAGTATTGAG	1680
GATTTCAAGA	AAGTAGAGAT	TAAAGTGGGG	CTTATCAAAG	AAGCTCAAAG	GATTGAAAAA	1740
TCCAATAAAT	TACTGCGCTT	AAAAGTGGAT	TTAGGCCGAA	ATCGTTTGAG	GCAGATCATC	1800
TCAGGGATCG	CTTTGGATTA	TGAGCCTGAA	AGCTTGGTGG	GTCAAATGGT	GTCCGTGGTG	1860
GCTAATTTAA	AACCCGCAAA	GCTTATGGGT	GAAATGAGTG	AGGGCATGAT	TTTAGCGGTG	1920
CGAGATAATG	ATAATCTGCG	TTTAATCAGC	CCTACCAGAG	AAAAAATTGC	AGGAAGTTTG	1980
ATCAGC						1986

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1026 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

993

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1026
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413

GGACGCATGA	TGAAAATTGT	AATAGACTTA	ATGGGGGCTG	ACCATGGGGT	TTTACCCATT	60
ATTGAGGGAG	TCTCAAGGGC	TTTAGAGAAT	AAGAGTTTTA	GCGTGGTTTT	AGTGGGGGAT	120
AAAGACAAAG	CGACCCCTTT	TATTCTAA	GAGTTAGCCA	GCAAAGTGA	AATGATCCAC	180
ACGCAAGATT	ACATTAAAT	GGAAGAAGCC	GCCACTGAGG	CGATTAAAGC	TAAGGAATCT	240
TCCATTTACT	TGGGCATGGA	TATTTTAAAA	AATGGGGCTG	ACGCTTTGAT	TTCAGCGGGG	300
CATAGCGGGG	CGACTATGGG	TTTAGCGACC	TTGCGTTTAG	GGCGTATCAA	GGGGGTTGAA	360
AGGCCTGCTA	TTTGCACTTT	AATGCCTAGC	GTGGGCAAAC	GCCCTAGCGT	GCTATTAGAC	420
GCAGGAGCGA	ACACGGATTG	CAAGCCTGAA	TATTTGATTG	ATTTTGCTCT	CATGGGGTAT	480
GAATACGCTA	AAAGCGTGTT	GCATTATGAC	AGCCCTAAAG	TGGGTCTTTT	GAGTAATGGT	540
GAAGAAGATA	TTAAGGGGAA	TACGCTCGTT	AAAGAAACGC	ATAAAATGTT	GAAAGCTTAT	600
GACTTTTTTT	ATGGCAATGT	GGAGGGGAGC	GATATTTTCA	AAGGGGTTGT	GGATGTAGTG	660
GTTTGCGATG	GCTTTATGGG	GAATGTGGTC	TTAAAGACAA	CTGAAGGGGT	CGCTAGTGCG	720
ATAGGCTCTA	TTTTTAAAGA	TGAAATTAAA	AGCTCTTTTA	AATCTAAAT	GGGGGCTTTG	780
ATGCTTAAGA	ACGCGTTTGG	TATTTTAAAA	CAAAAAACCG	ATTACGCTGA	ATATGGGGGA	840
GCACCGCTTT	TGGGCGTGAA	TAAAAGCGTG	ATCATTAGCC	ATGGCAAGAG	CAACGCTAGA	900
GCGGTTGAAT	GCGCGATTTA	TCAGGCTATT	ACGCGTGTTG	AAAGTCAGGT	TTGTTTGAGG	960
ATTACTCAAG	CGTTTGAGAG	TTTGAAATCT	CAATCTTTTG	AGAGCCAAAG	CGATCAACAA	1020
GACGCT						1026

(2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...759
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414

AACGCTCATG	CCTTTACCCA	TCCATTTAGC	GCACCAGCTC	GCTTTCGCCT	AGCTCAAAAA	60
AGAAAAGACA	ACACCTTGCC	TTTTTTAAGG	CCTGATGGCA	AGTCTCAAGT	GAGCGTGCGT	120
TATGAAAACA	ACAAGCCTGT	AAGCGTTGAT	ACGATTGTCA	TTTCCACCCA	ACATTCCCCA	180
GAAGTTTCAC	AAAAGCATTT	AAAAGAAGCG	GTGATTGAAG	AGATCGTGTA	TAAGGTTTTA	240
CCCAAAGAAT	ATTTGCATGA	CAATATCAAG	TTTTTTATAA	ACCCTACAGG	AAAATTTCGTC	300
ATCGGTGGGC	CTCAAGGCGA	TGCGGGTTTG	ACAGGTAGAA	AAATCATCTG	GGATACTTAT	360
GGAGGGTTTT	GCCCGCATGG	AGGGGGAGCG	TTTACCGGGA	AAGACCCTTA	CAAGGTGGAT	420
ATGAGCGCGG	CTTATGCGGC	CCGCTATGTG	GCTAAAAATT	TGGTAGCGAG	CGGGGTTTGC	480
GATAAAGCGA	CCGTGCAGCT	TGCTTATGCG	ATTGGGGTGA	TAGAGCCTGT	GTCTATTTAT	540

994

GTGAACACGC	ATAACACGAG	CAAGCATTCA	AGCGCGGAGT	TGGAAAAATG	CGTGAAATCG	600
GTTTTCAAAC	TCACGCCAAA	AGGCATCATT	GAAAGCTTGG	ATTTGTTAAG	ACCCATTTAT	660
TCGCTCACTT	CAGCTTATGG	GCATTTTGGG	CGCGAGTTAG	AAGAATTCAC	TTGGGAAAAG	720
ACTAACAAGG	TTGAAGAGAT	TAAAGCGTTC	TTTAAGCGT			759

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415

TCAACAATTC	ACAAGGAGTT	TAAATTGAAA	CAAAGAACGC	TGTCTATTAT	TAAACCGGAT	60
GCACCTAAGA	AAAAAGTGGT	AGGCCAAAAC	ATTGATCGCT	TTGAGAGTAA	CGGCTTGGA	120
GTGGTGGCCA	TGAAACGCTT	GCATTTGAGC	GTGAAAGACG	CTGAAAACTT	TTATGCGATC	180
CTCAGAGAGA	GACCCTTTTT	TAAAGATTTG	ATAGAGTTTA	TGGTGAGTGG	TCCGGTGGTG	240
GTTATGGTTT	TAGAAGGCAA	AGATGCGGTG	GCTAAAAACA	GAGAGCTTAT	GGGAGCGACT	300
GATCCCAAAC	TCGCCCCAAA	AGGTACTATC	AGAGCGGATT	TTGCTGAGAG	CATTGACGCT	360
AATGCGGTGC	ATGGGAGCGA	TAGCTTGGA	AACGCGCACA	ATGAAATCGC	TTTCTTTTTT	420
GCCGCTAGAG	AGTTT					435

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416

GGGCGAGGTG	GAATTTATAT	TGAACATGGC	AGGGTTAAAA	TGGTAGCTTT	AAGCAACGCT	60
CTTTCAAGGG	TTTTTGTTTC	TGTGGCTGGC	TATAAATTCC	CTTCTTTTAT	CCAAAAAAGC	120
ATCAACGCTC	TTTATGTTAA	GATCTTTAAA	ATTGATTTGA	GCGAGTTTGA	GCCTTTAGAA	180

995

AATTATAAGA	GTTTGAACGC	TCTTTTCATG	CGCTCTTTAA	AAAAAGAACG	CCCCTTTGAC	240
AAAGCCCCTA	ATATTTGCGAT	TGCGCCCTTG	GATGCTTTAA	TCAGTGAATG	CGCTTTTFTA	300
GACAACGATA	GCGCTTTTACA	AATTAAAGGC	ATGCCCTATA	AAGCGCATGA	ATTAGTGGGC	360
GAAATCAACC	CCTTAAGCCC	TTCTTTTTC	TATGTGAATT	TTTACCTTTC	GCCCAAAGAT	420
TACCACCACT	ACCACGCCCC	TTGCGATTTA	GAAATTTTAG	AGGCTCGTTA	TTTTCGGGG	480
AAATTACTAC	CAGTCAATAA	GCCCTCATT	CACAAAAACA	AAAATCTGTT	TGTGGGCAAT	540
GAAAGGGTCG	CGCTTGTTGC	AAAAGACGAT	TCAAGGCAA			579

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417

AACCATAATA	AAGGGGCGGA	AATTTTCGCTA	TGGGGTTTAA	CCCGCTTGGT	GGATAGAGAC	60
ATTGATAAGG	ATAACCCAAG	GACGAAAAAC	CGCCCCGAGC	TGGATGGTAG	GATCAGCGTT	120
AAAGGCATGG	TCATTTTTC	CGTTTCAAAC	GCTATTTTGT	TTGTGGGATG	GAGTAATTTT	180
ATCAACCCCTT	TAGCTTTCAA	GCTTTTCGTTA	CCTTTTTTAA	TCATTTTAGG	GGGGTATTTC	240
TATTTCAAGC	GCCTTTCTTC	TTTGGCGCAT	TTTGTCTGTT	GTTTGGCTTT	GGGTTTAGCC	300
CCCATTCGAG	GAAGCGTGGC	GGTTTTCGTT	GATATTCCTT	TATGGAATGT	CTTTTGGCT	360
TTAGGGGTGA	TGTTGTGGGT	GGCTGGGTTT	GATTTGCTCT	ATTCTTTACA	GGATATGGAG	420
TTTGATAAAG	AAAGGGGCTT	GTTTTCATT	CCTAGCCAAT	TAGGGGAAAA	ATGGTGCTTG	480
AATCTTTCAA	GGCTCTCGCA	CCTGTGGGCA	CTGATCTGCT	GGCTTTGTTT	TGTGAAATGC	540
TATCATGGGG	GGCTTTTTC	GTATTTGGGC	TTAGGGGTTT	CAGCCTTGAT	CTTACTCTAT	600
GAGCAGATTT	TAGTGGCCAG	AGATTATAAA	AACATTCCTA	AAGCCTTTT	TGTGAGTAAT	660
GGCTATTTGG	GGGTGGTGT	TTTATTTTT	ATCGTCCCTG	ATGTGGGGTT	CAAGCATGCA	720

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

996

(B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418

GTAATGGCTA	TTTGGGGGTG	GTGTTTTTTA	TTTTTATCGT	CCTTGATGTG	GGGTTCAAGC	60
ATGCATGAGT	TGGTTTTAAG	ATCCCAAGCT	TTAGGGTTTG	AAACGCGCTT	AGTCCAGTGC	120
GATTTATCGT	TTTCTTATGA	AAGGTTTATT	TCTAAAACCA	AACGCTCTTT	AGCGGTGTTA	180
GAAGAATTTG	ATTGGTTAAA	TTCTGGCTTT	GATTTTTCAC	GCTTGAACGT	TGAAAATGAC	240
ACTCTGGAAT	TACTCAAAGC	GCTGTATTTT	AAATTAGAAA	AATTAGAGAG	CCTGCTTTTA	300
AAAGAAAATT	TACTTGAATT	GGAGCAAAAG	GATCGCATCA	TCGCTTTAGG	GCATGGGCTA	360
GTTTGCCTAA	AAAAACAAAG	CCTGATAGCG	CCTCAAACCT	ACTATGGGCG	TTGCGTGTTA	420
GAGGGGAAAA	TCCTAGCCTT	TTTTGGCGTG	GCAAGGGATA	AAGATTTTTT	AGAAATCACT	480
CGCATGCACG	CCTTAGACAT	TAAGCGTTAT	GATTCTTCA	TTGTTGATAG	CGAAAGAAAA	540
GGCTTGAAAT	TA					552

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419

ACGGGAGCAA	TCATGTTATC	TTCTAATGAT	TTGTTTATGG	TCGTTTTAGG	GGCGATTTTA	60
TTGGTGTGG	TGTGCTTGGT	GGGGTATTG	TATCTTAAAG	AAAAAGAGTT	TTACCATAAA	120
ATGAGGCGTT	TAGAAAAAAC	TTAGATGAA	TCCTATCAAG	AAAATTATCT	CTATTCTAAG	180
CGTTTGAGAG	AAATTAGAGG	GCGTTTGAA	GGCCTTCTT	TAGAAAAAG	CGCTAAAGAG	240
GACAGCTCAT	TAAAAACGAC	TCTTTCGCAC	CTTTATAACC	AGTTGCAAGA	AATCCAAAAA	300
TCCATGGATA	AAGAGCGCGA	TTACTTAGAA	GAAAAATCA	TTACT		345

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

997

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420

GAGCCCATTA	AAAGCGACAA	AGAAGCCTTT	GATCTGGTCA	TGCAAAATCG	ATCGCATGAA	60
ATACAAGGCG	TATCACACAT	TAAGAATAAT	TATAAATTTT	TCACCAAAGA	GCTTGACAAT	120
TATATCAGCA	AAGGGTATCG	CATTGAAGAG	ATTTATGGCG	CGTTTTTGTG	GCTCAAAATC	180
GTAGCCATAG	GTTTAGAGTT	GGGCGAAGAC	GATCCGCAAG	TGGTGTGTTGA	GAGCATCAAC	240
GCTACAGGCG	TGCAATTAAA	AGGGCTGGAT	CTCATCCGCA	ACTATTGAT	GATGGGGGAA	300
AATTCTGACA	ACCAGAATCG	TCTTTATAAT	ACTTATTGGG	TGCCTTAGA	AAATTGGCTT	360
GGTGAAAAGG	ATTTGAATGA	TTTCATCAAA	ACCTATTTGA	GAATCTATTT	TGAGGATAGA	420
GTTAAAGAGG	GAGAGCGCGA	AGTGATTAC	GCGCTAAAAG	CCCACCACAG	AGACAATTTT	480
CCTAACAAATA	TACAAGGTCT	TATGAGCGAT	ATGCGAGAAT	ATGGCAGAAT	CTTTCAAATC	540
TTTTTAGACA	GAGATCATT	TTTTTTACAT	CGTGGAGACC	CGCAACAGTT	AGCGAATTTA	600
CGCTTGCGCG	TTAAAGATCT	CGTAAAAATC	AAATTTGGCG	TGGCAAAGCC	CTTGTGTTTG	660
CGTTGCGCCA	GAGATTTTGA	AGAAGGCAAA	TTGGATTATG	AAAACCTCCA	TGAAATCTTG	720
CAAAATCCTTA	TCAGCTACTT	CGTGCGCCGA	AGCGTGTGCG	GGGATTTCTAC	CCCTACGCTT	780
ACCAGAGTTC	TTTATTCTTT	ATACAGACAG	CTAGGGGAAG	ATGTTTCAGC	CGATGCATTG	840
AAGCGGTATT	TGGGCAAGAG	CGTTGGTCAA	ATGGCGTTCC	CTAATGACGA	TAAAATTAAA	900
GCGGCGTTTC	TTGTGCGTAA	CGCTTATGCA	GCAAATCAAG	TGTGCAAATT	CATCCTGCTT	960
GAGATTGAAA	AATTAGCAAC	GCTGAACCGC	CAAAGAAGA	GAATT		1005

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421

TTCTATGTCT	CGATCATTAA	ATGCACGCCT	TTATTGGTCC	AAATCGTAAT	CGTGTGTTTAT	60
GGTTTGCCCC	CCCTTGGGGT	CTATATGGAT	CCAATCCCGG	CAGGCATTAT	TGCGTTTTCT	120
TTTAAATGTG	GGGCATACGC	TTCAGAGACT	TTGAGGCGGA	GCTTTCTTTC	TGTCCCTAAA	180
GATCAATGGG	ATTCAAGCTT	GAGTTTGGGC	TTGAATTACT	TGCAAACCTT	TTGGCATGTC	240
ATCTTTTTTC	AAGCGCTCAA	AGTCGCCACG	GCCAAGCCTA	AG		282

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

998

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1383
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422

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TCAATAAAAC ATTTAGGCAA AAAAGAGGTG AAAACCTTAG GATTGTC TTC GCTTGGTGGG      60
ACTTTAGAAT TTTACGATTT TATCATCTTT GTATTTTTTA CAAGTATCAT TGCCAAACAC      120
TTTTTCCCAA ACACGCTTAG CCCTATCTGG TCTGAAATCA ACACTTATGG GATCTTTGCT      180
GCAGGTTATC TGGCGCGCCC GCTTGGTGGC ATAGTGATGG CCCACTTTGG GGATAAAATC      240
GGTCGTAAAA ACATGTTTCAT GCTCTCTATT TTATTAATGG TAATCCCAAC CTTTGCGCTA      300
GCTTTGATGC CAACTTTTAA TGATTGGGTG GGTTTTGGCG TGGATAGCAT GGGGCTTACC      360
CCTAAAAACG CTCATTATCT TGGTTACATA GCTCCTGTTT TTTTGGTGCT TGTTAGGATT      420
TGTCGAAGCG TCGCTGTGGG TGGTGAATTG CCTGGCGCTT GGGTTTTTGT CCATGAACAT      480
GCCCCACAAG GACAAAAAAA CACTTATATC GGTTTTTTAA CCGCTTCCGT AGTTTCTGGG      540
ATTTTGCTTG GGAGTTTGGT TTATATCGGG ATTTACATGG TTTTGACAA GCCTGTGTGT      600
GAAGATTGGG CTGGCGGGT TGCCTTTGGG CTGGAGGAA TTTTGGTAT CATTTCTGTG      660
TATTTGAGGC GCTTTTGA GAAACTCCC GTTTTTCAGC AAATGAAGCA GGACGATGCC      720
TTAGTCAAAT TCCCGCTTAA AGAGGTGTTT AAAAATCCC TCTTGGTAT ATCAATCTCC      780
ATGCTTATCA CTGGGTTTTT AACCGCTTGT ATTTTGATTT TTATCCTTTT TGTCCCGAAT      840
TTTACCCTTA CGCATCCCAA TTTTCATTTC ACTCCGTTTG AAAAAACCTA TTTTCAAATT      900
CTAGGACTTG TTGGTATTGT AAGTTCATT ATTTTCACCG GGTTTTTTGGC TGATAAAATC      960
AAACCGCACA AAGTTTGCAT GGCTTTTAGC GCGGCCTTTG GGTTTTTTGG CTTTTTATTC     1020
TTTAAGGAAT TTATTCTAA CGCGCCAAGT TTAGTCAATA CTATAATTTT ATACTTTTAA     1080
GCTTGCTTTT GCGCGGGCAT TATGAATTTT TGCCCCATTT TCATGAGCGA TGTGTTTAGC     1140
GCTAGAATCC GTTTTAGCGG GATTTCCCTT GCTTATAACA TAGCCTATGC TATAACCGCT     1200
GGCTTTACCC CTCAACTTTC AAGCTGGTTA AACGCAAAAG CTATAGCAGT GCCTGAAAGT     1260
TTGCAAAGTT ATGGTTTAA GCTTTATATC CTTATAGTTT CTTTAATTGC TTTTATTACA     1320
TCGCTTTTAA TGGCGCCAAT TTATCACAAA TCTAATACCC AACACGAAGT GTCGCCCACG     1380
GCA

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(2) INFORMATION FOR SEQ ID NO:1423:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1521
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423

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AAATCGCTCA AAAAGAAGTG CCGGAGCTTT TTGCAAGAAT ATGAGGTTTA TTCTTTGGAT      60
TTGGCTTTAA TGGTAGCTGG GGCAAAATAC AGAGGGGATT TTGAAAAGCG CCTGAAAAAA      120
ACGCTCAAAG AGATCCAGCA AAACGGCCGT ATCATTTTAT TCATTGATGA AATCCACACC      180
CTTTTAGGTG CAGGGAGCAG TAACGCTGGG AGCTTGGATG CGGCGAATAT ATTAAACCG      240

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999

GTTTTAAACGG	ATGGGAGCTT	GAAATGTTTG	GGGGCGACCA	CTTTTGAAGA	ATACCGCAGC	300
GTGTTTGAAG	AAGACAAGGC	TTTCAACAGG	CGCTTTTCTA	TAGTGAATGT	TGAAGAGCCT	360
TCTAAGGAAG	CGTGTTACTT	GATTTTAAAG	AATATTGCC	CCCTTTATGA	AGAACACCAC	420
CAGGTGCGTT	ATAATGAAAG	CGTGTTTAA	GCATGCGTGG	ATTTGACGAG	CTATTACATG	480
CATGATAAAT	TCTTGCCCGA	TAAGGCGATT	GAATTATTAG	ATGAGGTGGG	ATCAAGGAAA	540
AAGATCAACC	CTAAAAAAGG	CAAAAAATC	AGCGTTGATG	ACGTGCAAGA	AACGCTCGCT	600
CTCAAGCTTA	AAATCCCTAA	AATGCGTTTA	AATAGCGATA	AAAAAGCCCT	TTTAAGGAAT	660
TTGGAAAAAT	CGCTAAAAAA	TAAGATTTTT	GCCCAAACCG	AAGCGATCAA	CCTTGTCAGC	720
AATGCGATCA	AAATCCAGCA	TTGCGGCTT	TCTGCAAAAA	ATAAGCCTGT	GGGGAGCTTT	780
TTATTTCGTGG	GGCCTAGTGG	GGTAGGAAA	ACAGAATTGG	CTAAAGAATT	GGCCTTGAAT	840
TTGAATTTGC	ATTTTGAACG	CTTTGACATG	AGCGAATACA	AAGAAGCCCA	TAGCGTGGCA	900
AAGCTCATCG	GAAGTCCTAG	CGGTTATGTG	GGGTTTGAGC	AAGGGGGGTT	ATTGGTGAAT	960
GCGATTAAAA	AGCACCCGCA	TTGTTTGCTG	CTTTTAGATG	AGATAGAAAA	GGCCCACCCT	1020
AATGTGTATG	ATTTGTGTGT	GCAGGTGATG	GATAACGCCA	CTTTGAGCGA	TAATTTAGGC	1080
AACAAGGCGA	GTTTTAAGCA	TGTGATACTG	ATTATGACTT	CAAATGTGGG	GAGTAAGGAT	1140
AAGGACACGC	TAGGGTTTTT	TAGCACTAAA	AACGCCAAGT	ATGATAGAGC	CGTTAAAGAG	1200
CTTTTAAACC	CTGAATTGCG	ATCCAGAATT	GATGCGATCG	TGCCGTTTAA	CGCGCTCAGT	1260
TTGGAGGATT	TTGAACGCAT	TGTTTCTGTG	GAATTGGACG	GGTTAAAAGC	CCTAGCAATA	1320
GAGCAAGGCG	TGATCTTAAA	ATTCCATAAA	GAAGTTGTGA	AATGCATCGC	GCAAAAGAGC	1380
TACCAGAGGA	GTTTTGGTGC	GAGAGAAATT	AAAAAATCA	TTCAGAGGGA	AATCAACCCC	1440
CAATTAAGCG	ATATAGTGCT	TAAACAATCG	CTTAAAAAAC	CAACAAGATC	GTTGCGCATG	1500
AAGAGCACAT	TTCACAAAGT	G				1521

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424

GGAATAAAGT	TGATAAAATT	TGTGCGTAAT	GTGGTTTTAT	TCATTTTAAAC	AGCGATCTTT	60
TTAGCGTTCA	TGCTTTTAGT	GAGTTATTGC	ATGCCCCATT	ATAGCGTGGC	TGTCATTAGC	120
GGGGTGGAAG	TCAAAAGAAT	GAATGAAAT	GAAAACACGC	CCAATAATAA	GGAAGTAAAA	180
ACCCCTTGCTA	GAGATGTCTA	TTTTGTGCAA	ACTTACGACC	CTAAGGATCA	AAAAAGCGTG	240
ACCGTCTATC	GTAACGAAGA	CACGCGCTTT	GGCTTCCCTT	TTTATTTTAA	GTTTAATTCC	300
GCTGATATTT	CAGCTCTCGC	TCAAAGTTTA	GCTAATCAGC	AAGTGGAAGT	GCAATACTAT	360
GGCTGGCGGA	TCAATTTGTT	TAACATGTT	CCTAATGTGA	TTTTTTTAAA	ACCCCTAAAA	420
GAGAGCCATG	AGATGTCAAA	ACCCGTTTTT	AGCTGGATTT	TATACGCCCT	GCTACTAGTG	480
GGCTTTTTTA	TCAGTGCACG	TTCTGTTTGC	ACTTTATTTA	AGGGCAAAGC	TCAT	534

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

1000

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1914
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425

GCGCGGCTTT	TATTGTATAA	TCTTAAAAAT	TTTATTAAAG	GAAAAAGTTC	AATGTCTAAT	60
CAAGAATACA	CCTTCCAAAC	TGAAATCAAC	CAGCTTTTGG	ATTTGATGAT	CCACTCTTTG	120
TATTCTAATA	AAGAGATTTT	TTTAAGGGAG	TTGATTCTA	ACGCGAGCGA	CGCTTTGGAT	180
AAGCTGAATT	ATTTGATGCT	AACCGATGAG	AAATTAAAAAG	GGCTGAATAC	CACGCCTAGC	240
ATCCATTTGA	GTTTTGATAG	CCAAAAAATA	ACCTTAACGA	TTAAAGACAA	TGGTATAGGC	300
ATGGATAAAA	GCGATCTCAT	CGAGCATTTA	GGCAGCATCG	CTAAATCAGG	CACGAAGAGT	360
TTTTTAAGCG	CTTTGAGTGG	GGATAAGAAA	AAAGATAGCG	CCTTAATTGG	CCAATTTGGC	420
GTGGGCTTTT	ATTCGGCGTT	CATGGTAGCG	AGTAAGATTG	TCGTTCAAAC	CAAAAAAGTT	480
ACCAGTCATC	AAGCTTATGC	ATGGGTGAGC	GATGGTAAGG	GCAAGTTTGA	AATCAGCGAA	540
TGCGTCAAAG	AGGAGCAAGG	CACAGAAATC	ACCCTCTTTT	TAAAAGAAGA	AGATTCTCAT	600
TTTGCGAGCC	GTTCGGAGAT	TGATAGCGTT	GTTAAAAAGT	ATTCTGAGCA	TATCCCTTTC	660
CCTATTTTTT	TAACTTACAC	CGATACGAAA	TTTGAGGGCG	AAGGGGATAA	TAAAAAGAA	720
GTTAAAGAAG	AAAAATGCGA	TCAGATCAAT	CAAGCGAGCG	CTTTATGGAA	AATGAATAAG	780
AGCGAATTGA	AAGAAAAGGA	TTACAAAGAC	TTTTACCAAT	CGTTTGCACA	TGATAACAGC	840
GAGCCTTTGA	GCTATATCCA	TAATAAAGTG	GAAGGCTCTT	TAGAATACAC	GACGCTTTT	900
TATATCCCTA	GCAAAGCGCC	CTTTGATTTG	TTTAGGGTGG	ATTATAAAAG	CGGGGTCAAA	960
CTTTATGTTA	AACGGGTGTT	TATCACTGAT	GATGACAAAG	AATGTTTGCC	GTCTTATTTG	1020
AGGTTTGTAA	AAGCGGTGAT	TGACAGCGAA	GATTTGCCCT	TGAACGTGAG	TCGTGAAATC	1080
TTACAGCAGA	ATAAGATTTT	AGCCAATATC	CGTTCGGCTT	CAGTGAAAAA	GATTTTAAAGC	1140
GAGATTGAAA	GGCTGAGCAA	GGATAACAAG	AATTACCATA	AATCTATGA	GCCTTTTGGG	1200
AAAGTGTTAA	AAGAAGGCTT	GTATGGGGAT	TTTGAAAACA	AAGAAAAACT	TTTAGAATTG	1260
TTGAGATTCT	ATTCTAAAGA	CAAAGGAGAA	TGGATTCTTT	TAAAAGAATA	CAAAGAAAAT	1320
TTAAAGAAAA	ATCAAAAAAG	CATTTACTAC	CTTTTAGGCG	AAAATTTAGA	CTTATTAAAA	1380
GCGTCCCCC	TTTTAGAAAA	ATACGCTCAA	AAAGGCTATG	ATGTTTTGTT	ATTGAGCGAT	1440
GAAATTGATG	CGTTTGTGAT	GCCAGGCGTG	AATGAATACG	ATAAACGCC	CTTTAGAGAC	1500
GCTAGCCATA	GTGAGAGTTT	GAAAGAGCTT	GGTTTGGCAG	AAATCCATGA	TGAGGTAAAA	1560
GATCATTTTA	AAGATTTAAT	CAAAGCGTTT	GAAGAAAATC	TTAAGATGA	GATTAAAGGC	1620
GTAGAGCTTT	CTGGTCATCT	CACTTCAGCG	GTGGCTTTAA	TAGGCGATGA	ACCAAATGCG	1680
ATGATGGCTA	ATTGGATGCG	TCAAATGGGG	CAAAGCGTGC	CTGAAAGCAA	GAAAACTTTA	1740
GAATTAAACC	CTAACCATGC	GATTTTGCAA	AACTCTTAA	AATGCGAAGA	TAAAGAGCAG	1800
TTGAGCGCTT	TTATCTGGTT	GCTTTATGAT	GGGGCGAAGC	TTTTAGAAAA	AGGGGCTTTA	1860
AAAGACGCTA	AAAGTTTTTA	CGAACGCTA	AATAGCGTGC	TATTGAAGGC	GTTG	1914

(2) INFORMATION FOR SEQ ID NO:1426:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

1001

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426

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AAGCAATTG GTAGGCGAGT TTTTACCCAA ATTCTTAAA TGGTGCAATT TCAAAACACG      60
CTTATAAAAT TCCATGCCCT ATCCTTTAAA AACGCAAAAT TAATTTATAA TGCAAAATTA      120
AACAAAACAT GCTATAAAGA AAATTCAAAT ACTATCATT TAAGGATTAA AATGCTCACC      180
CAAGAAGATG TCTTAAACGC GTTAAAAACG ATCATCTACC CTAATTTTGA AAAGGATATT      240
GTCAGCTTTG GTTTTGTAA AAACATCACC TTGCATGACA ACCAATTAGG GCTTTTAATA      300
GAAATCCCTT CAAGCTCTGA GGAACGAGT GCGATTTTAA GGGAAAATAT CTCCAAAGCG      360
ATGCAAGAAA AAGGCGTGAA AGCTTTGAAT TTGGATATTA AAACCCCGCC TAAACCGCAA      420
GCTCCAAAGC CCACCACTAA AAATCTGGCT AAAAACATCA AGCATGTGGT CATGATAAGC      480
TCAGGCAAGG GCGGTGTGGG TAAAGCACC ACCAGCGTGA ATTTAAGCAT CGCTTTAGCG      540
AATTTAAACC AAAAAGTGGG GCTACTAGAC GCTGATGTGT ATGGCCCTAA TATCCCTAGA      600
ATGATGGGCT TGCAAAACGC TGATGTGATC ATGGATCCTA GCGGTAAAAA ACTCATTCCT      660
TTAAAAGCTT TTGGCGTTTC TGTGATGAGC ATGGGGCTTT TGTATGATGA GGGGCAGAGT      720
CTCATTGTGA GAGGACCCAT GCTCATGCGA GCGATTGAGC AGATGCTAAG CGATATTATT      780
TGGGGGGGAT TAGACGTGCT GGTGGTGGAT ATGCCCCCAG GAACAGGCGA TGCGCAGCTC      840
ACGCTAGCCC AAGCCGTGCC ACTCAGCGCA GGAATCACCG TTAACACGCC TCAAATCGTG      900
AGTTTAGATG ACGCTAAACG GAGTTTGGAC ATGTTTAAGA AACTACACAT TCCTATTGCG      960
GGCATTGTAG AAAATATGGG GAGTTTGTG TGCGAGCATT GCAAGAAAGA GAGCGAGATT     1020
TTTGGCTCAA ATTCCATGAG TGGATTATTA GAGGCTTATA ACACGCAGAT TTTAGCCAAG     1080
CTCCCTTTAG AGCCTAAAGT GCGTCTAGGG GGGGATAAGG GTGAACCGAT TGTGATTCTT     1140
CATCCCACTA GCGTGAGTGC TAAAATTTT GAAAAAATGG CAAAGGATTG GAGTGCTTTT     1200
TTAGACAAGG TGGAAAGGGA AAAACTAGCC GATAATAAGG ACATCCAGCC CACACAAACG     1260
CATGCTTATT CGCAT

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(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427

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CTAGGGTTTT TGGCTTTGCA TGGGTTTTTT CTCAGCGCTT TTGAGTATCA AGTGAGCGCT      60
AGAGTGGGAT CGTTTTGCGG TATCGCTTTC AACCAATCGA TCATCAATTC CAAAAAAGGG      120
ATTTACCCTA CAGGGAGTTA TGTAACCACT ACCGGGGCTT TACAAGTTGA TTCTAGTTTG      180
CTCCCTAAGG GGATTGAAAA CCACAAATTG GGTTTTGGGG TGGGGGGCGA AATAGGAGCG      240
TTAGCTTATG ATTCCACGAA ATTTTGTGAT GATGAAGCCA ACCCTAAGGC AGGGTTTCAG      300
CCAGCGAACT GGTATTACAT GGGCGCATGG GAGGGCTATT TGATGCAACA CAGCCAAAAT      360
TGGACCAGAG AGCAAAAGGC TCAAAACGCC AGGCCTTATG TGTTATACAA TTTGTATTTA      420
GATTATCAAT ATAAGGACAT TTTTGGGATT AAACATAGGC GTTACCCTTC TAAGGCTTTG      480
TTTTTGAGCG GGTTTAATCA AGGGTTTGAG ATTTTTTACC GGTGGAAGAA GTTTAAGATA      540
GTGTGGTTTA GCACCTTTGG AAGGGCTTTA GCCAATGAGC AATACATTAG GGATTTTAC      600

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SUBSTITUTE SHEET (RULE 26)

1002

GCTCCTGTCA	ATTACAAGCA	AAAAATCAAC	TACGGCATGC	ACAATTTCAA	CCTCGTTTAC	660
GAAAATAAAT	ACATTAGGAT	CGCGCCTTTT	ATTTGGTTTT	ACCCTAAGAA	TTTTAACGCT	720
CCTGGATTTG	AAATCACCCA	TGACACAAAA	TCTTATTGGA	AATCTCTTTG	GCGCATCCAA	780
ACGACTTTTT	ACGCATGGTT	TCCTCTCTAT	AGCGACTATT	TGTCTAAAGA	TTATTATAGG	840
GCCGCTTTAG	TGGGTAAAAA	AAGCGCGGCT	TTGTTTGTGT	TTCAAAGAGT	GAATTTCCGC	900
TCTTATCGTT	TTGGCTGGAG	CGTGTATAAG	AATTTTGGGA	ACGCGAGCGT	TCAGTTAGGT	960
TGGAATGGCT	CACCCATTGA	TCCTTTTTAC	GACACGAAAG	ATGATACCCC	TTATGAAGAC	1020
GCTTATTCCA	ATTTTTACAA	CGCTAATTCC	ATAACGATTA	ACGCTTTTAT	AGGGAAGAGC	1080
ATTAAGAATC	TTTTGGTGCA	ATTGTATGGG	AAATTAACCT	ATTCCCCAAG	GGCTGATGCG	1140
CAAAGCTTAG	GGGTTACTTT	TAAATATAAC	CTTAAAAAAC	ATATCTATTT	CATGCTAATG	1200
GTTAATGGCT	ATCAAATCAC	GATGCATAAG	GGTTATAAGG	TAGGGTTTTT	TACAAGCGGT	1260
TACAACCCTG	ATTCGCTCA	AACCATTCAA	AATAGAAGCT	ATTTGATGAG	CTCTATGAGT	1320
TATCGTTTTT						1329

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428

TACCCTACAA	ATACTATTAT	TGAAAGGATT	TTGATGTTTA	AAAAAATGTG	TTTGAGCCTG	60
CTAATGATAA	GCGGTGTTTG	TGTGGGGGCA	AAGGATTTGG	ATTTCAAGCT	GGATTATCGC	120
GCGACTGGGG	GGAAATTCAT	GGGGAAAATG	ACGGACTCTA	GTCCTTTAAG	TATCACTTCT	180
ATGAACGATG	AACCGGTGGT	GATTAAAAAC	CTTATTGTCA	ATAGGGGAAA	TTCAGTCGAA	240
GCGACTAAAA	AAGTAGAACC	CAAATTTGGC	GATAAGTTTA	AAAAAGAAAA	ACTCTTTGAT	300
CATGAATTAA	AATACTCGCA	ACAGATATTT	TACCGCCTGG	ATTGCAAGCC	TAACCAATTG	360
TTAGAAGTTA	AAATCATCAC	GGACAAGGGC	GAATATTACC	ATAAATTTTC	CAAA	414

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429

AGGATTGGCA	TGGACGCTTT	AGAAATCACC	CAAAAACCTCA	TCAGTTACCC	TACCATTACG	60
CCCAAAGAAT	GCGGTATTTT	TGAATACATT	AAATCGCTTT	TTCCTGCTTT	TAAAACCCCTA	120
GAATGTGAAA	AAAATGGCGT	GAAAAACCTT	TTTTTATACC	GCATTTTTTA	CCCCCTCAAA	180
AAGCATGCAG	AAAAAGAACA	TGCAAAAGAA	AAGCATGTAA	AAGAAAATGT	TAAGCCCTTG	240
CATTTTTGCT	TTGCAGGGCA	TATTGATGTC	GTGCCTCCTG	GGAACAATTG	GCAAAGTGAT	300
CCCTTTAAAC	CCATCATTA	AGAGGGGTTT	TTATACGGTC	GTGGGGCGCA	AGACATGAAG	360
GGGGGCGTTG	GGGCGTTTTT	GAGTGCAGT	TTAAATTTTA	ACCCTAAAAC	CCCTTTTTTG	420
CTTTCTATTT	TACTCACGAG	CGATGAAGAA	GGGCCAGGGA	TTTTTGCCAC	TAGGCTTATG	480
CTAGAAAAAC	TCAAAGAAAA	GGATTGCTG	CCTCATATGG	CGATTGTGGC	TGAACCCACT	540
TGCGAAAAAG	TCTTAGGCGA	TAGCATCAAA	ATTGGCCGAA	GAGGCTCTAT	TAATGGCAAA	600
CTCATTTTTAA	AAGGCGTTCA	AGGGCATGTG	GCTTACCCGC	AAAAATGCCA	AAACCCTATT	660
GATACGCTCG	CTTCAGTTTT	GCCTCTCATT	TCAGGAGTTC	ATTTAGACAA	TGGCGATGAG	720
TGTTTTGACC	CTTCAAAATT	AGTCATCACC	AACCTGTCATG	CAGGGTTAGG	GGCTAATAAT	780
GTTACACCAG	GGAGCGTAGA	AATTGCCTTT	AATGCGCGCC	ATTCTTTTAA	AACCACCCAA	840
GAGAGTTTGA	AAGAATATTT	GGAAAAGGTT	TTGAAAGATT	TGCCTTATAC	TTTAGAATTA	900
GAATCAAGCA	GTTGCGCTTT	CATCACGGCT	TCCCATTCAA	AGCTTACTAG	CGTTTTTCAA	960
GAAAATATTT	TAAAAACATG	CCACACCACC	CCCCTTTTAA	ACACCAAAGG	CGGCACGAGC	1020
GATGCGCGAT	TTTTTAGCGC	TCATGGTATA	GAAGTGGTGG	AGTTTGGCGC	CATTAAATGAC	1080
AGGATCCATG	CCGTTGATGA	AAGGGTGAGC	TTGAAGGAAT	TAGAGCTTTT	GGAAAAAGTG	1140
TTTTTGCGGG	TTTTAGAGGG	CTTGAGCGAG	AAA			1173

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430

ACAAGCCTTG	ATCACAAAAT	CACAGATTTT	TCTTGCCTGG	ATTTGAGGAT	CCAATCTAAA	60
GAAGTCAGTC	ATAATTTAAA	GGAATTATCA	AAAACGCTAA	TCAGCTATCC	TTTTGAAAAA	120
CATGTAGAAG	CTTTAGGGGA	ACAATGCAGT	AACTTCGTTT	CTATTCCCAT	TAACAATGAC	180
GACTATTCAA	ATATTGTCAC	TTTTGTGAGT	GATTTTATAA	ATCTTATAGC	TTCTTACAAT	240
TTATTAGAAT	CATTTTTCAG	TTTTTATAAA	GATAAATTAA	AATTGAGCGA	GCTTGTAAT	300
GAATATGCCA	ACGTAAACCA	TAACTGCTT	TTCAAAAAAT	TAATCAAACA	TTTAAGCGGC	360
AACAATCAAT	TGGTTAAAAA	TTTTTATCAG	TGTATAAGAG	AAATTATAAA	ATACAACGCC	420
CCTAATAAAG	AATACAAACC	CAATCAATTT	TTTATAATAG	GGAAAGGCAA	ACAAAAACAA	480
TTAGCAAAAA	TTTATCTCA	TTTAAAAGAA	CTTAGTGCAA	GTGAATTTAA	ACCACAAGAT	540
ATGGAAGACA	TCTTAAAAAA	GCTAGAGGAA	TTAGATAAAA	TTTTTAAAAC	TACCGACTTT	600
ACAAAATTCA	CACCAAAAAAC	TGAAATTAAG	GATATTATTA	AAGAAATAGA	CGAAAAATAC	660
CCTATCAATG	AAAATTTTAA	ACGGCAATTT	AATGAGTTTG	AATCAAATAT	TGAAAAACAT	720
GATGAAATAA	AAAAGGATTT	TGAGCGAAAC	AAAGAGTCGC	TGATCCGAGA	AATTGAAAAT	780
CACTGCAAAA	ATGAATGCAA	TAGCGAAGAA	GAGCCGGAGT	ATAAGATTAA	TGATCTGCTC	840
AAAAATATCC	AACAAATATG	CAAAAATTAT	ATAGAAAGTC	ATGCCGTTAA	TGATGTGTCT	900

1004

AAAGATATTA	AATCCATGAT	GTGTCAGTTT	TATTTGAAAC	AGATAGATTT	ATTAGTCAAT	960
TCAGAAATTG	TGCGATACAG	ATACAGCAAT	CTTTTGAAC	CAATACAAAG	ATCTTTATGG	1020
GAGAGTATAA	AAATTTTAGA	TAATGAAAGT	GGCATTTTATT	TGTTCCCTAA	AAATATTGGT	1080
GAAATCAAGG	ATAAATTTGA	AGCAAACAAG	GAAAAATTC	AACAAAGCAA	AAATGTTTCT	1140
GAGTTGCGAG	AATATTGCCG	AGAGTGTAA	CCCTATACAG	CGTTTAACTT	TCATCTAAAT	1200
ATAAATAATG	GTTTATCTCA	TCAATTTGAA	AAATTCGTGC	CAATCATGAA	AGAATACAAA	1260
GAGCCAAAAA	TCACAGATAA	TGACCTTGAA	GCCATATCAA	CCAAAGAGAC	TGGTCTTGCT	1320
AGCCAATTAT	CTGGGCACTG	GTTTTTTCAG	CTTTCGTTAT	TTAATAAAAC	AAACTTTAAT	1380
CCTAATAAAA	TTTGGAATTC	TTTAGAGTTC	AATAAAGAT	CAAAAATAAA	GTTTGATAAA	1440
GATTTAGAAA	TCATTTTGA	TAGTCATGAA	TCGTTCAATA	TCTCTAAAA	ATACTTGCAA	1500
GAAATAGATG	AAGAATCACT	AAAAAAGATC	AAACAATCAA	AAGATTTTTT	TTCAATTCAA	1560
AAAATAGAGA	GTAAGCATGA	TAATAACGAT	ATACTGCAAC	TTGAATTTTT	TGAGAATGAT	1620
ACAAGTTTTT	TTTTTGCTAA	AGGAAGTTTT	GCAGAAATTT	TAGAATACAA	CATGCAATTA	1680
AAAATAGATT	CTTTAATTAC	AAAAGAATTT	AATAAGCTTT	TAGCGATCGT	TCAAGATAGT	1740
CCCCAAGATA	GTTACCAATT	AAAAATTCGT	GTCCGACATA	ACAATAAGCT	TCCTAGAGAG	1800
AAATATACGG	AACATGAAAT	AAAACCTGAA	GTTTATGATT	GCAGAAATC	CCACGATCAC	1860
AATGAGCCAA	TCATCTTAAG	CCAGCAAAGC	ACCGGCTTCC	AATGGGCGTT	TAATTTTCATG	1920
TTTGCGTTTT	TTTATAATGT	GGGATCACAT	TTTAGTTTTA	ACCATAATAT	TATCTATGTC	1980
ATGGACGAGC	CAGCCACTCA	TTTGAGCGTG	CCAGCCAGAA	AGGAGTTTAG	GAAATTTTTTA	2040
AAAGAATACG	CTCATAAAAA	TCATGTTACT	TTTGTTTTAG	CCACCCATGA	CCCCTTTTTTA	2100
GTGGATACGG	ATCATTTAGA	TGAAATAAGG	ATTGTGGAAG	AGGAAACAGA	AGGCTCTGTA	2160
ATTAAGAATC	ACTTTAATA	TCCCCTAAAT	AATGCAAGCA	AAGACTCCGA	CGCTTTGGAC	2220
AAAATCAAAC	GCTCTTTAGG	AGTGGGCCAG	CATGTTTTTC	ATAACCCCCA	AAAACACCGA	2280
ATCATTTTTG	TAGAAGGCAT	CACGGATTAT	TGTTATTTGA	GCGCTTTTAA	ATTGTATTTG	2340
CGTTACAAAG	AATACAAGGA	CAACCCCAT	CCTTTCACCT	TCTTACCCAT	TTCAGGGCCT	2400
AAAAACGATT	CAAACGATAT	GAAAGAAACC	ATTGAAAAAC	TTTCCGAGTT	AGACAATCAC	2460
CCTATTGTTT	TGACAGACGA	TGACAGAAAA	TGCGTTTTTA	ACCAACAAGC	AACGAGCGAA	2520
CGATTTAAAA	GAGCTAATGA	AGAAATGCAT	GATCCCATCA	CCATCCTACA	ACTCTCAGAC	2580
TGCGATAGGC	ATTTCAAACA	AATTGAAGAT	TGTTTCAGCG	CAAACGATAG	AAACAAATAC	2640
GCTAAAAATA	AGCAAATGGA	ATTGAGCATG	GCTTTTAAAA	CAAGGCTTTT	GTATGGCGGA	2700
GAAGATGCGA	TAGAAAAACA	AACAAAAAGA	AATTTTAA	AATTATTCAA	ATGGATTGCA	2760
TGGGCTACAA	ACTTGATCAA	AAAC				2784

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431

CAAGCATTTG	GTATCAATAT	GTGTTCTAAA	AAAATAAGAA	ATCTCATTTT	ATGCTTTGGT	60
TTTATTTTAA	GCTTGTGCGC	TGAAGAAAAT	ATCACCAAAG	AAAACATGAC	TGAAACGAAC	120
ACGACTGAAG	AAAACACCCC	TAAAGACGCT	CCCATTCTTT	TGGAAGAAAA	ACGCGCCCAA	180
ACTCTAGAGC	TTAAAGAAGA	AAATGAAGTG	GCAAAAAAGA	TTGATGAAAA	AAGCCTGCTT	240
GAAGAAATCC	ATAAGAAAAA	ACGCCAGCTT	TACATGCTCA	AAGGGGAATT	GCATGAAAAG	300
AATGAATCCA	TCTTATTCCA	ACAAATGGCT	AAAAATAAGA	GCGGCTTTTT	TATAGGCGTG	360
ATCCTTGGCG	ATATAGGGAT	TAACGCTAAT	CCTTATGAGA	AGTTTGAAC	TTTAAGCAAT	420
ATCAAGCTT	CTCCCTTGCT	GTATGGTTTA	AGGAGCGGGT	ATCAAAAGTA	TTTCGCTAAC	480

1005

GGGATTAGCG	CCTTACGCTT	TTATGGGGAA	TATTTAGGGG	GGGCGATGAA	AGGGTTTAAA	540
AGCGATTCTT	TAGCTTCTTA	TCAAACCGCA	AGCTTGAATA	TTGATCTGTT	GATGGATAAG	600
CCTATTGACA	AAGAAAAAAG	GTTTGCCTTA	GGGATATTTG	GAGGCGTTGG	AGTGGGGTGG	660
AATGGGATGT	ATCAAAATTT	AAAAGAGATT	AGAGGGTATT	CACAGCCTAA	CGCCTTTGGG	720
TTGGTGTTAA	ATTTAGGGGT	GAGCATGACG	CTCAACCTCA	AACACCGCTT	TGAATTAGCC	780
CTAAAAATGC	CTCCCTTAAA	AGAAACTTCG	CAAACCTTTT	TATATTATTT	TAAAAGCACT	840
AATATTIATT	ATATTAGTTA	CAACTATTTA	TTG			873

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432

AGATTTTTTA	GAAAGCATAG	GGTTATAAGC	ATGAAAGAAA	TCGTTACAAT	AGAGAATGTG	60
TCTTTTAACT	ACCACAATCG	CGCTATTTTT	AAGGATTTTA	ATTTAAGCAT	TCAAGAAGGG	120
GATTTTTTAT	GCGTTTTAGG	GGAGAGCGGG	AGCGGTAAAA	GCACGCTTTT	AGGCTTGATT	180
TTAGGGCTTT	TAAACCCAG	TCTGGGGAGC	GTTAAAATCT	TTAATGAGAC	CCTTTCAAAC	240
AACGCTTTTT	TACGCCAAAA	AATAGGCTAT	ATCGCTCAGG	GCAATTCCTT	ATTCCCTCAT	300
TTAAACGCCT	TACAAAACAT	GACTTTTTGC	CTTAATTTAC	AAGGCATAAA	CAAACAAGCC	360
GCTCAAAAAG	AAGCCAAAGC	CTTAGCGTTA	AAAATGGGGT	TAGACGAGAG	CCTTATGGAT	420
AAATTCCTTA	ATGAATTGAG	TGGGGGGCAA	GCCCAAAGAG	TGGGCATTAT	TAGGGGGATT	480
ATCCACAGGC	CAGAACTCAT	TTTATTAGAT	GAGCCTTTTA	GCGCTTTAGA	TAGTTTGAAT	540
CGTAAGAATT	TACAGGATCT	CATCAAGAA	ATACACCAA	ATTCTTGCGC	TACTTTCATT	600
ATGGTAACGC	ATGATGAAAA	CGAGGCGCAA	AAGTTAGCCA	CAAAAACCTT	AGAAATCAAA	660
GCCCTTAAAC	AAGAGCAG					678

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

1006

(B) LOCATION 1...1782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433

ATGGCTGATT	TATTGTCCAG	TTTGAAAAAC	CTTTCTAGTA	GTAGTGGGGT	GTATCAATAT	60
TTTGATAAAA	ACCGCCAATT	ACTCTACATC	GGTAAGGCGA	AAAATTTAAA	AAAGCGCATC	120
AAAAGCTATT	TTTCTGTCCG	TAATAATGAA	ATCACGCCCC	ATCCTCGCAC	AAGCTTACGC	180
GTCCAAATGA	TGGTCAAACA	GATCGCTTTT	TTAGAAACCA	TTTGTAGTGA	AAACGAGCAA	240
GACGCTTTGA	TTTTGGAAAA	TTCTTTGATC	AAGCAGCTCA	AGCCTAAATA	CAACATTCTT	300
TTAAGAGACG	ATAAAACTTA	CCCTTATATT	TACATGGATT	TTTCTATTGA	TTTCCCTATC	360
CCTTTAATCA	CACGAAAAAT	CTTAAACAG	CCTGGCGTTA	AATATTTTGG	CCCTTTTACG	420
AGCGGGGCTA	AGGATATTTT	GGACAGCTTG	TATGAATTGC	TCCCTTTGGT	TCAAAAAGAAA	480
AATTGCATCA	AGGATAAAAA	GGCATGCTAG	TTTTATCAAA	TAGAGCGTTG	TAAAGCCCCA	540
TGCGAGGATA	AAATCACTAA	AGAAGAATAT	TTAAAAATCG	CTAAGAATG	TTTAGAAATG	600
ATTGAAATA	AAGACAGGCT	CATCAAAGAG	CTTGAATTGA	AAATGGAGCG	CCTTTCTAGT	660
AACTTGCGTT	TTGAAGAAGC	CTTAATTTAT	AGGGATAGGA	TTGCAAAAAT	CCAAAAATC	720
GCCCCTTTCA	CTTGCAATGA	TTTAGCCAAA	CTCTACGATT	TGGATATTTT	TGCTTTTTTAT	780
GGTGGGAACA	ACAAGGCGGT	GTTAGTGAAA	ATGTTTCATG	GTGGGGGTAA	AATCATTCTT	840
TCAGCGTTTG	AAAAAATCCA	CTCTCTCAAC	GGGTTTGACA	CTGATGAAGC	GATGAAACAA	900
GCCATTATCA	ATCATTACCA	ATCGCATTTG	CCTTTGATGC	CTGAACAAAT	CTTATTGAGC	960
GCTTGTCTTA	ATGAAACGCT	TAAAGAATTG	CAAGAGTTTA	TCTCTCACCA	ATATTCTAAA	1020
AAAATCGCTC	TTAGCATTCC	TAAAAAGGGT	GATAAGCTCG	CTTTAATAGA	AATCGCTATG	1080
AAAAACGCTC	AAGAGATTTT	TAGCCAAGAA	AAAACCTCTA	ATGAAGATCG	GATCTTAGAA	1140
GAAGCGCGAT	CGCTCTTCAA	TTTAGAGTGC	GTGCCCTTATA	GGGTAGAAAT	CTTTGACACA	1200
AGCCACCATT	CAACAGCCCA	ATGCGTGGGG	GGAATGCTCG	TGTATGAAAA	CAATGCATTT	1260
CAAAAAGACT	CITATCGGCG	CTACCATCTA	AAAGGCTCTA	ACGAATATGA	TCAAATGAGC	1320
GAATTGCTCA	CCAGAAGGGC	TTTAGACTTT	GCTAAAGAGC	CACCGCCTAA	TTTGTGGGTG	1380
ATAGATGGAG	GGAGGGCGCA	ATTAAACATC	GCTTTAGAAA	TTTTAAAAAG	CAGCGGGAGT	1440
TTTGTAGAAG	TGATCGCTAT	TTCTAAAGAA	AAAAGGGATT	CTAAGGCTTA	TCGTTCTAAA	1500
GGGGGTGCTA	AAGACATTAT	CCATACGATT	AGTCATACTT	TTAAATTGCT	CCCTAGCGAC	1560
AAACGCTTGC	AGTGGGTGCA	AAAATTGCGC	GATGAAAGCC	ACCGGTATGC	GATAAACTTC	1620
CATAGATCCA	CTAAACTTAA	AAACATGAAA	CAATTCGCTC	TTTTAAAAAG	AAAGGGCATA	1680
GGAGAAGCCA	CGGTGAAAAA	ATTGTTGGAT	TATTTTGGGA	GTTTGAAGC	GATAGAAAAA	1740
GCGAGCGATC	AGGAAAAAAA	CGCCGTTTTA	AAAAAACGAA	AA		1782

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434

AGGAAAAACA	TGAAAAAAG	ATTGAATATA	GGGCTTGTGG	GTTTAGGGTG	CGTGGGGAGC	60
ACGGTTCGCTA	AAATCTTACA	AGAAAAATCA	GAAATCATT	AAGACAGAGC	CGGCGTGGAA	120
ATTAAAAATTA	AAAAAGCGGT	GGTCCGAGAC	GTGAAAAAAC	ACAAGGGCTA	TGCTTTTGAA	180
ATCAGTGATG	ATTTAGAAAG	CGTGATAGAA	GATAAAGGGA	TTGATATTGT	CGTGGAGCTT	240
ATGGGTGGGG	TGGAAGCGCC	TTATCTTTTA	GCTAAAAAAA	CTTTAGCCAA	ACAAAAAGCC	300
TTCGTTACAG	CCAATAAAGC	CATGTTAGCG	TACCACCGCT	ATGAATTAGA	ACAAATCGCT	360

SUBSTITUTE SHEET (RULE 26)

1007

AAAAACACCC	CCATAGGCTT	TGAAGCGAGC	GTGTGTGGGG	GTATCCCCAT	TATCAAGGCT	420
TTAAAGACG	GCTTGAGCGC	TAATCACATC	CTTTCTTTTA	AAGGGATTTT	AAACGGCACG	480
AGCAATTACA	TTTTAAGCCA	GATGTTTAAA	AATCAAGCGA	GCTTTAAGGA	CGCTTTGAAA	540
GACGCCGAGC	ATTTAGGCTA	TGCGGAATTG	AACCCTGAAT	TTGACATTAA	GGGCATTGAT	600
GCGGCCGACA	AATTATTGAT	TTTAGCGTCT	TTAGCGTATG	GCATTGATGC	GAAATTAGAA	660
GAAATCTTGA	TTGAAGGCAT	TGAAAAGATA	GAGCCAGATG	ACATGGAATT	TGCAAAAGAG	720
TTTGGTTATA	GCATCAAAC	TTTAGGCATC	GCTAAAAAAC	ACCAGGATTG	CATTGAATTA	780
AGGGTGCATC	CAAGCATGAT	TAAAAATGAA	TGCATGCTCT	CTAAAGTGGA	TGGGGTGATG	840
AACGTCATCA	GCGTCATAGG	GGATAAGGTG	GGCGAGACTT	TGTATTATGG	GGCTGGGGCT	900
GGAGGAGAGC	CTACCGCAAG	CGCGGTCATT	AGCGATATTA	TAGAAATCGC	AAGGAAAAAA	960
AGCTCTCTAA	TGCTGGGCTT	TGAAACCCCT	CAAAAACCTCC	CCCTAAACC	CAAAGAAGAA	1020
ATCCAATGCG	CTTACTATGC	GCGCTTGTTA	GTGAGCGATG	AAAAAGGGGT	TTTTTCTCAA	1080
ATCAGCGCGA	TTTAGCCCA	AAATGATATT	TCGCTCAACA	ATGTCTTGCA	AAAAGAAATC	1140
CCGCAATCCA	ACAAGGCTAA	AATCTTATTT	TCCACGCACA	CCACCAACGA	AAAATCTATG	1200
CTGAACGCCC	TTAAAGAGCT	TGAAAATTTA	CAAAGCGTGT	TGGATACCCC	TAAAATGATC	1260
CGTTTGAAA	AT					1272

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435

AGTCGCTTTA	AAAGAGCAAT	TGAACAAGCT	TTTAGGCTAG	TGGCCATGAT	AGATTGCGCG	60
ATTATTGGAG	GTGGTCCTGC	AGGTTTGAGT	GCGGGGCTTT	ATGCCACTAG	AGGCGGTGTT	120
AAAAACGCCG	TTTATTTTGA	AAAAGGAATG	CCTGGGGGGC	AAATCACTGG	CAGTAGTGAG	180
ATTGAAAATT	ATCCGGGCGT	TAAGGAAGTG	GTGAGCGGAT	TGGATTTTCAT	GCAACCATGG	240
CAGGAGCAAT	GCTTTTCGCTT	TGGTTTAAAG	CATGAGATGA	CCGCCATTCA	AAGGGTTTCT	300
AAAAAAGGTT	CTCATTTTGT	TATTTTGGCA	GAAGATGGCA	AGACTTTTGA	AGCTAAGAGC	360
GTGATCATCG	CTACCGGTGG	TAGCCCTAAA	CGCACAGGTA	TCAAGGGCGA	GTCAGAATAT	420
TGGGGTAAAG	GCGTTAGCAC	TTGTGCAACA	TGCGATGGCT	TCITTTACAA	AAATAAGGAA	480
GTAGCGGTGC	TTGGTGGAGG	CGATACCGCC	GTAGAAGAGG	CGATTTATCT	AGCCAATATC	540
TGCAAAAAAG	TCTATCTCAT	CCACAGAAGA	GATGGTTTTA	GGTGTGCGCC	TATCACTTTA	600
GAGCATGCTA	AAAACAATAG	TAAGATTGAG	TTTTTAACCC	CITATGTGGT	GGAAGAAATC	660
AAGGGCGATG	CTTCTGGCGT	GTCTTCTTTA	AGCATTAATA	ACACAGCCAC	TAACGAAAAA	720
AGAGAATTAG	TCGTGCCGGG	GCTTTTTTATT	TTTGTGGGTT	ATGATGTGAA	TAACGCCGTG	780
TTGAAGCAAG	AAGATAACTC	CATGCTATGC	GAATGCGATG	AATACGGCTC	TATTGTCGTG	840
GATTTTTCCT	TGAAGACGAA	TGTTTCAGGC	TTGTTTGGCG	CAGGAGATAT	TCGCATTTTT	900
GCCCCCAAGC	AAGTGGTTTG	TGCGGCAAGC	GATGGTGCTA	CGGCAGCCTT	AAGCGTGATT	960
TCTTATTTAG	AACACCAT					978

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid

1008

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436

AAATTATGGG AGTTTAGCTT GCGTGTITTT ATCATTTCCTT TAAATCAAAA AGTGTGCGAT	60
AAATTTGGTT TGGTTTTTAG AGACACCACA ACTTTACTCA ATAATATCAA CGCCACCCAC	120
CACCAAGCGC AAATTTTGA TGCGATTTAT TCCAAGACTT TTGAAGGCGG GTTGCACCCC	180
CTAGTTAAAA AGCATTTACA CCCTTATTTT ATCAGCGCAA ATATCAAAGA CATGGGGATT	240
GCAACCAGTC TCATCAGTGA GGTTCCTAAG TTTTATTACG CTTTAAAAATA CCATGCGAAA	300
TTTATGAGCT TGGGGGAGCT TGGGTGCTAT GCGAGCCATT ATTCGTTGTG GCAAAAATGC	360
ATAGAGCTCA ATGAAGCGAT CTGTATTTTA GAAGACGATA TAACCTTGAA AGAGGATTTT	420
AAAGAGGGCT TGGATTTTTT AGAAAAACAC ATCCAAGAGT TAGGCTATGC GCGTTTGATG	480
CATTTATTGT ATGATGCCAG CGTGAAAAGT GAGCCTTTAA ACCATGAAAA CCAAGAGATA	540
CAAGAGCGTG TGGGGATCAT TAAAGCTTAT AGCCATGGGG TGGGGACGCA AGGCTATGTG	600
ATCAGCCCCA AGATTGCCAA AGTTTTTTTG AAACACAGCC GAAAATGGGT TGTTCCTGTG	660
GATACGATAA TGGACGCTAC TTTTATCCAT GGCGTGAAAA ATCTGGTGTG ACAACCTTTT	720
GTGATCGCTG ATGATGAGCA AATCTCTACG ATAGCGCGAA AAGAAGAACC CTATAGCCCT	780
AAAATCGCTC TAATGAGAGA ACTCCATTTT AAATTTTGA AATGGTGGCA GTTTGTA	837

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437

GGGGATTTTA TAATTTCTAA CATCAGCATA CACCCAAAAA CCATGTTTAA AAACGCTTTA	60
AATATACAAG ATTTTTCATT TAAAAATCAT ACTAGTACAG CCATTATTGG CACAAATGGT	120
GCTGGAAAAAT CAACGCTTAT CAACACTATT CTAGGCATTA GATCAGACTA TAATTTTAAA	180
GCACAAAACA ATAATATTCC ATACCACGAC AATGTTATAC CACAACGCAA GCAATTGGGA	240
GTGTCTCTA ACCTATTCAA CTACCCACCT GGATTAAACG CAAACGACCT TTTTAAATTC	300
TATCAATTTT TTCACAAAAA CTGCACTCTA GATTTGTTTG AAAAAAATCT TTTAAATAAA	360
ACCTACGAAC ACCTAAGCGA CGGACAAAAA CAGCGCTTAA AAATTGACTT AGCTCTTAGC	420
CATCACCCAC AATTAGTTAT TATGGATGAA CCAGAAACCA GTTTAGAGCA AAACGCTCTT	480

SUBSTITUTE SHEET (RULE 26)

1009

ATAAGACTAT	CAAATCTCAT	AAGCTTGCGC	AACACCCCAAC	AACTTACAAG	TATCATCGCC	540
ACTCATGATC	CTATTGTCTT	AGATAGTTGC	GAATGGGTAT	TGCTCCTTAA	GAATGGCAAC	600
ATTGCTCAAT	ACAAACCTTT	AAATTCTATA	TTAAAATCTG	TAGCTAAAAC	TTTAACTTT	660
AAAGAAAAAC	CAACCACAAA	AGACTTATTA	GCGTTACTAA	AGGATATT		708

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438

ATTTATCTC	ATCTCGCTCC	CATTATGCAC	TATCAATTAA	CAAGTTTCAA	TATAATACAA	60
GATCTTTT	TAAC TTGTC	TGTGTTAAGG	ATCAAAATGC	GCGTGTGTTGT	TTGCTTTT	120
GGGGTTT	TATCTAACGG	CTTGGCTCGT	TTTGGCTATG	TGGTTTAAAT	CCCCCTACTC	180
ATTTTATCAG	GGAGTTTAAC	CCCACACCAA	AGCTTCCAAC	TGGGTATTGC	GGTGCTAATG	240
GGCTATGTTT	TTGGGAGCTT	TTTAATCCAA	TTTTTAAGCC	CGTTAATGTC	ATTAGAAAGC	300
ATCGCTAAAA	TCAGTTTAA	ATTAATCACT	TTGAGTTT			339

(2) INFORMATION FOR SEQ ID NO:1439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439

AGTATGGGCG	GATTCAACAG	CATATGGCAT	TGGGTCATG	TTTTATTAGT	GATTGTGTTG	60
TTATTTGGGG	CTAAAAAGAT	CCCAGAATTG	GCTAAAGGTT	TAGGCAGTGG	GATTAAAGAAT	120
TTCAAAAAAG	CCGTGAAAGA	CGATGAAGAA	GAGGCTAAAA	ACGAGCTAAA	AACCCTAGAC	180
GCTCAAGCAA	CACAAACCAA	AGTGCATGAA	ACTAGCGAAA	TTAAAAGCAA	ACAAGAAAGT	240

1010

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440

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AGAAAAACCA ACCACAAAAG ACTTATTAGC GTTACTAAAG GATATTTAAT GGGTGCAATT      60
TTATCTATTT TAAAACCTGA AATCAAATCT TATCTCACCA ATACAAGCGC GCTATTTTGG      120
ACTTTTATTT ATCCTATTTT AATGCTCCTA TTAATAATTT TTGTTTTTTC AAAAAATACC      180
ACTGAAATTT TTTACTTTAA TAACATTATA GGTCTAATGG GACTTCTTAT TATTTCTAGC      240
GCGATCTTTG GTCTCACACA AGCTATAACA AGCTCTAGAT CGCATAATAT ATTCTTATTC      300
TACATGCTAT CACCAGCAAC TTTCAAACAA ATAACCTAG CATTAATCGC TTCAAGACTA      360
ATCGTTGTAA TCCTATATGC TTTTATCTTT ATTGTCTCT CTTTTTATGC GCTCAATATC      420
ATCACTATTC TTAATTTTAA AGCGCTTATT TTGGGGTTTA TTAGCATTTT TTCAAGCGCA      480
TTGTTTGTGT TTTGCTTGGC AATTTTGTGA GCTAGAATTT TTCAAAACGA ACAAGCATC      540
TTAGGATTTT GTAATATCAT CAATCTCTAT GCGCTAATGT CTGTGAATGT TTTTGTTCCT      600
TTAGAATACC TACCTAATAT TGGTCAATTA TTTATCAAAA CATCTATTTT TTAATACCTT      660
AATCAACTTC TAATCAAAGC TTTTCAAGGG ATTGATACTA TACTGGTTTT AGCAACTTCA      720
ACATTTTTC TATTGGTGG CATTATTTTA TTTTACTAA GCGCTAATCG CATGTTACTA      780
ACACCAAAG AACGCATGCG T                                     801

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(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441

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AGAAAACAAG AAATGAAAAA ACTTCTTTTA CTCTTAGAGC ATAAGATCGT AAAAATTGGC      60
TTAATTATTG TGATTGTGTT AGTGGGTTTT TTTCTTTTTT ATGAACAAGA AATCAAAGAA      120

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1011

AAAGCTGTTA	ATGTTTCTCA	AGGTAAATTC	CCCACTTCAT	CTTATTTGTT	TCAAGCTTAC	180
GAAGGCATTA	AGAATAAAAT	AGATACTATC	AATCAAGTGA	AGCCAAACGA	TGAAACTAAA	240
AGCGTTAATG	AGAATATAGA	AAAAACACAA	AAAGATTTAG	ATGATTTTAA	TGCGCTAGTG	300
CAAAAGTTAC	CAAAATTGCG	TAAGGACTTT	AATAAAACAC	TTATTAAACC	ACAAAGTCCA	360
TTTTTCAACT	ACAATACCGC	TAACGAAGAT	GAAAAAAACC	GCCTGGTGAT	TTTAGCGTCT	420
CGTATTAGCA	GCCAAAAAGA	AACGCAACCT	CCCATTCTTA	TAAAAAATAG	CGTTTCTCAC	480
ATAAAATCCA	AAGAAAAACG	AGAACTTGAA	AAAGAATGGG	CAAAACCTAG	TGTTTCTTTT	540
GGTTCCTTTT	CCTTGCTTTC	CAGTCTTCT	TCTTTTTCTT	CTTTTGAAGT	TTCTTTTTTA	600
TCAAGGGGAA	TAGGATTGGA	TTGTGAGAAG	CTCAAATCCT	TTTTAAAGC	TTTTTCAAGT	660
TCGCTATTTT	CCTTATTATC	TTCATTGTTT	TGCCATCCAC	TTTCTCTTTT	TTGCTCTCTA	720
ATAGGATTAA	TCTTTTGTTT	TTCTAAGTTT	TCTAGAGAGC	TAGTGAATGC	GTCTAACAAT	780
TCGCTTGAGT	TTTCATCATT	GTCAAGGCTA	GGATCA			816

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442

AAAATCTTCA	AAAAGGCTTT	AAGGCATAAA	ATGGAAAAAG	TTTGCCTGAG	CGCATGGGGG	60
TTGCCTAAGA	TTTTAGAAGA	AAGATTAAAA	GAAAAATATG	GCGATGATTG	GGAAAAACAT	120
GTTAAGGCTA	AAGCAATAAA	CGAAGAAGAG	CTTGAAGAAC	AAGTCAAAGC	TAAAGCCAAA	180
GAGCAACAAA	AGACACAAAG	AGAAAAACA	CTCAATGGAT	TTTTAAAAAA	AGTTGGTTTA	240
AAAAAGCGTG	ATATGTTACA	AAGCACTATG	TTATTTGATG	AAGTCAAAGA	AGCTGATGTG	300
CTTTTTCAAG	CAGAGCGTAA	AATTGGCGAT	TGGATTTTTA	GCAGTGCGGT	GTTCTTTTTT	360
GCTCTAGCCC	TTATAGAAGC	CATTATTATT	GTATGCTTAT	TGCCGTTAAA	AGAAAAAGTG	420
CCTTATTAG	TAACCTTTTC	AAACGCTACA	CAAAATTTTG	CCATAGTCCA	AAGAGCAGAC	480
AAGAGCATCC	GTGCTAATCA	AGCGCTTGTG	AGACAATTGG	TAGCGTCTTA	TGTTAATAAT	540
AGAGAAAATA	TTTCAAGTAT	AAAAGAGCAA	AACGAAATAG	CCCACGAAAC	CATTAGGTTG	600
CAAAGCGCAT	TTGAAGTGTG	GGATTTTTTT	GAAAAACTGG	TTTCTTATGA	GCATAGCATT	660
TACACTAATA	TAAATCTAAC	ACGAAAAAAT	AGCATTATCA	ATATCGCTTT	AATCAGTAAA	720
ACCCAAGCCA	ATATTGAAAT	ATCCGCACAA	CTTTTTTATA	AAGAAAAAGT	AGAAAGCGAA	780
AAGCGTTATA	GAATAATTAT	GACCTTTGAA	TTTGAACCTA	TTGAAATTGA	TACAAAATCT	840
GTTCCCTTAA	ACCCCTACAG	CTTTATTGTT	ACAGGTTATG	ATGTAAGTGA	AATTGCGATT	900
TTAAAGATT	TAGATGAGAA	AAATAAAGTC	AAAGATGATG	GTGTGAAATC	TAGGATTATC	960
CATGTCGAGA	AAAAAGACCC	TCATATGAGC	CAGTATAAAG	ATGTTAAGGA	GCAA	1014

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

1012

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443

GTTGTGGTAA	TAAGGTTAGT	CCTAAACATG	CTAACATGTC	AAATTAGCTA	TATAAGGATA	60
AGTTATCTTG	TCTCTGTTAG	CGATTTTGTG	ATTGCAAGG	AAAGATTTAT	GGATGAAATT	120
AAAACGCTGT	TAGTGGATTT	TTTCCCGCAG	GCAAAGCATT	TTGGGATAAT	CTTAATCAAG	180
GCTATTGTTG	TCTTTTGTAT	AGGTTTTTAT	TTTTCGTTTT	TCTTACGGAA	CAAAACCATG	240
AAACTCTTAT	CCAAAAAGGA	TGAGATTTTG	GCGAATTTTG	TCGCGCAGGT	TACTTTTATC	300
TTAATCCTTA	TCATTACTAC	AATCATCGCG	CTCAGCACGC	TAGGCGTCCA	AACCACCTCT	360
ATTATCACTG	TTTTAGGAAC	GGTGGGGATT	GCGGTGGCGT	TGGCTTTAAA	AGATTATCTT	420
TCAAGCATTG	CTGGAGGGAT	AATCCTTATT	ATTTTACACC	CTTTCAAAAA	AGGAGACATC	480
ATTGAAATCT	CTGGCCTAGA	GGGCAAAGTA	GAAGCGCTTA	ATTTTTTTAA	TACTTCTTTA	540
CGCTTGCATG	ACGGGCGCTT	GGCGGTTTG	CCTAATAGAA	GTGTCGCTAA	TTCTAATATT	600
ATCAATAGCA	ATAACACTGC	GTGTCGGCGC	ATTGAATGGG	TCTGTGGGGT	AGGGTATGGG	660
AGCGATATTG	AACTGGTGCA	TAAGACTATA	AAAGATGTTA	TTGACGGGAT	GGAAAAAATT	720
GATAAAAACA	TGCCCCACTT	CATTGGAATC	ACGGATTTTG	GACAAAGTTC	GCTGAACTTC	780
ACCATTAGGG	TTTGGGCAAA	GATTGAAGAC	GGGATCTTTA	ATGTGAGGAG	CGAACTCATT	840
GAACGCATCA	AAAACGCCCT	GGACGCTAAT	CGTATTGAAA	TCCCTTTCAA	CAAGCTAGAT	900
ATTTCTATCA	ACAAACAAGA	CTCTTCTAAG				930

(2) INFORMATION FOR SEQ ID NO:1444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444

AGCAAAAGAA	CACAACAAAC	CTTTTTTCTA	TTCAATTGATG	AAACTAAAGA	CTACATTATG	60
CATCCTATAA	TGTTTGCCTA	TATCGCTAAC	GCGCTCGCTC	AAGCTAGAAA	GATCAACGGA	120
ACACTTTTGA	TGGCGTTTCA	AAAAATATCT	CAAGTCAAAAG	AATTAGGCAT	TGATAAAGCA	180
AAGAGTTTGA	TAGGCAACCT	TTCTCAAGTG	ATTATCTACC	CCACAAAAGA	TACTGATGAA	240
TTAATAGAAT	GTGGCGTCCC	ATTAAGCGAT	AGTGAAATCA	ATTTCTTACA	CAACACGGAC	300
ATGAGAGCCA	GACAAGTGCT	AGTAAAAAAT	ATCGTTACAA	ACGCTTCAGC	TTTTATTGAA	360
ATTGATTTAA	AAAAGATTTG	CAAGAACTAC	TTTATATTCT	TGATAGCAAT	GCTGGTAATA	420
GAAAAATCCT	CAATGATCTT	AAAAAAGCAA	ACCAAGAAAC	TTATAAGGAA	GAGTATT	477

1013

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...774
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445

CTCCTTAAAA	ATATTGATGA	GAAAAAGCTT	TCCGTAAGTA	AGGTAAATGA	AAAAAGGCAC	60
ATGGATTTTA	AAAAATGCCC	TAATTTTGAA	AAAAAATGTG	CGTTTCCTTG	TTTCTCAAAT	120
TTGGTTTTAC	TTATTGAAAT	CCACTCTAAA	GGACTACACA	TGCAAAAAAA	GAAACCCAAG	180
AACCCGCAAC	CGAATTTATT	TAGCATCTTA	GATAAGGGCG	ATGTTGCAAC	AAACAATCCT	240
GTTGAAGAGT	CAGACAAGGC	CAATAAAATA	CAAGAGCCAC	TCCCTTATGT	CGTGAAAAACG	300
CAAATCAATA	AAGCAAGCAT	GATTTCTAGA	GATCCTATTG	AATGGGCAAA	GTATTTAAGC	360
TTTGAAAAAC	GAGTCTATAA	GGATAATAGT	AAAGAAGATG	TCAATTTCTT	TGCCAATGGT	420
GAGATAAAAG	AAAGTTCTCG	TGTTTATGAA	GCGAATAAAG	AAGGGTTTGA	AAGGCGCATC	480
ACTAAAAGAT	ACGATCTGAT	TGATAGAAAT	ATTGATAGAA	ATAGAGAATT	TTTTATAAAA	540
GAAATTGAAA	TTCTAACCCA	CACAAACAGC	TTAAAAGAAT	TGAAAGAGCA	AGGGTTAGAA	600
ATCCAATTGA	CCCACCATAA	TGAAACGCAT	AAGAAAGCCT	TAGAAAATGG	CAATGAAATC	660
GTTAAAGAAT	ACGACCATCT	TAAAGATATT	TACCAAGAAG	TAGAAAGAAC	AAAAGATGGT	720
GGATTGGTAA	GAGAAATAAT	CCCCAGTATT	TCTAGCGCTG	AGTATTTTAC	CCTT	774

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...274
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446

Asp	Ala	Arg	Ser	Phe	Phe	Leu	Arg	Leu	Val	Ala	Met	Ala	Leu	Cys	Leu
1				5					10					15	
Ile	Leu	Ile	Asn	Ser	Arg	Gly	Val	Ala	Met	Gly	Tyr	Ala	Ser	Lys	Leu
			20				25						30		
Ala	Leu	Lys	Ile	Cys	Leu	Val	Gly	Leu	Cys	Leu	Phe	Ser	Thr	Leu	Gly
		35				40					45				
Asp	Glu	His	Leu	Glu	Gln	Lys	Gly	Asn	Tyr	Ile	Tyr	Lys	Gly	Glu	Glu

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1014

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      50      55      60
Ala Tyr Asn Asn Lys Glu Tyr Glu Arg Ala Ala Ser Phe Tyr Lys Ser
65      70      75      80
Ala Ile Lys Asn Gly Glu Ser Leu Ala Tyr Ile Leu Leu Gly Ile Met
      85      90      95
Tyr Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val Glu
      100      105      110
Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn Asn
      115      120      125
Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu Lys
      130      135      140
Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr Asn
145      150      155      160
Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val Pro
      165      170      175
Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His Lys
      180      185      190
Gly Asn Val Glu Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser Gly
      195      200      205
Asn Asp Gln Leu Gly Ile Glu Pro Asp Lys Asp Lys Ala Val Val Tyr
      210      215      220
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Glu Gly Leu
225      230      235      240
Ser Glu Pro Tyr Arg Tyr Gly Leu Gly Val Glu Lys Asp Lys Lys Lys
      245      250      255
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
      260      265      270
Cys Lys

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(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447

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Thr Met Lys Asn Thr Ser Ser Ser Thr Thr Leu Thr Met Asn Asp Thr
1      5      10      15
Ile Ala Ala Ile Ala Thr Pro Leu Gly Lys Gly Ala Ile Ser Ile Ile
      20      25      30
Lys Ile Ser Gly His Asn Ala Leu Asn Ile Leu Lys Gln Leu Thr Gln
      35      40      45
Lys Gln Asp Phe Thr Pro Arg Tyr Ala Tyr Val Cys Asp Ile Phe Ser
      50      55      60
Asp Gly Val Leu Leu Asp Lys Ala Leu Val Ile Tyr Phe Lys Ala Pro
65      70      75      80
Tyr Ser Phe Thr Gly Glu Asp Val Cys Glu Ile Gln Cys His Gly Ser
      85      90      95
Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala Cys Leu Asn Leu Gly Ala
      100      105      110

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1015

Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys Lys Ala Phe Leu Asn His
 115 120 125
 Lys Met Asp Leu Ser Glu Ile Glu Ala Ser Val Gln Leu Ile Leu Cys
 130 135 140
 Glu Asp Glu Ser Val
 145

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448

Asn Leu Ile Tyr Arg Ser Ser Gln Arg Ser Ala Ala Ala Cys Val Val
 1 5 10 15
 Arg Leu Asn Lys Glu Pro Met Ile Glu Tyr Leu Lys Ser Asn Ile Lys
 20 25 30
 Leu Ile Asp Glu Met Ile Ala Ser Gly Tyr Glu Asp Lys Glu Thr Leu
 35 40 45
 Lys Lys Arg Arg Asp Ala Met Gln Ala Trp Val Asp Lys Pro Val Leu
 50 55 60
 Leu Glu Pro Asp Ser Asn Ala Gln Tyr Ala Val Ile Glu Ile Asp
 65 70 75 80
 Val Ala Glu Ile Thr Glu Pro Ile Leu Ala Cys Pro Asn Asp Pro Asp
 85 90 95
 Asp Val Ala Thr Leu Ser Glu Val Leu Ala Asp Thr Thr Gly Lys Arg
 100 105 110
 Pro His Ala Ile Asp Glu Val Phe Ile Gly Ser Cys Met Thr Asn Ile
 115 120 125
 Gly His Phe Arg Ala Phe Gly Glu Ile Val Lys Asn Ala Pro Pro Ser
 130 135 140
 Gln Ala Arg Leu Trp Val Val Pro Pro Ser Lys Met Asp Glu Gln Glu
 145 150 155 160
 Leu Ile Asn Glu Gly Tyr Tyr Ala Ile Phe Gly Ala Ala Gly Ala Arg
 165 170 175
 Thr Glu Val Pro Gly Cys Ser Leu Cys Met Gly Asn Gln Ala Arg Val
 180 185 190
 Arg Asp Asn Ala Val Val Phe Ser Thr Ser Thr Arg Asn Phe Asp Asn
 195 200 205
 Arg Met Gly Arg Gly Ala Lys Val Tyr Leu Gly Ser Ala Glu Leu Gly
 210 215 220
 Ala Ala Cys Ala Leu Leu Gly Arg Ile Pro Thr Lys Glu Glu Tyr Met
 225 230 235 240
 Asn Leu Val Ser Glu Lys Leu Glu Ser Gln Lys Asp Lys Ile Tyr Arg
 245 250 255
 Tyr Met Asn Phe Asn Leu Met Glu Asn Phe Arg Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:1449:

1016

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449

```

Lys Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu
1      5      10      15
Phe Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu
20      25      30
Phe Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro
35      40      45
Cys Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe
50      55      60
Ser Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys
65      70      75      80
Thr Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala
85      90      95
Ser Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala
100     105     110
Ile Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met
115     120     125
Asn Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile
130     135     140
Gln Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Glu Thr
145     150     155     160
Tyr Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Ile Ile Ala Leu Leu
165     170     175
Thr Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Asn Thr
180     185     190
Pro Thr Tyr Val Pro Thr Val Asn Lys Thr Gln Leu Glu Asn His Thr
195     200     205
Glu Leu Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys
210     215     220
Glu Gln Leu Gly Met Leu Ala Thr Phe Ile Ser Pro Asn Ser Pro Val
225     230     235     240
Ile Glu Tyr Asp Asp Asp Gly Leu Ile Gly Glu Arg Leu Arg Gln Ile
245     250     255
Thr Glu Ser Leu Asn Val Glu Val Lys His Gln Glu Asn Ile Ser Tyr
260     265     270
Lys Gln Ala Thr Ser Phe Ser Lys Asn Phe Arg Lys His Asp Ala Phe
275     280     285
Phe Lys Asn Ser Thr Leu Ile Leu Asn Thr Pro Thr Thr Lys Ser Gly
290     295     300
Leu Ile Leu Ser Gln Ile Gly Leu Leu Glu Tyr Lys Pro Leu Lys Ile
305     310     315     320
Leu Ser Thr Gln Ile Asn Phe Asn Pro Ser Leu Leu Leu Leu Thr Gln
325     330     335
Pro Lys Asp Arg Lys Asn Leu Phe Ile Val Asn Ala Leu Gln Asn Ser
340     345     350
Asp Glu Thr Leu Ile Glu Tyr Ala Ser Leu Leu Glu Ser Asp Leu Arg
355     360     365

```

SUBSTITUTE SHEET (RULE 26)

1017

```

His Asp Trp Val Asn Tyr Ser Ser Ala Ile Gly Leu Glu Met Phe Leu
 370                               375                               380
Asn Thr Leu Asp Pro His Phe Lys Lys Ser Phe Gln Glu Ser Leu Glu
 385                               390                               395                               400
Asp Asn Gln Val Arg Tyr His Asn Gln Ile Tyr Gln Ala Leu Gly Tyr
                               405                               410                               415
Ser Phe Glu Pro Ile Lys Asn Glu Ser Glu Thr Lys Lys Glu
                               420                               425                               430

```

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450

```

Tyr Leu Asp Asn Tyr Leu Asn Thr Phe Ile Phe Asn Gly Phe Leu Arg
 1                               5                               10                               15
Lys Ile Asp Tyr Tyr Ala Ser Gly Lys Leu Lys Arg Ile Gly Ala Val
 20                               25                               30
Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr Asn
 35                               40                               45
Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala Glu
 50                               55                               60
Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys Glu
 65                               70                               75                               80
Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu Gln
 85                               90                               95
Val Asp Ser Asn Leu Leu Pro Lys Asn Ile Glu Lys His Ser Leu Lys
 100                              105                              110
Ile Gly Val Gly Gly Ile Leu Gly Ala Leu Ala Tyr Asp Ser Thr Lys
 115                              120                              125
Thr Leu Ile Asp Gln Ala Thr His Gln Ile Tyr Gly Ser Glu Leu Phe
 130                              135                              140
Tyr Leu Ile Gly Arg Trp Gly Phe Leu Gly Asn Ala Pro Trp Lys
 145                              150                              155                              160
Asp Ser Leu Ile Glu Ser Asp Ala His Thr Arg Asn Tyr Val Leu Tyr
 165                              170                              175
Asn Ser Tyr Leu Phe Tyr Ser Tyr Gly Asp Lys Phe His Leu Lys Leu
 180                              185                              190
Gly Arg Tyr Leu Ser Asn Met Asp Phe Met Ser Ser Tyr Thr Gln Gly
 195                              200                              205
Phe Glu Leu Asp Tyr Lys Ile Asn Ser Lys Ile Ala Leu Lys Trp Phe
 210                              215                              220
Ser Ser Phe Gly Arg Ala Leu Ala Phe Gly Gln Trp Ile Arg Asp Trp
 225                              230                              235                              240
Tyr Ala Pro Ile Val Thr Glu Asp Gly Arg Lys Glu Val Tyr Asp Gly
 245                              250                              255
Ile His Ala Ala Gln Leu Tyr Phe Ser Ser Lys His Val Gln Val Met
 260                              265                              270
Pro Phe Ala Tyr Phe Ser Pro Lys Ile Tyr Gly Ala Pro Gly Val Lys

```

1018

```

      275      280      285
Ile His Ile Asp Ser Asn Pro Lys Phe Lys Gly Leu Gly Leu Arg Ala
290      295      300
Gln Thr Thr Ile Asn Val Ile Phe Pro Val Tyr Ala Lys Asp Leu Tyr
305      310      315      320
Asp Val Tyr Trp Arg Asn Ser Lys Ile Gly Glu Trp Gly Ala Ser Leu
      325      330      335
Leu Ile His Gln Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Phe Gly
      340      345      350
Tyr Tyr Gln Asn Phe Gly Asn Ala Asn Ala Arg Ile Gly Trp Tyr Gly
      355      360      365
Asn Pro Ile Pro Phe Asn Tyr Arg Asn Asn Ser Val Tyr Gly Gly Val
370      375      380
Phe Ser Asn Ala Ile Thr Ala Asp Ala Val Ser Gly Tyr Val Phe Gly
385      390      395      400
Gly Gly Val Tyr Arg Gly Phe Leu Trp Gly Ile Leu Gly Arg Tyr Thr
      405      410      415
Tyr Ala Thr Arg Ala Ser Glu Arg Ser Ile Asn Leu Asn Leu Gly Tyr
      420      425      430
Lys Trp Gly Ser Phe Ala Arg Val Asp Val Asn Leu Glu Tyr Tyr Val
      435      440      445
Val Ser Met His Asn Gly Tyr Arg Leu Asp Tyr Leu Thr Gly Pro Phe
450      455      460
Asn Lys Ala Phe Lys Ala Asp Ala Gln Asp Arg Ser Asn Leu Met Val
465      470      475      480
Ser Met Lys Phe Phe Phe
      485

```

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451

```

Val Tyr Ala Gly Leu Ala Ile Ala Ile Gly Met Leu Ile Asp Ser Ser
1      5      10      15
Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala Asn Thr Lys
      20      25      30
Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu Ile Ala Val
      35      40      45
Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe Val Pro Ile
      50      55      60
Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro Leu Ala Gln
      65      70      75      80
Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser Ile Thr Ile
      85      90      95
Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro His Ser Glu
      100      105      110
Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro Leu Leu Glu
      115      120      125

```

1019

```

Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala Phe Val Phe
130      135      140
Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys Asn Phe Met
145      150      155      160
Pro Ala Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu Thr Thr Pro
      165      170      175
Ser Ile Ser Leu Asp Gln Ser Lys Asp Leu Met Leu Asn Ile Glu Ser
      180      185      190
Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val Ala Arg Thr
      195      200      205
Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn Gln Thr Asp
210      215      220
Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val Lys Thr Lys
225      230      235      240
Asp Glu Leu Val Arg Lys Asn His Gly Phe Phe Lys Arg Leu
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452

```

Trp Leu Phe Leu Thr Cys Tyr Gly Ser Val Ile Lys Lys Gly Tyr Ile
1      5      10      15
Arg Gly Asp Leu Met Arg Ile Val Arg Asn Leu Phe Leu Val Ser Phe
      20      25      30
Val Ala Tyr Ser Ser Ala Phe Ala Ala Asp Leu Glu Thr Gly Thr Lys
      35      40      45
Asn Asp Lys Lys Ser Gly Lys Lys Phe Tyr Lys Leu His Lys Asn His
      50      55      60
Gly Ser Glu Thr Glu Thr Lys Asn Asp Lys Lys Leu Tyr Asp Phe Thr
      65      70      75      80
Lys Asn Ser Gly Leu Glu Gly Val Asp Leu Glu Lys Ser Pro Asn Leu
      85      90      95
Lys Ser His Lys Lys Ser Asp Lys Lys Phe Tyr Lys Gln Leu Ala Lys
      100      105      110
Asn Asn Ile Ala Glu Gly Val Ser Met Pro Ile Val Asn Phe Asn Lys
      115      120      125
Ala Leu Ser Phe Gly Pro Tyr Phe Glu Arg Thr Lys Ser Lys Lys Thr
      130      135      140
Gln Tyr Met Asp Gly Gly Leu Met Met His Ile Arg Phe
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
 (B) TYPE: amino acid

1020

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453

```

Pro Lys Ile Ala Pro Leu Ala Met Ala Leu Asn Pro Lys Thr Phe Gln
1           5           10           15
Pro Leu Trp Ile Ala Leu Val Arg Ala Thr Leu Leu Gly Trp Gly His
          20           25           30
Arg Asn Leu Ser His Val Ala Gly Val Leu Asn Ala Ser Phe Leu Ala
          35           40           45
His Phe Ile Lys Asp Pro Val Lys Thr Ala Lys Leu Ser His Lys Phe
          50           55           60
Asn Asp Glu Arg Pro Tyr Pro Met Pro Ala Phe Ser Gln Phe Ser Asp
65           70           75           80
Gln Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys
          85           90           95
Asn Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His
          100          105          110
Ser Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu
          115          120          125
Ala Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg
          130          135          140
Ala Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys
145          150          155          160
Leu Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala
          165          170          175
Gln Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys
          180          185          190
His Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val
          195          200          205
Leu Ser Phe Leu Ala Tyr Asp Trp Lys Arg Lys Val Trp Ser Glu Val
210          215          220
His
225

```

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...381

1021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454

```

Thr Trp Arg Tyr Gln Leu Gly Ser Leu Lys Gly Lys Ile Gln Met Ile
1      5      10      15
Lys Ser Val Glu Ile Glu Asn Tyr Lys Asn Phe Glu His Leu Lys Met
20      25      30
Glu Asn Phe Lys Leu Ile Asn Phe Thr Gly Gln Asn Asp Ala Gly
35      40      45
Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys Asp
50      55      60
Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn Ile
65      70      75      80
Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr Phe
85      90      95
Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu Phe
100     105     110
Glu His Ala Thr Ile Pro Leu Thr Ile Gln Tyr Pro Thr Gln Thr Ser
115     120     125
Tyr Ser Lys Asp Ile Asn Leu Asn Ser Asp Asp Ala His Met Thr Asn
130     135     140
Leu Ile Asn Thr Thr Ile Thr Lys Pro Gln Leu Gln Phe Ser Tyr Asn
145     150     155     160
Pro Ser Leu Ser Pro Met Thr Met Thr Tyr Glu Phe Glu Arg Gln Asn
165     170     175
Leu Gly Leu Ile His Ser Asn Leu Asp Lys Ile Ala Gln Thr Tyr Lys
180     185     190
Glu Asn Ala Met Phe Ile Pro Ile Glu Leu Ser Ile Val Asn Ser Leu
195     200     205
Lys Ala Leu Glu Asn Leu Gln Leu Ala Ser Lys Glu Lys Glu Leu Ile
210     215     220
Glu Ile Leu Gln Cys Phe Asn Pro Asn Ile Leu Asn Ala Asn Thr Ile
225     230     235     240
Arg Lys Ser Val Tyr Ile Gln Ile Lys Asp Glu Asn Thr Pro Leu Glu
245     250     255
Glu Ser Pro Lys Arg Leu Leu Asn Leu Phe Gly Trp Gly Phe Ile Lys
260     265     270
Phe Phe Ile Met Val Ser Ile Leu Ile Asp Asn Arg Val Lys Tyr Leu
275     280     285
Phe Ile Asp Glu Ile Glu Ser Gly Leu His His Thr Lys Met Gln Glu
290     295     300
Phe Leu Lys Ala Leu Phe Lys Leu Ala Gln Lys Leu Gln Ile Gln Ile
305     310     315     320
Phe Ala Thr Thr His Asn Lys Glu Phe Leu Leu Asn Ala Ile Asn Thr
325     330     335
Ile Ser Asp Asn Glu Thr Gly Val Phe Lys Asp Ile Ala Leu Phe Glu
340     345     350
Leu Glu Lys Glu Ser Ala Ser Gly Phe Ile Arg His Ser Tyr Ser Met
355     360     365
Leu Glu Lys Ala Leu Tyr Arg Gly Met Glu Val Arg Gly
370     375     380

```

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

1022

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455

```

Thr His Cys Leu Phe Leu Gly Gly Ser Ile Lys Ile Leu Leu Ile Leu
1      5      10      15
Lys Glu Gly Ile Asp Leu Asn His Gly Tyr Tyr Gln Leu Gly Lys Tyr
      20      25      30
Thr Ile Lys Asp Asp Phe Ile Pro Ser Lys Lys Ala Val Val Glu Asp
      35      40      45
Val Leu Ile Gln Ser Ser Asn Val Gly Met Ile Lys Ile Ser Lys Ser
      50      55      60
Leu Asn Pro Glu Asp Phe Tyr Asn Gly Leu Leu Gly Tyr Gly Phe Ser
      65      70      75      80
Gln Lys Thr Gly Ile Asp Leu Ser Leu Glu Ala Thr Gly Lys Ile Pro
      85      90      95
Pro Leu Ser Ala Phe Lys Arg Glu Val Leu Lys Gly Ser Val Ser Tyr
      100      105      110
Gly Tyr Gly Leu Asn Ala Thr Phe Leu Gln Leu Leu Arg Ala Tyr Ala
      115      120      125
Val Phe Ser Asn Glu Gly Lys Leu Thr Thr Pro Tyr Leu Val Gln Arg
      130      135      140
Glu Thr Ala Pro Asn Gly Asp Ile Tyr Ile Pro Ser Pro Lys Pro Thr
      145      150      155      160
Phe Gln Val Ile Ser Pro Lys Ser Ala Arg Lys Met Lys Glu Thr Leu
      165      170      175
Ile Lys Val Val Arg Tyr Gly Thr Gly Lys Asn Ala Gln Phe Glu Gly
      180      185      190
Leu Tyr Ile Gly Gly Lys Thr Gly Thr Ala Arg Val Ala Lys Asn Gly
      195      200      205
Ser Tyr Ser Ala Glu Ser Tyr Asn Ser Ser Phe Phe Gly Phe Ala Glu
      210      215      220
Asp Glu Arg Gln Val Phe Thr Ile Gly Val Val Ile Leu Gly Ser His
      225      230      235      240
Gly Lys Glu Glu Tyr Tyr Ala Ser Lys Ile Ala Ala Pro Ile Phe Lys
      245      250      255
Glu Ile Thr Glu Ile Leu Val Arg Tyr Asn Tyr Leu Ser Pro Ser Ile
      260      265      270
Ala Ile Gln Asn Ala Leu Glu Lys Asn Arg Leu Lys
      275      280

```

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456

SUBSTITUTE SHEET (RULE 26)

1023

```

Asp Lys Lys Ile Leu Leu Ile Ile Gln Gly Lys Phe Met Glu Phe His
1      5      10      15
Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser Ala Leu Val Ala
      20      25      30
Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile Val Phe Lys Leu
      35      40      45
Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu Ser Ile Leu Ile
      50      55      60
Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val Ser Ala Ser Phe
      65      70      75      80
Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala Trp Ile Val Ile
      85      90      95
Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser Gly Tyr Phe Glu
      100      105      110
Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu Asp His Arg Ile Leu
      115      120      125
Val Ile Leu Ile Gly Phe Cys Leu Ala His Phe
      130      135

```

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457

```

Pro Lys Pro Lys Gly Val Cys Pro Lys Asn Leu Met Ser Lys Arg Ala
1      5      10      15
Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro Lys Pro Lys Ile Lys
      20      25      30
Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala Tyr Pro Leu Lys Pro
      35      40      45
His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser Leu Leu Ala Pro Ile
      50      55      60
Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn Ala Ile Lys Pro Asp
      65      70      75      80
Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met Pro Met Lys Ile Gln
      85      90      95
Lys

```

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1024

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458

```

Arg Asn Asp Phe Lys Gly Val Arg Lys Met Ala Leu Arg Val Leu Leu
1      5      10      15
Phe Phe Cys Phe Leu Phe Leu Gln Ala Glu Asp Lys Ser Gln Glu Leu
20      25      30
Ser Ser Ile Gln Lys Gln Met Ala Leu Val Asp Lys Lys Leu Ala Lys
35      40      45
Asp Asp Asn Val Trp Leu Lys Lys Phe Glu Asn Tyr Lys Ile Tyr Asn
50      55      60
Gln Ile Tyr Thr Glu Lys Glu Ser Val Arg Gln Glu Leu Arg Arg Leu
65      70      75      80
Lys Asn Lys Lys Ser Lys Asp Leu Leu Lys Ile Ser Thr Leu Glu His
85      90      95
Thr Leu Lys Ala Leu Glu Ser Gln Gln Lys Met Phe Glu Ser Tyr Gly
100     105     110
Val Asn Pro Phe Lys Asp Leu Ile Glu Arg Pro Asn Ile Pro Asn Ile
115     120     125
Pro Asn Ile Ala Asn Pro Ile Ala Ile Ile Asp Gly Ile Ser Phe Ile
130     135     140
Lys Ser Met Arg Leu Lys His Glu Asn Leu Lys Asn Asn Gln Thr Ser
145     150     155     160
Leu Gly Glu Val Leu Lys Leu Leu Asp Gln Lys His Gln Leu Leu Asn
165     170     175
Gln Trp His Ala Leu Asp Lys Ser Ala Lys Leu Ser Asp Glu Ile Tyr
180     185     190
Gln Thr Gln Ala Lys Arg Leu Glu Leu Gln Gly Ala Gln Asn Ile Leu
195     200     205
Lys Thr Thr Ile Gly Ile Phe Gln Lys Asp Ser Asp Glu Ala Ile Ser
210     215     220
Ile Val Lys Ser Gln Val Lys Asn Gln Leu Phe Lys Leu Val Tyr Val
225     230     235     240
Phe Leu Ala Ala Leu Leu Ser Val Val Phe Ala Trp Ile Leu Lys Ile
245     250     255
Ile Ser Ser Lys Tyr Ile Glu Asn Asn Glu Arg Val Tyr Thr Val Asn
260     265     270
Lys Ala Ile Asn Phe Val Asn Val Ser Val Ile Val Leu Ile Phe Leu
275     280     285
Phe Ser Tyr Leu Glu Asn Val Thr Tyr Leu Val Thr Val Leu Gly Phe
290     295     300
Ala Ser Ala Gly Leu Ala Ile Ala Met Lys Asp Leu Phe Met Ser Leu
305     310     315     320
Leu Gly Trp Phe Ile Leu Ile Gly Gly Ser Val His Val Gly Asp
325     330     335
Arg Val Arg Ile Ala Lys Gly Thr Asp Ile Phe Ile Gly Asp Val Leu
340     345     350
Asp Ile Ser Met Leu His Ile Thr Ile Leu Glu Asp Val Thr Phe Thr
355     360     365
Thr Tyr Thr Asn Asn Arg Arg Ala Gly Arg Ile Ile Phe Val Pro Asn
370     375     380
Asn Tyr Ile Phe Thr Thr Met Phe Ala Asn Tyr Ser His Phe Gly Met
385     390     395     400
Lys Thr Val Trp Asp Gly Val Asp Phe Cys Val Thr Phe Asp Ser Asp
405     410     415
Phe Lys Lys Ala Ser Lys Ile Ala Leu Asn Ile Ala Thr Glu Leu Ser
420     425     430

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SUBSTITUTE SHEET (RULE 26)

1025

```

Lys Glu Tyr Thr Asp Ile Thr Tyr Lys Gln Leu Asn Lys Met Arg Asp
      435                      440                      445
Arg Tyr Ser Leu Arg Ser Leu Ser Val Lys Pro Arg Cys Phe Leu Met
      450                      455                      460
Pro Glu Asn Asn Gly Ile Lys Ile Ser Val Trp Tyr Gln Thr Asn Ser
465      470                      475                      480
Tyr Ala Thr Met Ser Leu Arg Ser Lys Ile Val Ala Glu Ile Val Glu
      485                      490                      495
Ala Phe Leu Lys Glu Glu Asn Ile His Ile Ala Tyr Thr Thr Ser Lys
      500                      505                      510
Leu Leu Lys Val Asp Ala Asp Ala Leu Gly Asp Gly Phe Gly Asn Lys
      515                      520                      525
Arg Glu Gln Lys
      530

```

(2) INFORMATION FOR SEQ ID NO:1459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459

```

Arg Ser Glu Arg Met Gln Glu Ile Leu Ile Pro Leu Lys Glu Lys Ser
1      5      10      15
Tyr Lys Val Phe Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys
      20      25      30
Ala Leu Ile Ile Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr
      35      40      45
Leu Leu Glu Arg Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu
      50      55      60
Ser Gly Glu Lys Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn
      65      70      75      80
Asn Ala Phe Glu Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu
      85      90      95
Gly Gly Gly Val Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr
      100     105     110
Phe Arg Gly Ile Asp Phe Ile Asn Ile Pro Thr Thr Leu Leu Ala Gln
      115     120     125
Val Asp Ala Ser Val Gly Gly Lys Thr Gly Ile Asn Thr Pro Tyr Gly
      130     135     140
Lys Asn Leu Ile Gly Ser Phe His Gln Pro Lys Ala Val Tyr Met Asp
      145     150     155     160
Leu Ala Phe Leu Lys Thr Leu Glu Lys Arg Glu Phe Gln Ala Gly Val
      165     170     175
Ala Glu Ile Ile Lys Met Ala Val Cys Phe Asp Lys Asn Leu Val Glu
      180     185     190
Arg Leu Glu Thr Lys Asp Leu Lys Asp Cys Leu Glu Glu Val Ile Phe
      195     200     205
Gln Ser Val Asn Ile Lys Ala Gln Val Val Val Gln Asp Glu Lys Glu
      210     215     220
Arg Asn Ile Arg Ala Gly Leu Asn Tyr Gly His Thr Phe Gly Met Leu

```

SUBSTITUTE SHEET (RULE 26)

1026

```

225          230          235          240
Ile Glu Asn Glu Thr Asn Tyr Glu Arg Phe Leu His Gly Glu Ala Ile
          245          250          255
Ala Ile Gly Met Arg Met Ala Asn Asp Leu Ala Leu Ser Leu Gly Met
          260          265          270
Leu Thr Leu Lys Glu Tyr Glu Arg Ile Glu Asn Leu Leu Lys Lys Phe
          275          280          285
Asp Leu Ile Phe Asn Tyr Gln Ile Thr Asp Ile Gln Lys Phe Tyr Glu
          290          295          300
Arg Leu Phe Leu Asp Lys Lys Ser Glu Asn Gln Thr Leu Lys Phe Ile
305          310          315          320
Leu Pro Lys Gly Val Gly Ala Phe Glu Ile Ala Ser His Ile Pro Lys
          325          330          335
Glu Thr Ile Leu Lys Val Leu Glu Lys Trp His
          340          345

```

(2) INFORMATION FOR SEQ ID NO:1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460

```

Lys Ser Lys Ser Met Lys Leu Arg Arg Gly Lys Ile Met Pro Phe Ser
1          5          10          15
Lys Phe Leu Glu Asn Leu Thr Ala Pro Phe Lys Arg Ile Lys Asn Arg
          20          25          30
Ser Leu Val Leu Ala Leu Gly Phe Leu Ile Leu Thr Phe Cys Leu Leu
          35          40          45
Leu Phe Leu Ile Leu Ser Asp Val Ser Arg Leu Ile Ser Ser Lys Asp
50          55          60
Phe Leu Tyr Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp
65          70          75          80
Glu Asn Tyr Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu
          85          90          95
Ala Phe Leu Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys
          100          105          110
Arg Glu Ser Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe
          115          120          125
Phe Ile Ser Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg
130          135          140
Leu Asp Thr Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu
145          150          155          160
Asn Ala Phe Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile
          165          170          175
Ala Gly Val Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr
          180          185          190
Leu Lys Lys Pro
195

```

1027

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461

```

Met Lys Pro Leu His Phe Ser His Leu Asp Arg Glu Gln Ser Gly Asp
1          5          10          15
Val Gly Phe Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu
20          25          30
Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu
35          40          45
Leu Lys Lys Ile Leu Leu Glu Asn Arg Lys Lys Ser Val Leu Glu
50          55          60
Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln
65          70          75          80
Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser
85          90          95
Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
100         105         110
Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
115         120         125
Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr
130         135         140
Leu Ile Asn Lys Tyr Leu Pro Ser Ala Gln Ser Gln Leu Pro Leu Lys
145         150         155         160
Ile Ser Lys Asp Ser Asp Gly Leu Leu Val Gln Phe Gly Val Ser Ile
165         170         175
Asp Leu Gln

```

(2) INFORMATION FOR SEQ ID NO:1462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 452 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462

SUBSTITUTE SHEET (RULE 26)

1028

Phe Lys Arg Tyr Phe Ile Thr Met Lys Ile Phe Gly Thr Asp Gly Val
 1 5 10 15
 Arg Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu
 20 25 30
 Gly Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys
 35 40 45
 Ile Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn
 50 55 60
 Ala Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile
 65 70 75 80
 Gly Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg
 85 90 95
 Cys Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp
 100 105 110
 Asn Gly Ile Lys Phe Phe Asn Ser Tyr Gly Tyr Lys Leu Lys Glu Glu
 115 120 125
 Glu Glu Arg Ala Ile Glu Glu Ile Phe His Asp Glu Glu Leu Leu His
 130 135 140
 Ser Ser Tyr Lys Val Gly Glu Ser Val Gly Ser Ala Lys Arg Ile Asp
 145 150 155 160
 Asp Val Ile Gly Arg Tyr Ile Ala His Leu Lys His Ser Phe Pro Lys
 165 170 175
 His Leu Asn Leu Gln Lys Leu Arg Ile Val Leu Asp Thr Ala Asn Gly
 180 185 190
 Ala Ala Tyr Lys Val Ala Pro Val Val Phe Ser Glu Leu Gly Ala Asp
 195 200 205
 Val Leu Val Ile Asn Asp Glu Pro Asn Gly Cys Asn Ile Asn Glu Gln
 210 215 220
 Cys Gly Ala Leu His Pro Asn Gln Leu Ser Gln Glu Val Lys Lys Tyr
 225 230 235 240
 Arg Ala Asp Ile Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Leu Val
 245 250 255
 Val Ala Asp Asn Leu Gly Asn Ile Val His Gly Asp Lys Leu Leu Gly
 260 265 270
 Val Leu Gly Val Tyr Gln Lys Ser Lys Asn Ala Leu Ser Ser Gln Ala
 275 280 285
 Val Val Ala Thr Ser Met Ser Asn Leu Ala Leu Lys Glu Tyr Leu Lys
 290 295 300
 Ser Gln Asp Leu Glu Leu Lys His Cys Ala Ile Gly Asp Lys Phe Val
 305 310 315 320
 Ser Glu Cys Met Arg Leu Asn Lys Ala Asn Phe Gly Gly Glu Gln Ser
 325 330 335
 Gly His Ile Ile Phe Ser Asp Tyr Ala Lys Thr Gly Asp Gly Leu Val
 340 345 350
 Cys Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Leu Val Ser
 355 360 365
 Ser Ile Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn
 370 375 380
 Leu Asn Ile Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser
 385 390 395 400
 Ala Leu Leu Lys Glu Leu Asp Gln Leu Glu Ile Arg His Leu Ile Arg
 405 410 415
 Tyr Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp
 420 425 430
 Glu Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu
 435 440 445
 Gly Gln Leu Cys
 450

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

SUBSTITUTE SHEET (RULE 26)

1029

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463

```

Asn His Gln Arg Ile Arg Ser Arg Gln Gln Phe Arg Lys Pro Phe Asp
1          5          10          15
Pro Phe Arg Arg Ala Ser Glu Leu Lys Val Arg Ser Cys Lys Gln Ile
20          25          30
Phe Asp Lys Gly Leu Lys Pro Tyr Lys Lys His Ser Val Cys Leu Lys
35          40          45
Pro Phe Phe Arg Phe Cys Phe Leu Lys Ile His Ala Tyr Gln Gln Arg
50          55          60
Tyr Arg Ala Phe Ala Leu Thr Leu Phe Ser Cys Lys Phe Phe Asn Ala
65          70          75          80
Cys Lys Ile Phe Ile Pro Ile Ile Asp Phe Lys Ile Val Phe Ile Pro
85          90          95
Ile Leu Lys His Gln Ala Lys Leu Lys Arg Val Ser Asn Ala Tyr
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464

```

Lys Arg Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala
1          5          10          15
Cys Ser Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys
20          25          30
Lys Ile Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn
35          40          45
Glu Asn Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu
50          55          60
Gly Tyr Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe
65          70          75          80
Ser Pro Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val
85          90          95
Val Tyr Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu

```

SUBSTITUTE SHEET (RULE 26)

1030

```

      100      105      110
Ser Leu Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu
      115      120      125
Gln Leu Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr
      130      135      140
Ile Gln Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser
145      150      155      160
Leu Ile Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn
      165      170      175
Cys Ile Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly
      180      185      190
Ile Ile Ile Leu Lys Ala Cys Ala
      195      200

```

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465

```

Lys Glu Ser Leu Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu
1      5      10      15
Phe Thr Ala Ser Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala
      20      25      30
Ser Ser Tyr Gln Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu
35      40      45
Ile Leu Asp Gly Leu Asp Gly Arg Val Ala Arg Leu Thr Asn Thr Thr
50      55      60
Ser Lys Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe
65      70      75      80
Gly Val Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe
      85      90      95
Gly Arg Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala
100      105      110
Ile Arg Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr
115      120      125
Ser Phe Ile Gly Ile Pro Ile Pro Ala Ala Ala Val Leu Val Val Leu
130      135      140
Cys Val Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu
145      150      155      160
Lys Leu Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser
165      170      175
Asn Ile Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu
180      185      190
Phe Ile Leu Val Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu
195      200      205
Glu Ala Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile
210      215      220
Arg Trp Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser
225      230      235      240

```

SUBSTITUTE SHEET (RULE 26)

1031

Ala

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466

```

Tyr Leu Pro Ala Ser Glu Asn Ala Pro Leu Pro Ser Ser Val Phe Ser
1      5      10      15
Ser Ile Val Ala Leu Ser Leu Lys Ile Asp Ser Leu Phe Ser Leu Phe
20      25      30
Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro Phe Ala Leu Arg
35      40      45
Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His Tyr Gly Leu Glu
50      55      60
Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu Lys Val Gly Val
65      70      75      80
Tyr Gln Ser Phe Asp Leu Glu Val Leu Glu Lys Phe Leu Leu Glu Arg
85      90      95
Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile Arg Ser Val Leu
100     105     110
Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Gln Lys Val Lys Ala
115     120     125
Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Gln Lys Lys Glu Leu
130     135     140
Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn Lys Asp Arg Asn
145     150     155     160
Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe Lys Glu Leu Gln
165     170     175
Glu His Ala Leu Phe Glu Ala Phe Asn Ala Ile Lys Thr Ser Thr Phe
180     185     190
Glu Ser Leu Asp Ser Lys Ile Glu Ala Tyr Phe Gly Leu His Ala Pro
195     200     205
Leu Glu Glu Tyr Phe Lys Ser Val Leu Val Met Asp Lys Asp Ile Glu
210     215     220
Ile Gln Lys Asn Arg Lys Asn Phe Leu Trp Gly Val Tyr Gln Ser Phe
225     230     235     240
Leu Glu Ile Gly Asp Ile Lys Glu Ile Ala Ile
245     250

```

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

1032

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467

```

Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1      5      10      15
Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn
      20      25      30
Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
      35      40      45
Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
      50      55      60
Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu
      65      70      75      80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
      85      90      95
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
      100     105     110
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
      115     120     125
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
      130     135     140
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
      145     150     155     160
His Val Lys Phe Ile Phe Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
      165     170     175
Ile Leu Gly Gln Leu Gln Ile Phe Ser Lys Lys Ala Phe Gln Lys Asp
      180     185     190
Tyr Phe Glu Lys Asn Pro Leu Leu Ile Pro Val Ser Ser Gly Pro Tyr
      195     200     205
Val Ile Ala Ser Phe Asp Val Gly Lys Lys Ile Thr Tyr Gln Arg Asn
      210     215     220
Pro Asn Tyr Trp Ala Lys Asn Leu Pro Ser Arg Lys Gly Gln Phe Asn
      225     230     235     240
Phe Asp Gln Ile Lys Phe Glu Tyr Tyr Lys Asp Glu Thr Val Ala Leu
      245     250     255
Gln Ala Phe Leu Ser Gly Ala Tyr Asp Trp Arg Leu Glu Ser Thr Ala
      260     265     270
Lys Val Trp Ala Arg Gly Tyr Val Gly Lys Ala Met Asp Asn Lys Lys
      275     280     285
Ile Thr Lys Tyr Leu Ile Ala His Lys Met Pro Ser Gly Met Gln Gly
      290     295     300
Phe Phe Phe Asn Thr Arg Arg Glu Ile Phe Lys Asp Lys Arg Val Arg
      305     310     315     320
Glu Ala Leu Phe Tyr Ala Phe Asp Phe Glu Trp Ala Asn Lys Asn Leu
      325     330     335
Phe Phe Ser Gln Tyr Lys Arg Thr Thr Ser Phe Phe Ser Asn Ser Ile
      340     345     350
Tyr Ala Ser Pro Pro Leu Pro Ser Pro Glu Glu Lys Ala Leu Leu Ala
      355     360     365
Pro Tyr Glu Lys Ser Leu Asp Glu Arg Val Phe Lys Glu Pro Tyr Ile
      370     375     380
Val Pro Arg Thr Asp Gly Pro Asp Val Leu Gly Tyr Asn Leu Arg Glu
      385     390     395     400
Asn Leu Lys Tyr Ala Gln Lys Leu Leu Glu Ser Ala Gly Phe Ser Tyr
      405     410     415

```

SUBSTITUTE SHEET (RULE 26)

1033

Lys Asn Met Arg Leu Val Asp Lys Asn Asn Lys Pro Phe Ser Phe Thr
 420 425 430
 Leu Leu Leu Asn Ser Pro Ala Phe Glu Arg Leu Ala Leu Ala Phe Ala
 435 440 445
 Lys Asn Leu Arg Val Leu Gly Ile Glu Met Lys Ile Gln Arg Val Asp
 450 455 460
 Leu Ser Gln Tyr Val Asn Arg Ile Lys Ser Tyr Asp Phe Asp Met Ile
 465 470 475 480
 Val Gly Val Ile Gly Gln Ser Ser Phe Pro Gly Asn Glu Gln Arg Phe
 485 490 495
 Tyr Phe Gly Ser Leu Ser Ala Lys Ala Lys Gly Thr Arg Asn Tyr Ala
 500 505 510
 Arg Ile Ser Ser Lys Ala Val Asp Asp Leu Ile Glu Arg Ile Ile His
 515 520 525
 Ala Lys Asp Tyr Lys Glu Gln Leu Ala Ala Ile Gln Ala Met Asp Arg
 530 535 540
 Val Leu Leu Arg Gly Phe Tyr Ala Ile Pro His Phe Tyr Leu Pro Asn
 545 550 555 560
 Tyr Arg Ile Ala Ala Tyr Asn Tyr Ile Gly Met Pro Glu Ile Ser Pro
 565 570 575
 Ser Tyr Gly Phe Ser Pro Tyr Leu Trp Trp Ile Lys Lys Glu Arg Gly
 580 585 590
 Pro Lys

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468

Ser Val Ile Gly Val Tyr Ile Ile Ser Leu Lys Glu Ser Gln Arg Arg
 1 5 10 15
 Leu Asp Thr Glu Lys Leu Val Leu Glu Ser Asn Glu Lys Phe Lys Gly
 20 25 30
 Arg Cys Val Phe Gln Ile Phe Asp Ala Ile Ser Pro Lys His Gln Asp
 35 40 45
 Phe Glu Lys Leu Leu Gln Glu Leu Tyr Asn Ala Gln Ser Leu Leu Gln
 50 55 60
 Ser Asp Trp Tyr His Ser Tyr Val Gly Ala Gly Leu Thr Leu Pro Glu
 65 70 75 80
 Leu Gly Cys Tyr Leu Ser His Tyr Leu Leu Trp Lys Glu Cys Val Lys
 85 90 95
 Leu Asp Gln Pro Val Val Ile Leu Glu Asp Asp Val Thr Leu Glu Ser
 100 105 110
 His Phe Met Gln Ala Leu Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe
 115 120 125
 Val Arg Leu Tyr Gly Cys Tyr Trp Tyr Tyr His Glu Thr Lys Phe His
 130 135 140
 Val Leu Pro Lys Glu Phe Val Phe Pro Pro Phe Asp His Ser Phe Lys

SUBSTITUTE SHEET (RULE 26)

1034

```

145          150          155          160
Asn Asn Pro Ile Leu Glu Lys Phe Lys Lys Phe Phe Asp Val Ser Arg
          165          170          175
Phe Leu Asn Leu Ser Thr His Lys Val Ile His Leu Tyr Ser Gln Lys
          180          185          190
Asn Thr Lys Lys Leu Leu Arg Asn Ala
          195          200

```

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469

```

Phe Ser Glu Arg Asp Phe Glu Leu Phe Arg Gln Lys Thr Asn Pro Tyr
1          5          10          15
Glu Arg Cys Ser Cys Gly Phe Gly Phe Leu Ser Asp Ala Ser Lys Arg
          20          25          30
Ser Leu Asn Pro Thr Leu Met Met Asn Asn Asn Thr Leu Pro Lys
          35          40          45
Pro Leu Glu Glu Ser Leu Asp Leu Lys Glu Phe Ile Ala Leu Phe Lys
          50          55          60
Thr Phe Phe Ala Lys Glu Arg Gly Ser Ile Ala Leu Glu Asn Asp Leu
65          70          75          80
Lys Gln Ala Phe Thr Tyr Leu Asn Glu Val Asp Ala Ile Gly Leu Pro
          85          90          95
Ala Pro Lys Ser Val Lys Glu Ser Asp Leu Ile Val Val Lys Leu Thr
          100          105          110
Lys Leu Gly Thr Leu His Leu Asp Glu Ile Tyr Glu Ile Val Lys Arg
          115          120          125
Leu Arg Tyr Ile Val Val Leu Gln Asn Ala Phe Lys Pro Phe Thr His
130          135          140
Leu Lys Phe His Glu Arg Leu Asn Ala Ile Ile Leu Pro Pro Phe Phe
145          150          155          160
Asn Asp Leu Ile Leu Leu Leu Asp Asp Glu Gly Gln Ile Lys Gln Gly
          165          170          175
Ala Asn Ala Thr Leu Asp Ala Leu Asn Glu Ser Leu Asn Arg Leu Lys
          180          185          190
Lys Glu Ser Thr Lys Ile Ile His Tyr Ala His Ser Lys Glu Leu
          195          200          205
Ala Pro Tyr Leu Val Asp Thr Gln Ser His Leu Lys His Gly Tyr Glu
210          215          220
Cys Leu Leu Leu Lys Ser Gly Phe Ser Ser Ala Ile Lys Gly Val Val
225          230          235          240
Leu Glu Arg Ser Ala Asn Gly Tyr Phe Tyr Leu Leu Pro Glu Ser Ala
          245          250          255
Gln Lys Ile Ala Gln Lys Ile Ala Gln Ile Gly Asn Glu Ile Asp Cys
          260          265          270
Cys Ile Val Glu Met Cys Gln Thr Leu Ser Arg Ser Leu Gln Lys His
          275          280          285

```

SUBSTITUTE SHEET (RULE 26)

1035

```

Leu Leu Phe Leu Lys Phe Leu Phe Lys Glu Phe Asp Phe Leu Asp Ser
290                295                300
Leu Gln Ala Arg Leu Asn Phe Ala Lys Ala Tyr Asn Leu Glu Phe Val
305                310                315                320
Met Pro Ser Phe Thr Gln Lys Lys Met Ile Leu Glu Asn Phe Ser His
                325                330                335
Pro Ile Leu Lys Glu Pro Lys Pro Leu Asn Leu Lys Phe Glu Lys Ser
                340                345                350
Met Leu Ala Val Thr Gly Val Asn Ala Gly Gly Lys Thr Met Leu Leu
                355                360                365
Lys Ser Leu Leu Ser Ala Ala Phe Leu Ser Lys His Leu Ile Pro Met
370                375                380
Lys Ile Asn Ala His His Ser Thr Ile Pro Tyr Phe Arg Glu Ile His
385                390                395                400
Ala Ile Ile Asn Asp Pro Gln Asn Ser Ala Asn Asn Ile Ser Thr Phe
                405                410                415
Ala Gly Arg Met Lys Gln Phe Ser Ala Leu Leu Ser Lys Glu Asn Met
                420                425                430
Leu Leu Gly Val Asp Glu Ile Glu Leu Gly Thr Asp Ala Asp Glu Ala
                435                440                445
Ser Ser Leu Tyr Lys Thr Leu Leu Glu Lys Leu Leu Lys Gln Asn Asn
450                455                460
Gln Ile Val Ile Thr Thr His His Lys Arg Leu Ser Val Leu Met Ala
465                470                475                480
Glu Asn Lys Glu Val Glu Leu Leu Ala Ala Leu Tyr Asp Glu Glu Lys
                485                490                495
Glu Arg Pro Thr Tyr Thr Phe Leu Lys Gly Val Ile Gly Lys Ser Tyr
                500                505                510
Ala Phe Glu Thr Ala Leu Arg Tyr Gly Val Pro Pro Phe Leu Ile Glu
                515                520                525
Lys Arg Lys Pro Ser Met Ala Lys Ile Arg Lys Asn
530                535                540

```

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470

```

Lys Leu Thr Glu Lys Ile Met Leu Glu Thr Pro Lys Val Leu Leu Lys
1          5          10          15
Asn Leu Gln Asp Cys Lys Ile His Phe Ile Gly Ile Gly Gly Ile Gly
20        25        30
Ile Ser Gly Leu Ala Lys Tyr Leu Lys Ala Gln Gly Ala Lys Ile Ser
35        40        45
Gly Ser Asp Ile Ala Ile Ser Pro Ser Val Lys Tyr Leu Lys Ala Leu
50        55        60
Gly Val Glu Ile Asn Ile Pro His Asp Pro Lys Ala Ile Asn His Gln
65        70        75        80
Asp Val Ile Ile His Ser Ala Ile Ile Lys Glu Asp Asn Thr Glu Ile

```

SUBSTITUTE SHEET (RULE 26)

1036

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

- (A) NAME/KEY: misc_feature

1037

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471

```

Ala Val Thr Ala Ile Leu Gly Trp Asp Glu Glu Gly Lys Leu Lys Phe
1           5           10           15
Gly Lys Ile Arg His Lys Tyr Leu Glu Thr Ser Asn Val Asn Ala Gly
20           25           30
Asn Ala Leu Thr Asn Leu Ile Leu Met Gln Arg Gly Tyr Ser Met Asn
35           40           45
Ala Arg Ala Phe Gly Ala Gly Asp Asp Met Ile Lys Glu Ala Ile Ser
50           55           60
Leu Lys Lys
65

```

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472

```

Lys Leu His Arg Gly Ser Gln Lys Gln Asn Pro Ile Asn Asp Pro Thr
1           5           10           15
Trp Glu Ile Val Gly Phe Asp Ser Ala Thr His Lys Met Lys Ser Ala
20           25           30
Pro Met Thr Leu Asp Phe Lys Gly Asn Lys Leu Thr Tyr Ser Leu Asp
35           40           45
Lys Ser Glu Asn Met Ile Leu Thr Lys Leu Phe Tyr Gln Asp Ser Lys
50           55           60
Leu Leu Lys Thr Ser Gln Glu Arg Lys Pro Arg Gly Ile Phe Arg Asp
65           70           75           80
Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
85           90           95
Val Val Glu Pro Val Ala Arg Ile Gly Ile Leu Ala Phe Thr Asn Asp
100          105          110
Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
115          120          125
Thr Ile Asn Gly Glu Asn Arg Pro Leu Ser Gly Asn Arg His Phe Arg
130          135          140
Val Gly Arg Arg Gly Gln Ala Gln Val Trp Glu Asn Gln Ala Gln Ile
145          150          155          160
Phe Arg Asn Glu Gln Arg Glu Cys Arg Glu Arg Pro Asn Gln Ser His
165          170          175
Phe Asn Ala Lys Arg Leu Phe Tyr Glu Arg
180          185

```

(2) INFORMATION FOR SEQ ID NO:1473:

(1) SEQUENCE CHARACTERISTICS:

1038

(A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473

```

Trp Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser
1          5          10          15
Pro Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu
20          25          30
Arg Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu
35          40          45
Ala Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser
50          55          60
Lys Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His
65          70          75          80
Lys Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu
85          90          95
Leu Ile Ile Ser Asp Ala Asn Lys Glu Ala Tyr Thr Ile Thr Gln Lys
100          105          110
Tyr Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser
115          120          125
Lys Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val
130          135          140
Glu Ser Val Phe Lys Asp Leu Arg Glu Ser Lys Lys Val Ser Phe Asn
145          150          155          160
Ala Gln Asp Cys Val Asn Ile Leu Lys Gln Arg Leu
165          170

```

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474

```

Met Gln Lys Ser Ile Phe Lys Ile Thr Leu Leu Val Phe Leu Phe
1          5          10          15
Leu Arg Asn Ala Val Gly Leu Asp Asp Lys Lys Ala Ala Pro Lys Ser
20          25          30

```

1039

```

Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
      35      40      45
Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
      50      55      60
Thr Gln Tyr Glu Phe Pro Lys Ile Lys Glu Ile Leu Glu Gln Ser Glu
      65      70      75      80
Glu Glu Trp Leu Gly Val Ala His Glu Glu Cys Val Ala Leu Val Met
      85      90      95
Leu Ile Ser Pro Lys Ala Ser Ile Glu Asn Ser Pro Ile Tyr Lys Asn
      100      105      110
Cys Tyr Glu Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe
      115      120      125
Tyr Ile Glu Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Glu
      130      135      140
His Glu Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Glu Pro Pro
      145      150      155      160
Lys Ser Glu Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala
      165      170      175
Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser
      180      185      190
Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met
      195      200      205
Glu Glu Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr
      210      215      220
Lys Glu Glu Ala Leu Lys Gln Leu Glu Asn Ala Ala Lys Ser Phe Lys
      225      230      235      240
Asn Lys Pro Ala Leu Val Glu Lys
      245

```

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475

```

Ser Gly Cys Tyr Phe Glu Ser Asn Ser Asp Val Tyr Val Val Ile Ile
1      5      10      15
Gly Leu Ala Asp Gln Lys Ile Gly Val Ile Val Asp Tyr Leu Ile Gly
      20      25      30
Gln Glu Glu Val Val Ile Lys Ser Leu Gly Tyr Tyr Leu Lys Asn Thr
      35      40      45
Arg Gly Ile Ala Gly Ala Thr Val Arg Gly Asp Gly Lys Ile Thr Leu
      50      55      60
Ile Val Asp Val Gly Ala Met Met Glu Met Ala Lys Ser Ile Lys Val
      65      70      75      80
Asn Ile Thr Thr Leu Met Asn Glu Ser Glu Asn Thr Lys Ser Lys Asn
      85      90      95
Ser Pro Ser Asp Tyr Val Val Leu Ala Ile Asp Asp Ser Ser Thr Asp
      100      105      110
Arg Ala Ile Ile Arg Lys Cys Leu Lys Pro Leu Gly Ile Thr Leu Leu

```

```

      115      120      125
Glu Ala Thr Asn Gly Leu Glu Gly Leu Glu Met Leu Lys Asn Gly Asp
  130      135      140
Lys Ile Pro Asp Ala Ile Leu Val Asp Ile Glu Met Pro Lys Met Asp
  145      150      155      160
Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys Tyr Asn Lys Phe Lys Asn
      165      170      175
Leu Pro Leu Ile Ala Val Thr Ser Arg Val Thr Lys Thr Asp Arg Met
      180      185      190
Arg Gly Val Glu Ser Gly Met Thr Glu Tyr Ile Thr Lys Pro Tyr Ser
      195      200      205
Gly Glu Tyr Leu Thr Thr Val Val Lys Arg Ser Ile Lys Leu Glu Gly
      210      215      220
Asp Gln Ser
225

```

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476

```

Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Glu Leu Ser Pro
 1      5      10      15
Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu Gly Phe Val
      20      25      30
Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His Leu Glu Leu
      35      40      45
Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly Lys Arg Leu
      50      55      60
Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp Phe Tyr Gly
      65      70      75      80
Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg Pro Glu Thr
      85      90      95
Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln Tyr His Leu
      100      105      110
Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val Ser Val Ser
      115      120      125
Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser Asp Ile Ser
      130      135      140
Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg Phe Cys Leu
      145      150      155      160
Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp His Met Pro
      165      170      175
Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala Arg Asn Tyr
      180      185      190
Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala Leu Phe Gly
      195      200      205
Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe Leu Ala Ala
      210      215      220

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1041

Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr Asp Gln Leu
 225 230 235 240
 Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp Ala Glu Phe
 245 250 255
 Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly Val Leu Lys
 260 265 270
 Ser Phe Leu Arg
 275

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477

Lys Ala Val Leu Phe Asn Pro Leu Pro Thr Lys Arg Ser Val Met Pro
 1 5 10 15
 His Ser Leu Lys Lys Arg Phe Leu Ile Val Tyr Thr Leu Ser Thr Leu
 20 25 30
 Leu Leu Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn
 35 40 45
 Asn Leu Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala
 50 55 60
 Ile Ala Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro
 65 70 75 80
 Leu Lys Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu
 85 90 95
 Asp Ala Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala
 100 105 110
 Ser Phe Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys
 115 120 125
 Lys Gln Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly
 130 135 140
 Val Ser Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile
 145 150 155 160
 Pro Leu Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe
 165 170 175
 Val Ala Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
 180 185

(2) INFORMATION FOR SEQ ID NO:1478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1042

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478

```

Asn Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu
1      5      10      15
Leu Phe Phe Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys
20     25     30
Phe Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys
35     40     45
Asp Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser
50     55     60
Ile Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe
65     70     75     80
Phe Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro
85     90     95
Glu Thr Leu Gly Tyr Leu Val Phe Ala Leu Leu Phe Leu Ala Ile Gln
100    105    110
Ser Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp
115    120    125
Lys Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Phe Lys Asp
130    135    140
Phe Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile
145    150    155    160
Tyr Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser
165    170    175
Ser Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Tyr
180    185    190
Pro Lys Ile Ala Gln Leu Phe Asn Gln Phe Thr Pro Leu Asn Asn Arg
195    200    205
Asp Leu Glu Ser Gln Ile Glu Ser Met Met Asp Lys Val Gly Phe Lys
210    215    220
Ser Gln Gly Ile Phe Val Met Asp Ala Ser Lys Arg Asp Gly Arg Leu
225    230    235    240
Asn Ala Tyr Phe Gly Gly Leu Gly Lys Asn Lys Arg Val Val Leu Phe
245    250    255
Asp Thr Leu Ile Ser Lys Val Gly Thr Glu Gly Leu Leu Ala Ile Leu
260    265    270
Gly His Glu Leu Gly His Phe Lys Asn Lys Asp Leu Leu Lys Asn Leu
275    280    285
Gly Ile Met Gly Gly Leu Leu Ala Leu Val Phe Ala Leu Ile Ala His
290    295    300
Leu Pro Pro Leu Val Phe Glu Gly Phe Asn Val Ser Gln Thr Pro Ala
305    310    315    320
Ser Leu Ile Thr Ile Leu Leu Leu Phe Leu Pro Val Phe Ser Phe Tyr
325    330    335
Ala Met Pro Leu Ile Gly Phe Phe Ser Arg Lys Asn Glu Tyr Asn Ala
340    345    350
Asp Lys Phe Gly Ala Ser Leu Ser Ser Lys Glu Thr Leu Ala Lys Ala
355    360    365
Leu Val Ser Ile Val Asn Glu Asn Lys Ala Phe Pro Tyr Ser His Pro
370    375    380
Phe Tyr Val Phe Leu His Phe Thr His Pro Pro Leu Leu Glu Arg Leu
385    390    395    400
Lys Ala Leu Asp Tyr Glu Ile Glu
405

```

1043

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479

```

Ile Arg Arg Arg Pro Ile Val Ser Asn Gln Leu Lys Asp Leu Phe Glu
1      5      10      15
Arg Gln Lys Glu Ala Asn Ala Ser Ser Lys Gln Glu Asp Asn Glu Glu
20     25     30
Ile Leu Gln Phe Ile Gly Phe Ile Ile Gly Asp Glu Glu Tyr Ala Ile
35     40     45
Pro Ile Leu Asn Ile Leu Glu Ile Val Lys Pro Ile Gly Tyr Thr Arg
50     55     60
Val Pro Glu Thr Pro Asn Tyr Val Leu Gly Val Phe Asn Leu Arg Gly
65     70     75     80
Asn Val Phe Pro Leu Ile Ser Leu Arg Leu Lys Phe Gly Leu Lys Ala
85     90     95
Glu Lys Gln Asn Lys Asp Thr Arg Tyr Leu Val Val Arg His Asn Asp
100    105    110
Arg Ser Leu Gly Phe Ser Ser Leu Ser Gly Leu Met Pro Ser Glu Ser
115    120    125
Ala Ser Thr Ile Asp Pro Ser Gln Lys Leu Cys Ala Ile Thr Ile Ile
130    135    140

```

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480

```

Ser Phe Ser Ile Asn Ser Phe Lys Lys Ala Lys Gly Met Lys Ser Thr
1      5      10      15
Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala Val Val Ile Val
20     25     30
Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys Val Glu Ser Val

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1044

```

      35          40          45
Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys Ala Gln Leu Val
  50          55          60
Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe Met Gly Ala Asn
  65          70          75          80
Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala Ile Asn Asp Thr
      85          90          95
Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala Asn Pro His Val
      100          105          110
Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu Arg Met Ile Thr
      115          120          125
Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn Thr Ala Leu Asn
      130          135          140
Glu Asn Met Thr Asn Gln Ile His Ser Leu Lys Ser Ile Thr Arg Ser
      145          150          155          160
Asp Pro Tyr Tyr Lys Glu Val Asn Gly Asp Lys Ile Tyr Gly Met Asp
      165          170          175
Ile Thr Leu Pro Leu Met Gly Lys Asn Gln Asn Val Ile Gly Ala Leu
      180          185          190
Asn Phe Phe Leu Asn Ile Asp Ala Phe Tyr Thr Asp Val Val Gly Lys
      195          200          205
Lys Lys Ser Asn Thr Phe Leu Met Gly Lys Asp Gly Arg Ile Leu Ile
      210          215          220
Asn Pro Asn Arg Glu Ile Gln Asp Lys Ile Leu Ser Ala Ile Asn Pro
      225          230          235          240
Asp Lys Arg Val Ala Lys Ala Val Glu Tyr Tyr Asn Gln Asn Glu Ala
      245          250          255
Gly Thr Leu Ser Tyr His Ser Leu Ser Gly Asn Thr Glu Thr Phe Leu
      260          265          270
Ala Ile Gln Pro Phe Asp Phe Phe Glu Glu Lys Gly Asn Asn Gly Gln
      275          280          285
Ser Leu Ala Leu Gly Asn Trp Glu Ile Cys Gln
      290          295

```

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481

```

Gly Val Phe Tyr Asn Ser Ser Leu Pro Gln Pro Pro Thr Lys Asn Pro
 1          5          10          15
Leu Thr Arg Glu Tyr Arg Phe Leu Lys Arg Leu Ser Leu Ile Tyr Ala
      20          25          30
Ser Ser Phe Ile Val Phe Ile Leu Lys Asn Ala Leu Lys Leu Phe Leu
      35          40          45
Ile Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Leu Leu
      50          55          60
Val Lys Pro Phe Phe Tyr Leu Phe Asp Leu Val Ala His Leu Ser Thr
      65          70          75          80

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1045

Arg Ile Asp Leu Ile Asp Lys His Val Lys Val Tyr His His Gln Lys
 85 90 95
 His His His Lys Pro
 100

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482

Phe Ile Thr Gly Ile Glu Ile His Pro Gly Ala Lys Ile Gly Arg Gly
 1 5 10 15
 Leu Phe Ile Asp His Gly Met Gly Val Val Ile Gly Glu Thr Thr Glu
 20 25 30
 Ile Gly Asp Asp Val Thr Ile Tyr His Gly Val Thr Leu Gly Gly Thr
 35 40 45
 Gly Lys Phe Lys Gly Lys Arg His Pro Thr Leu Gly Asn Arg Val Val
 50 55 60
 Val Gly Ala Gly Ala Lys Val Leu Gly Ala Ile Cys Val Gly Asp Asp
 65 70 75 80
 Val Arg Ile Gly Ala Asn Ala Val Val Leu Ser Asp Leu Pro Thr Gly
 85 90 95
 Ser Thr Ala Val Gly Ala Lys Ala Lys Thr Ile Thr Lys Asp Arg
 100 105 110

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483

Lys Gly Phe Leu Gly Val Lys Lys Val Ile Val Phe Ile Lys Lys Lys
 1 5 10 15
 Gly Glu Met Val Val Asn Ser Lys Val Gln Thr Leu Lys Val Phe Ser

SUBSTITUTE SHEET (RULE 26)

1046

```

      20      25      30
Lys Phe Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu
      35      40      45
Glu Ala His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr
      50      55      60
Glu Ile Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu
      65      70      75      80
Thr Val Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe
      85      90      95
Lys Tyr Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala
      100      105      110
Leu Ala Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr
      115      120      125
Tyr Asn Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys
      130      135      140
Ser Leu Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe
      145      150      155      160
Asn Glu Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys
      165      170      175
His Pro Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys
      180      185      190
Ile Ala Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp
      195      200      205
Ile Ile Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp
      210      215      220
Asn Thr Leu Leu Thr Ser Glu Asn Arg Arg Ser Trp Arg Lys Lys Ile
      225      230      235      240
Gly Tyr Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp
      245      250      255
Asn Ile Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val
      260      265      270
Cys Lys Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu
      275      280      285
Lys Thr Gln Val Gly Glu Gly Gly Ala Lys Leu Ser Gly Gly Gln Lys
      290      295      300
Gln Arg Ile Gly Ile Ala Arg Ala Leu Tyr Asp Asn Pro Glu Ile Leu
      305      310      315      320
Val Leu Asp Glu Ala Thr Ser Ala Leu Asp Asn Glu Thr Glu Ser Lys
      325      330      335
Ile Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val
      340      345      350
Ile Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp
      355      360      365
Met Ser Gln His Lys Asp Asn Leu Gly
      370      375

```

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...229

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1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484

```

Ala Tyr Lys Lys Gly Glu Ile Met Ala Leu Glu Val Val Leu Trp Asp
1      5      10      15
Phe Asp Gly Val Ile Phe Asp Ser Met His Leu Lys Tyr Glu Gly Phe
      20      25      30
Lys Ala Leu Phe Gln Lys His Gly Asn Asp Ser Lys Glu Gly Leu Lys
      35      40      45
Gln Phe Glu Val Tyr His Tyr Gln Ser Gly Gly Ile Ser Arg Asn Glu
      50      55      60
Lys Ile Gln Tyr Phe Tyr Asn Glu Ile Leu Lys Thr Pro Ile Ala Gln
      65      70      75      80
Glu Glu Ile Asp Ala Leu Ala Leu Glu Phe Gly Ala Ile Ile Glu Gln
      85      90      95
Lys Leu Phe Asp Arg Gly His Leu Asn Ser Glu Val Met Ala Phe Ile
      100     105     110
Asp Lys His Tyr Gln Asn Tyr Ile Phe His Ile Ala Ser Ala Ala Leu
      115     120     125
His Ser Glu Leu Gln Val Leu Cys Glu Phe Leu Gly Ile Thr Lys Tyr
      130     135     140
Phe Lys Ser Val Glu Gly Ser Pro Pro Asp Lys Pro Lys Ile Ile Ala
      145     150     155     160
Asn Ile Ile Gln Lys Tyr Ala Tyr Asp Pro Ser Arg Met Leu Met Ile
      165     170     175
Gly Asp Ser Val Asn Asp Tyr Glu Ser Ala Lys Ala Asn Lys Val Ala
      180     185     190
Phe Leu Gly Tyr Asn Ser Lys Val Leu Lys Asn Leu Val Gly Gln Asp
      195     200     205
Gly Tyr Gln Gly Lys Tyr Leu Glu Ser Phe Lys Gly Phe Asp Leu Gln
      210     215     220
Asn Phe Ala Lys Glu
225

```

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485

```

Asn Lys Ser Met Gln His Leu Val Leu Ile Gly Phe Met Gly Ser Gly
1      5      10      15
Lys Ser Ser Leu Ala Gln Glu Leu Gly Leu Ala Leu Lys Leu Glu Val
      20      25      30
Leu Asp Thr Asp Met Ile Ile Ser Glu Arg Val Gly Leu Ser Val Arg
      35      40      45
Gly Ile Phe Glu Glu Leu Gly Glu Asp Asn Phe Arg Met Phe Glu Lys
      50      55      60
Asn Leu Ile Asp Glu Leu Lys Thr Leu Lys Thr Pro His Ile Ile Ser
      65      70      75      80
Thr Gly Gly Gly Ile Val Met His Glu Asn Leu Lys Gly Leu Gly Thr

```

1048

[illegible]

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486

1	Phe	Phe	Lys	Gly	Leu	Val	Met	Leu	Ser	Arg	Asp	Ile	Val	Gln	Tyr
				5					10					15	
Ser	Lys	Ile	Arg	Thr	Glu	Leu	Tyr	Ala	Tyr	Leu	Thr	Tyr	Leu	Phe	Ser
			20					25					30		
His	Asn	Ile	Arg	Asn	His	Leu	Pro	Glu	Ile	Thr	Leu	Asp	Tyr	Leu	Asn
		35					40					45			
Arg	Gln	Ile	Ser	Lys	Met	Gln	Ala	Glu	Ile	Lys	Met	Ala	Lys	Ser	Phe
		50				55					60				
Phe	Val	Leu	Asp	Ala	Lys	Gly	Met	Leu	Met	Leu	Lys	Pro	Ser	Gln	Phe
65					70					75					80
Lys	Glu	Gln	Gly	His	Lys	Glu	Gly	Leu	Leu	Glu	His	Asp	Leu	Thr	Glu
				85						90				95	
Gly	Ile	Glu	Leu	Glu	Ser	His	Val	Ser	Phe	Ser	Asp	Lys	Tyr	Tyr	Phe
			100					105					110		
Tyr	Gln	Ala	Val	Asn	Glu	Lys	Arg	Cys	Ile	Leu	Thr	Asp	Pro	Tyr	Pro
		115					120					125			
Ser	Lys	Lys	Gly	Asn	His	Leu	Val	Val	Ser	Ala	Ser	Tyr	Pro	Val	Tyr
		130				135					140				
Asp	Gln	Asn	Asn	Asp	Leu	Ala	Phe	Val	Val	Cys	Leu	Gln	Ile	Pro	Leu
145					150					155				160	
Arg	Val	Ala	Ile	Glu	Ile	Ser	Ser	Pro	Ser	Lys	Tyr	Phe	Lys	Thr	Phe
				165						170				175	
Ser	Glu	Gly	Ser	Met	Val	Met	Tyr	Phe	Met	Ile	Ser	Ile	Met	Leu	Thr
			180					185					190		
Leu	Val	Ser	Leu	Leu	Leu	Phe	Val	Lys	Cys	Ile	Ser	Ser	Phe	Trp	Thr
		195					200					205			
Ala	Ile	Val	His	Phe	Ser	Ser	Phe	Asp	Ile	Lys	Glu	Val	Phe	His	Pro
		210				215					220				
Ile	Val	Leu	Leu	Thr	Leu	Ala	Leu	Ala	Thr	Phe	Asp	Leu	Val	Lys	Ala
225					230					235				240	
Ile	Phe	Glu	Glu	Glu	Val	Leu	Gly	Lys	Asn	Ser	Gly	Asp	Asn	His	His
				245					250					255	

1049

Ala Ile His Arg Thr Met Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala
 260 265 270
 Leu Ala Ile Glu Ala Leu Met Leu Val Phe Lys Phe Ser Val Ser Glu
 275 280 285
 Pro Asp Lys Ile Thr Tyr Ala Val Tyr Leu Ala Ile Gly Val Ala Val
 290 295 300
 Leu Leu Ile Ser Leu Ala Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu
 305 310 315 320
 Pro Lys Arg Glu Arg
 325

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487

Glu Ser Tyr Gln Thr Val Phe Thr Arg Gln Arg Tyr Tyr Gln Arg Leu
 1 5 10 15
 Phe Arg Arg Ala Val Cys Arg Asn Leu Arg Val Cys Glu Phe Thr Asn
 20 25 30
 Gln Asn Asn Lys Arg Gly Asp Cys Gln Arg Gln Gln Leu Phe Tyr Gly
 35 40 45
 Ala Tyr His Gly Glu Cys Leu Ser His Phe Arg Ile Ala Lys Thr His
 50 55 60
 Cys Gly Ala Ser Pro Phe Ile Val Ser Asp Phe Asn Phe Ile Gly Phe
 65 70 75 80
 Ile Val Pro Pro Ser Asn His Phe Ile Cys Gly Ser Gln Leu Lys Ser
 85 90 95
 Arg Pro Phe Arg Ala Ile Cys Leu Ala Arg Ile Ser Lys His Cys Gln
 100 105 110
 Ser Leu Phe Thr Leu Val Cys His Arg Val Phe Tyr Gly Val Pro Tyr
 115 120 125
 Phe Met Leu Gly Val Ile Glu Arg Tyr Tyr Phe Trp His Asp His Glu
 130 135 140
 Asn Pro Pro Ser Ile Gln Pro Ala Arg Tyr Arg Val Ser Gly Asn Cys
 145 150 155 160
 Asp Arg Val Cys Gly His Tyr Phe Asn Arg Phe Gly Tyr His Gly Ala
 165 170 175
 Phe Arg Arg Asn Gln Pro Gly Leu Arg Tyr Asn Leu
 180 185

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

1050

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488

```

Gly Val Leu Arg Phe Ser Ile Phe Phe Lys Val Val Ala Leu Phe Met
1          5          10          15
Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser Ser
20          25          30
Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln Phe
35          40          45
Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg Ala
50          55          60
Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile Glu
65          70          75          80
Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His Arg
85          90          95
Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe Ile
100          105          110
Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His Ser
115          120          125
Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu Leu
130          135          140
Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu Arg
145          150          155          160
Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser Val
165          170          175
Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn Glu
180          185          190
Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg Val
195          200          205
Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr Lys
210          215          220
Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys Arg
225          230          235          240
Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe Ala
245          250          255
Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu Lys
260          265          270
Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu Ile
275          280          285
Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Ser Asn Tyr Ile
290          295          300
Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met Ile
305          310          315          320
Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp Phe
325          330          335
Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys Glu
340          345          350
Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro Ser
355          360          365
Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala Leu
370          375          380
Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg Ile
385          390          395          400
Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu Glu
405          410          415

```

1051

Ala Asp Asn Glu Glu Leu Pro Pro Pro Arg Lys Phe Glu Arg Gly Glu
 420 425 430
 Gly Asn Glu Gly Asn Arg Lys Ser Gln Leu Trp Gly
 435 440

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489

Arg Lys Thr Lys Arg Glu Asn Met Phe Lys Arg Leu Arg Arg Leu Arg
 1 5 10 15
 Ser Ser Glu Asn Leu Arg Ala Met Val Arg Glu Thr Arg Leu Asn Ile
 20 25 30
 Asn Asp Phe Ile Ala Pro Leu Phe Val Ile Glu Ser Asp Ser Gly Ile
 35 40 45
 Lys Asn Glu Ile Ser Ser Met Pro Gly Val Tyr Gln Met Ser Ile Glu
 50 55 60
 Pro Leu Leu Lys Glu Cys Glu Glu Leu Val Gly Leu Gly Ile Lys Ala
 65 70 75 80
 Val Leu Leu Phe Gly Ile Pro Lys His Lys Asp Ala Thr Gly Ser His
 85 90 95
 Ala Leu Asn Lys Asp His Ile Val Ala Lys Ala Thr Arg Glu Ile Lys
 100 105 110
 Lys Arg Phe Lys Asp Leu Ile Val Ile Ala Asp Leu Cys Phe Cys Glu
 115 120 125
 Tyr Thr Asp His Gly His Cys Gly Ile Leu Glu Asn Ala Ser Val Ser
 130 135 140
 Asn Asp Lys Thr Leu Lys Ile Leu Asn Leu Gln Gly Leu Ile Leu Ala
 145 150 155 160
 Glu Ser Gly Val Asp Ile Leu Ala Pro Ser Asn Met Met Asp Gly Asn
 165 170 175
 Val Leu Ser Leu Arg Lys Ala Leu Asp Lys Ala Gly Tyr Phe His Thr
 180 185 190
 Pro Ile Met Ser Tyr Ser Thr Lys Phe Ala Ser Ser Tyr Tyr Gly Pro
 195 200 205
 Phe Arg Asp Val Ala Asn Ser Pro Pro Ser Phe Gly Asp Arg Lys Ser
 210 215 220
 Tyr Gln Met Asp Tyr Ala Asn Gln Lys Glu Ala Leu Leu Glu Ser Leu
 225 230 235 240
 Glu Asp Glu Lys Gln Gly Ala Asp Ile Leu Met Val Lys Pro Ala Leu
 245 250 255
 Ala Tyr Leu Asp Ile Val Lys Glu Ile Arg Asp His Thr Leu Leu Pro
 260 265 270
 Leu Ala Leu Tyr Asn Val Ser Gly Glu Tyr Ala Met Leu Lys Leu Ala
 275 280 285
 Gln Lys His Asn Leu Ile Asn Tyr Glu Ser Val Leu Leu Glu Thr Met
 290 295 300
 Thr Cys Phe Lys Arg Ala Gly Ala Asp Met Ile Ile Ser Tyr His Ala

SUBSTITUTE SHEET (RULE 26)

305 310 315 320
Lys Glu Val Ala Asn Leu Leu Gln Arg Asn
 325 330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490

Ser	Ala	Gly	Arg	Ile	Leu	Ala	Glu	Asp	Ile	Ile	Cys	Val	His	Ala	Leu
1				5					10					15	
Pro	Lys	Phe	Asn	Gln	Ser	Ala	Met	Asp	Gly	Tyr	Gly	Phe	Lys	Met	Gln
			20					25					30		
Asp	Leu	Gly	Gln	Lys	Thr	Gln	Val	Ile	Gln	His	Ile	Phe	Ala	Gly	Asp
		35					40					45			
Asp	Val	Ser	Ala	Leu	Glu	Val	Lys	Glu	Asn	Glu	Cys	Val	Lys	Ile	Met
	50					55					60				
Thr	Gly	Ala	Met	Val	Pro	Lys	Gly	Ile	Glu	Thr	Ile	Val	Pro	Ile	Glu
65					70					75					80
Cys	Met	Leu	Glu	Ser	His	Lys	Asp	Phe	Ala	Leu	Ala	Pro	Lys	Asp	Phe
				85				90						95	
Lys	Ile	His	Ala	Asn	Ile	Arg	Gln	Lys	Gly	Glu	Asn	Ala	Ser	Leu	Asn
			100					105					110		
Ser	Val	Leu	Val	Pro	Lys	Asn	Thr	Arg	Leu	Asn	Tyr	Gly	His	Ile	Ala
		115					120					125			
Leu	Ile	Ala	Ser	Gln	Gly	Phe	Lys	Glu	Ile	Lys	Ala	Phe	Arg	Lys	Leu
		130				135					140				
Lys	Ile	Ala	Leu	Phe	Ser	Ser	Gly	Asp	Glu	Leu	Val	Pro	Leu	Gly	Gln
145					150					155					160
Asn	Ala	Leu	Glu	Cys	Gln	Val	Tyr	Asp	Val	Asn	Ser	Val	Gly	Val	Phe
				165				170						175	
Asn	Met	Leu	Lys	Asn	Tyr	Asn	Thr	His	Phe	Leu	Gly	Val	Leu	Lys	Asp
			180					185					190		
Asp	Lys	Asn	Leu	Gln	Leu	Lys	Ile	Leu	Glu	Leu	Gln	Gly	Tyr	Asp	Val
		195					200					205			
Ile	Leu	Ser	Ser	Ala	Gly	Val	Ser	Val	Gly	Asp	Lys	Asp	Phe	Phe	Lys
		210				215					220				
Asp	Ala	Leu	Lys	Glu	Arg	Asn	Ala	Leu	Phe	Tyr	Tyr	Glu	Lys	Val	Asn
225					230					235					240
Leu	Lys	Pro	Gly	Lys	Pro	Val	Thr	Leu	Ala	Gln	Leu	Asn	Gln	Ser	Ile
					245				250					255	
Ile	Ile	Gly	Leu	Pro	Gly	Asn	Pro	Leu	Ser	Cys	Leu	Leu	Val	Leu	Arg
			260					265					270		
Val	Leu	Ile	Leu	Pro	Leu	Leu	Glu	Arg	Leu	Ser	Leu	Asn	Lys	Asp	Phe
		275					280					285			
Lys	Leu	Lys	Pro	Phe	Lys	Ala	Gln	Ile	Asn	Ala	Pro	Leu	Lys	Leu	Asn
					295					300					
Asn	Lys	Arg	Thr	His	Leu	Ile	Leu	Gly	Asn	Tyr	Ser	Asn	His	Gln	Phe
305					310					315					320

1053

Ile Pro Tyr Asn Asn Arg Tyr Glu Ser Gly Ala Ile Gln Ala Leu Ala
 325 330 335
 Gln Val Asp Ser Ile Ala Leu Ile Asp Glu Gly Val Gly Leu Val Gln
 340 345 350
 Gly Glu Ile Glu Ile Leu Arg Phe Glu Asn
 355 360

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491

Gly Asn Tyr Gly Leu Glu Ile Arg Phe Lys Glu Met Ala Val Leu Lys
 1 5 10 15
 Lys Met Ile Gly Leu Val Ala Val Leu Ser Val Leu Leu Ala Arg Asp
 20 25 30
 Asn Pro Phe Glu Pro Glu Ile Asn Ser Lys Asn Leu Gln Gly Gly Phe
 35 40 45
 Ser Gly Ile Tyr Asp Asp Tyr Leu Lys Glu Ile His Val Asp Leu Pro
 50 55 60
 Thr Ser Ala Arg Ile Leu Lys Lys Ile Thr Leu Thr Tyr Gln Asp Ile
 65 70 75 80
 Asp Gly Ser Ile His Ser Lys Val Val Gly Ile Asp Lys Ser Ile Asp
 85 90 95
 Trp His Tyr Pro Leu Lys Leu Ser Gln His Thr Leu Asn Gln Asp Ala
 100 105 110
 Phe Glu Lys Arg Tyr Gln Ile Gln Asp Phe Asp Phe Leu Met Ala Asn
 115 120 125
 Asn Thr Met Ile Leu Arg Ser Pro Tyr Lys Ile Leu Arg Ser Phe Val
 130 135 140
 Leu Val Asn Pro Tyr Arg Ile Val Leu Asp Thr Gln Lys Gly Pro Leu
 145 150 155 160
 Asp Ile Tyr Gln Asn Met Asp Leu Asn Gln Lys Phe Phe Ser His Ile
 165 170 175
 Lys Val Gly Thr His Lys Asp Tyr Tyr Arg Ile Thr Leu Ile Leu Asp
 180 185 190
 Gly Lys Tyr Arg Tyr Leu Leu Glu Lys Asn Gly Ala Tyr Glu Leu
 195 200 205
 Lys Leu Lys
 210

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

1054

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492

```

Lys Ala Val Ala Thr Pro His His Thr Pro Leu Trp Leu Ser Val Tyr
1      5      10      15
Glu Ser Phe Lys Glu Ala Leu Asp Phe Lys Glu Val Ile Leu Val Val
20     25     30
Ser Glu Leu Asp Tyr Val Tyr Ile Gln Arg His Tyr Pro Lys Ile Lys
35     40     45
Leu Val Lys Gly Gly Ala Ser Arg Gln Glu Ser Val Arg Asn Ala Leu
50     55     60
Lys Val Ile Asp Ser Thr Tyr Thr Ile Thr Ser Asp Val Ala Arg Gly
65     70     75     80
Leu Ala Asn Met Glu Ala Leu Lys Ser Leu Phe Leu Thr Leu Gln Gln
85     90     95
Thr Ser His Tyr Cys Ile Ala Pro Tyr Leu Pro Cys Tyr Asp Thr Ala
100    105    110
Ile Tyr Tyr Asn Glu Ala Leu Asp Arg Glu Ala Ile Lys Leu Ile Gln
115    120    125
Thr Pro Gln Leu Ser His Thr Lys Thr Leu Gln Ser Ala Leu Asn Gln
130    135    140
Gly Gly Phe Lys Asp Glu Ser Ser Ala Ile Leu Gln Ala Phe Pro Asn
145    150    155    160
Ser Val Ser Tyr Ile Glu Gly Ser Lys Asp Leu His Lys Leu Thr Thr
165    170    175
Ser Gly Asp Leu Lys Phe Phe Thr Pro Phe Phe Asn Pro Ala Lys Asp
180    185    190
Thr Phe Ile Gly Met Gly Phe Asp Thr His Ala Phe Ile Lys Asp Lys
195    200    205
Pro Met Val Leu Gly Gly Val Val Leu Asp Cys Glu Phe Gly Leu Lys
210    215    220
Ala His Ser Asp Gly Asp Ala Leu Leu His Ala Val Ile Asp Ala Ile
225    230    235    240
Leu Gly Ala Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn
245    250    255
Asp Pro Lys Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val
260    265    270
Leu Asp Phe Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala
275    280    285
Thr Ile Phe Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile
290    295    300
Leu Glu Asn Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser
305    310    315    320
Leu Lys Val Thr Thr Met Glu Lys Met Gly Phe Ile Gly Lys Gln Glu
325    330    335
Gly Leu Leu Val Gln Ala His Val Ser Met Arg Tyr Lys Gln Lys Leu
340    345    350

```

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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1055

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493

```

Cys Leu Gly Met Cys Phe Ile Leu Lys Pro Phe Leu Ser Cys Leu Lys
1      5      10      15
Trp Ala Asn Pro Ser Leu Lys Pro Leu Ser Asn Ala Val Leu Arg Leu
      20      25      30
Ser Arg Gly Glu Ile Glu Asp Val Phe Val Gly Glu Cys Phe Asn Ser
      35      40      45
Asp Lys Gln Lys Tyr Trp Arg Ile Leu Glu Asp Lys Thr Ala His Phe
50      55      60
Ile Glu Ala Ser Leu Lys Ser Met Ala Ile Leu Leu Asn Lys Asp Ala
65      70      75      80
Lys Met Tyr Ala Asp Phe Gly Leu His Phe Gly Met Ala Phe Gln Ile
      85      90      95
Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp Ala Asn Thr Leu Gly Lys
100      105      110
Pro Asn Phe Ser Asp Phe Lys Glu Gly Lys Thr Thr Leu Pro Tyr Leu
115      120      125
Leu Leu Tyr Glu Lys Leu Asn Gln His Glu Gln Gly Leu Leu Ile Ser
130      135      140
Tyr Phe Lys Gln Asp Ser His Glu Ile Ile Glu Trp Thr Lys Glu Lys
145      150      155      160
Phe Lys Gln His Gly Ile Ile Glu Glu Thr Leu Lys Ile Ala Gln Val
165      170      175
Tyr Ser Lys Lys Ala Leu Glu Ala Ile Lys Gly Glu Asn Asn Leu Ile
180      185      190
Leu Glu Lys Leu Ala Gln Asp Val Ile Tyr Arg Thr Phe
195      200      205

```

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494

```

Lys Lys Val Lys Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly
1      5      10      15
Leu Phe Phe Leu Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn

```

1056

```

      20      25      30
Ser Phe Leu Gly Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser
      35      40      45
Lys Ala Ala Ser Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu
      50      55      60
Gly Cys Thr Gln Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg
      65      70      75      80
Ile Asp Tyr Lys Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala
      85      90      95
Asp Asp Arg Glu Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly
      100      105      110
Leu Gly Thr Ala Gln Asn Tyr Gln Glu Ala Ile Asp Ala Tyr Ala Arg
      115      120      125
His Ala Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495

```

Ser Ser Lys Thr Ala Phe Arg Ala Lys Gln Ile Ile Thr Ala Thr Asp
1      5      10      15
Ile Ser Ala Gln Lys Arg Gln Glu Arg Leu Ala Ser Met Gly Lys Ile
      20      25      30
Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val Gly Ser Ile Ser
      35      40      45
Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu Lys Thr Lys Pro
      50      55      60
Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val Glu Arg Ile Ile
      65      70      75      80
Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala Asn Arg Thr Lys
      85      90      95
Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu Ala Leu Asn Cys
      100      105      110
Tyr Thr Tyr Ser Lys Asp Ile Asp Phe Leu Phe Asn Phe Ser Asp Glu
      115      120      125
Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val Leu Gln Asn Phe
      130      135      140
Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu Glu Ser Glu Gln
      145      150      155      160
Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu Phe Ile Val Phe
      165      170      175
Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys Ser Ala Leu Phe
      180      185      190
Glu Pro Phe Glu Thr Thr Lys Leu Lys Gly Asn Gly Leu Gly Leu Ala
      195      200      205
Leu Ser Leu Gln Val Val Lys Ala His Glu Gly Ser Ile Ala Leu Leu
      210      215      220

```


1057

Glu Asn Gln Glu Lys Thr Phe Glu Ile Lys Ile Leu Asn Ala Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496

Lys Pro Lys Thr Ile Leu Lys Lys Gly Leu Leu Met Lys Thr Phe Glu
 1 5 10 15
 Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val Leu Phe Met Lys Val
 20 25 30
 His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val His
 35 40 45
 Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp Asp
 50 55 60
 Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr Leu
 65 70 75 80
 Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr Ser
 85 90 95
 Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys His
 100 105 110
 Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly
 115 120 125
 Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln
 130 135 140
 Lys Ser Ile Trp Met Leu Glu Ala His Leu Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497

SUBSTITUTE SHEET (RULE 26)

1058

```

Gly Ile Cys Met Gln Glu Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile
1      5      10      15
Ala Ser Trp Ile Lys Glu Ile Glu Ser Gly Phe Ile Asp Ala Leu Phe
20     25     30
Ser Lys Ile Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala
35     40     45
Leu Leu Asp Glu Lys Thr Asp Ala Ile Leu Leu Asp Lys Ala Leu Asn
50     55     60
Leu Cys Ala Ile Val Glu Met Ile Gln Thr Ala Ser Leu Leu His Asp
65     70     75     80
Asp Val Ile Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn
85     90     95
Ala Leu Phe Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr
100    105    110
Ser Lys Ala Phe Phe Glu Leu Ser Lys Met Gly Glu Ser Ile Ala Gln
115    120    125
Ala Pro Leu
130

```

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498

```

Cys Met Leu Phe Ser Lys Leu Phe Ala Pro Thr Leu Lys Glu Pro Pro
1      5      10      15
Lys Asp Ala Val Leu Lys Ser Pro Lys His Pro Gly Asn Gly Gly His
20     25     30
Pro Leu Gln Ile Gly Ser Gly Ile Tyr Asn Phe Leu Pro Leu Ala Lys
35     40     45
Lys Val Leu Asp Lys Ile Glu Asn Val Thr His Lys Arg Met Gln Glu
50     55     60
His Gly Ala Gln Asn Ile Leu Met Ser Phe Val Val Leu Ala Ser Leu
65     70     75     80
Trp Glu Lys Ser Gly Arg Leu Asp Lys Tyr Gly Lys Glu Leu Leu Val
85     90     95
Phe Lys Asp Arg Lys Asp Asn Asp Phe Val Leu Ser Pro Thr Leu Glu
100    105    110
Glu Asn Ile Thr Glu Ile Ala Ala Asn Phe Ile Lys Ser Tyr Lys Gln
115    120    125
Leu Pro Val His Leu Tyr Gln Ile His Thr Lys Phe Arg Asp Glu Ile
130    135    140
Arg Pro Arg Phe Gly Leu Val Arg Ala Arg Glu Phe Ile Met Lys Asp
145    150    155    160
Gly Tyr Ser Phe His Glu Asp Ala Glu Ser Leu Asp Lys Glu Ile Leu
165    170    175
Asn Thr Gln Ser Ala Tyr Lys Glu Ile Leu Ser Asp Leu Gly Leu Asp
180    185    190

```

1059

Phe Arg Ile Val Glu Ala Asp Ser Gly Ala Ile Gly Gly Ser Lys Ser
 195 200 205
 Arg Glu Phe Val Val Leu Thr Glu Cys Gly Glu Asp Thr Ile Val Val
 210 215 220
 Cys Gln Asn Cys Asp Tyr Ala Ala Asn Ile Glu Ile Ala Lys Arg Ser
 225 230 235 240
 Lys Arg Thr Glu Pro Leu Met Ser Pro Ser Ala Leu Ala Lys Phe Pro
 245 250 255
 Thr Pro Asn Thr Thr Ser Ala Pro Ser Val Ala Glu Phe Phe Lys Thr
 260 265 270
 Glu Pro Tyr Phe Val Leu Lys Ala Leu Val Asn Lys Val Ile His Lys
 275 280 285
 Asp Lys Glu Thr Leu Ala Cys Phe Phe Val Arg Gly Asp Asp Asn Leu
 290 295 300
 Glu Glu Thr Lys Ala Leu Asn Thr Leu Asn Leu Leu Gly Ala Asn Ala
 305 310 315 320
 Leu Glu Leu Arg Glu Ala Asn Glu Glu Asp Leu Asn Lys Ala Gly Leu
 325 330 335
 Ile Ala Gly Phe Ile Gly Pro Tyr Gly Leu Lys Lys His Val Cys Tyr
 340 345 350
 Ile Ile Phe Asp Glu Asp Leu Lys Glu Gly Asp Cys Leu Ile Val Gly
 355 360 365
 Ala Asn Glu Lys Asp Phe His Ala Val Gly Val Asp Leu Lys Gly Phe
 370 375 380
 Glu Asn Leu Val Tyr Ala Asp Ile Val Gln Val Lys Glu Ser Asp Cys
 385 390 395 400
 Cys Pro Asn Cys Gln Gly Ala Leu Lys Tyr His Lys Ser Leu Glu Val
 405 410 415
 Gly His Ile Phe Lys Leu Gly Gln Ser Tyr Ala Lys Ser Leu Lys Ala
 420 425 430
 Ser Phe Leu Asp Lys Asn Gly Lys Glu Arg Phe Phe Glu Met Gly Cys
 435 440 445
 Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu Glu Gln Lys
 450 455 460
 Ser Asp Asp Leu Gly Cys Val Trp Thr Lys Asn Thr Ala Pro Phe Asp
 465 470 475 480
 Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln Lys Lys Leu
 485 490 495
 Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val Asp Ala Leu
 500 505 510
 Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg Asp Phe Glu
 515 520 525
 Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln Thr Leu Glu
 530 535 540
 Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu Lys Gln Thr
 545 550 555 560
 Ile Lys Asp Ile Glu Leu Glu Glu Lys Ile Leu Glu Met Leu Ala Ser
 565 570 575
 Glu

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

1060

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499

```

Ile Arg Glu Pro Gln Val Ala Ile Met Thr Ala Met Met Arg Tyr Phe
1           5           10           15
His Ile Tyr Ala Thr Thr Phe Phe Phe Pro Leu Ala Leu Leu Phe Ala
20           25           30
Val Ser Gly Leu Ser Leu Leu Phe Lys Ala Arg Gln Asp Thr Gly Ala
35           40           45
Lys Ile Lys Glu Trp Val Leu Glu Lys Ser Leu Lys Lys Glu Glu Arg
50           55           60
Leu Asp Phe Leu Lys Gly Phe Ile Lys Glu Asn His Ile Ala Met Pro
65           70           75           80
Lys Lys Ile Glu Pro Arg Glu Tyr Arg Gly Ala Leu Val Ile Gly Thr
85           90           95
Pro Leu Tyr Glu Ile Asn Leu Glu Thr Lys Gly Thr Gln Thr Lys Ile
100          105          110
Lys Thr Ile Glu Arg Gly Phe Leu Gly Ala Leu Ile Met Leu His Lys
115          120          125
Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly Ile Phe Cys Val
130          135          140
Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met Val Ala Phe Lys
145          150          155          160
Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly Ser Val Val Phe
165          170          175
Phe Gly Ala Ile Tyr Trp Ser Leu
180

```

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500

```

Leu Ile Lys Ser Lys Ser Lys Lys Trp Leu Leu Val Gly Glu Gly Ala
1           5           10           15
Asn Ser Glu Ile Phe Glu Ala Ser Met Gln Ser Leu Leu Lys Thr Asp
20           25           30
Gly Val Tyr Ser Asn His Lys Pro Ile Tyr Gln Glu Phe Tyr Glu Leu
35           40           45
Asn Ser His Asn Gly Leu Tyr Tyr Gln Pro Asn Val Phe Phe Ala Tyr
50           55           60
Glu Ser Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp Asn
65           70           75           80
Phe Ser Lys Phe Val Ser His Arg Leu Gln
85           90

```

1061

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501

```

Met Leu Glu Ser Val Asn Val Lys Ile Ser Ala Asp Asp Ile Lys Ser
1           5           10           15
Lys Asn Val Ala Ala Val Met Ile Thr Ala Ser Leu Pro Pro Phe Ala
          20           25           30
Arg Gln Gly Asp Lys Ile Asp Ile His Ile Ser Ser Ile Gly Asp Ala
          35           40           45
Lys Ser Ile Gln Gly Gly Thr Leu Val Met Thr Pro Leu Asn Ala Val
          50           55           60
Asp Gly Asn Ile Tyr Ala Leu Ala Gln Gly Ala Ile Ile Ser Gly Asn
65           70           75           80
Ser Ser Asn Leu Leu Ser Ala Asn Ile Ile Asn Gly Ala Thr Ile Glu
          85           90           95
Arg Glu Val Ser Tyr Asp Leu Phe His Lys Asn Ala Met Thr Leu Ser
          100          105          110
Leu Lys Asn Pro Asn Phe Lys Asn Ala Ile Gln Val Gln Asn Thr Leu
          115          120          125
Asn Lys Val Phe Gly Asn Lys Val Ala Ile Ala Leu Asp Pro Lys Thr
          130          135          140
Ile Gln Ile Thr Arg Pro Glu Arg Leu Ser Met Val Glu Phe Leu Ala
145          150          155          160
Leu Val Gln Glu Ile Pro Ile Tyr Tyr Arg Ala Lys Asn Lys Ile Ile
          165          170          175
Val Asp Glu Lys Ser Gly Thr Ile Val Ser Gly Val Asp Ile Ile Val
          180          185          190
His Pro Ile Val Val Thr Ser Gln Asp Ile Thr Leu Lys Ile Thr Lys
          195          200          205
Glu Pro Leu Asn Asp Ser Lys Asn Met Gln Asp Leu Asp Asn Asn Met
          210          215          220
Ser Leu Asp Thr Ala His Asn Thr Leu Ser Ser Asn Gly Lys Asn Ile
225          230          235          240
Thr Ile Ala Gly Val Val Lys Ala Leu Gln Lys Ile Gly Val Ser Ala
          245          250          255
Lys Gly Met Val Ser Ile Leu Gln Ala Leu Lys Lys Ser Gly Ala Ile
          260          265          270
Ser Ala Lys Trp Arg Tyr Tyr Asp Lys Gln Gln
          275          280

```

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid

1062

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502

```

Thr Gly His Gly Arg Leu Gly Trp Ile Leu Asn Pro Lys Lys Ala Lys
1      5      10      15
Phe Ile Ala Leu Lys Gln Ala Trp Ile Tyr Glu Arg Met Leu Ser Phe
20      25      30
Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg Leu Leu Thr Ala
35      40      45
Leu Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp Leu Glu Ile Gln
50      55      60
Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys Ile Gln Ala Leu
65      70      75      80
Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys Val Val Ser Lys
85      90      95
Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn Ala Asn Val Ser
100     105     110
Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn Met Ser Leu Gly
115     120     125
Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu Thr Gln Ser Lys
130     135     140
Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu Leu Lys Lys Thr
145     150     155     160
Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly Ile Glu Asn Tyr
165     170     175
Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala Ile Lys Asn Leu
180     185     190
Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser Pro Asp Leu Ile
195     200     205
Ala Ile Ala Lys Leu Glu Ile Leu Lys Ser Gln Leu Glu Ile
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503

1063

```

Ile Val Phe His Gln Gly Ser Leu Ser Val Ser Gly Leu Phe Lys Met
1      5      10      15
Arg Ile Leu Ser Phe Lys Lys Asn Lys Arg Ala Val Phe Ser Leu Tyr
20      25      30
Leu Phe Ile Ala Leu Leu Ala Leu Ser Leu Leu Ala Pro Leu Trp Val
35      40      45
Asn Asp Arg Pro Leu Phe Ile Tyr Lys Asp Asn Lys Ala Tyr Phe Pro
50      55      60
Met Phe Lys Asn Tyr Ala Glu Val Glu Phe Gly Gly Asp Phe Phe Thr
65      70      75      80
Pro Thr Asp Tyr Asn Asp Pro Tyr Val Gln Asn Thr Leu Leu Lys Asp
85      90      95
Ala Phe Ile Ile His Ala Leu Ile Pro Tyr Ser Tyr Asp Thr Ile Ile
100      105      110
Met Asp Leu Asp Ser Pro Ala Pro Thr Pro Pro Ser Phe Lys His Leu
115      120      125
Leu Gly Thr Asp Asp Gln Ala Arg Asp Val Leu Ala Arg Leu Val Tyr
130      135      140
Gly Tyr Arg Val Ser Leu Val Phe Gly Ile Leu Leu Thr Leu Phe Ser
145      150      155      160
Val Leu Ile Gly Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly
165      170      175
Leu Val Asp Leu Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile
180      185      190
Pro Met Leu Phe Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn
195      200      205
Phe Trp Ile Ile Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu
210      215      220
Ser Gln Val Val Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr
225      230      235      240
Thr Lys Ala Ala Arg Ala Leu Gly Val Asn Asp Leu Lys Ile Ile Phe
245      250      255
Tyr His Val Leu Pro Asn Ala Leu Val Ala Thr Ile Thr Tyr Ile Pro
260      265      270
Phe Leu Met Ala Ala Ser Ile Ser Thr Leu Val Ser Leu Asp Phe Leu
275      280      285
Gly Phe Gly Met Pro Ile Gly Ser Ala Ser Leu Gly Glu Leu Val Asn
290      295      300
Gln Gly Lys Asp Asn Leu Thr Thr Pro His Leu Ala Val Val Ala Phe
305      310      315      320
Val Ala Ile Ser Leu Leu Leu Ser Val Leu Val Phe Ile Gly Glu Gly
325      330      335
Val Arg Asp Ala Phe Asn Ala Asn Met Leu Lys
340      345

```

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504

SUBSTITUTE SHEET (RULE 26)

Arg Gly Tyr Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser
 1 5 10 15
 His Phe Ser Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg
 20 25 30
 Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn
 35 40 45
 Leu Val Met Arg Leu Asn Pro Arg Phe Lys Pro His Asn Gly Glu Ile
 50 55 60
 Leu Phe Glu Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Met Gln
 65 70 75 80
 His Leu Arg Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser
 85 90 95
 Ser Leu Asn Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr
 100 105 110
 Phe Leu His His Lys Asn Ala Ser Gln Val Leu Leu Lys Glu Gln Val
 115 120 125
 Leu Asn Ala Met Lys Gln Val Gln Leu Asp Glu Lys Phe Leu Asp Arg
 130 135 140
 Tyr Pro Tyr Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Cys Ile Ala
 145 150 155 160
 Met Gly Ile Ile Asn Ala Pro Lys Leu Leu Ile Cys Asp Glu Pro Thr
 165 170 175
 Thr Ala Leu Asp Ala Gln Ile Gln Asn Gln Ile Leu Asp Leu Leu Lys
 180 185 190
 Gln Leu Ser Val Glu Lys Asn Ile Ala Leu Leu Phe Ile Ser His Asp
 195 200 205
 Leu Lys Ala Val Lys Arg Leu Ala Asp Arg Val Tyr Val Leu Lys Lys
 210 215 220
 Gly Glu Ile Val Glu Thr Asn Leu Thr Lys Glu Leu Phe Asn Asp Pro
 225 230 235 240
 Lys His Glu Tyr Ser Lys Leu Leu Ile Gln Ala Ser Asn Leu Pro Ala
 245 250 255
 Lys Asn Leu Lys Ala Leu Asp Glu Thr Leu Leu Glu Val Lys Asp Phe
 260 265 270
 Ser Val Tyr Tyr Leu Gln Lys Arg Phe Phe Arg Pro Ser Leu Lys Lys
 275 280 285
 Pro Leu Ile Ala Ser Val Asp Phe Ser Leu Lys Ala Lys Glu Asn Ile
 290 295 300
 Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Ser Leu Ala Leu Gly
 305 310 315 320
 Leu Leu Lys Leu Ala Leu Asn Ser Gly Glu Glu Lys Ile Leu Gly Gln
 325 330 335
 Ser Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile
 340 345 350
 Leu Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu
 355 360 365
 Ser Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys
 370 375 380
 Ala Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu
 385 390 395 400
 Val Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser
 405 410 415
 Gly Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys
 420 425 430
 Pro Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser
 435 440 445
 Ile Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln
 450 455 460
 Asp Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala
 465 470 475 480
 Phe Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr
 485 490 495
 Gly Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys
 500 505 510

1065

Arg Leu Leu Glu Ser Arg Leu
515

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505

Gly	Gly	Leu	Met	Asn	Thr	Ile	Ile	Arg	Tyr	Ala	Ser	Leu	Trp	Gly	Leu	1	5	10	15
Cys	Ile	Thr	Leu	Thr	Leu	Ala	Gln	Thr	Pro	Ser	Lys	Thr	Pro	Asp	Glu	20	25	30	
Ile	Lys	Gln	Ile	Leu	Asn	Asn	Tyr	Ser	His	Lys	Asn	Leu	Lys	Leu	Ile	35	40	45	
Asp	Pro	Pro	Thr	Ser	Ser	Leu	Glu	Ala	Thr	Pro	Gly	Phe	Leu	Pro	Ser	50	55	60	
Pro	Lys	Glu	Thr	Ala	Thr	Thr	Ile	Asn	Gln	Glu	Ile	Ala	Lys	Tyr	His	65	70	75	80
Glu	Lys	Ser	Asp	Lys	Ala	Ala	Leu	Gly	Leu	Tyr	Glu	Leu	Leu	Lys	Gly	85	90	95	
Ala	Thr	Thr	Asn	Leu	Ser	Leu	Gln	Ala	Gln	Glu	Leu	Ser	Val	Lys	Gln	100	105	110	
Ala	Met	Lys	Asn	His	Thr	Ile	Ala	Lys	Ala	Met	Phe	Leu	Pro	Thr	Leu	115	120	125	
Asn	Ala	Ser	Tyr	Asn	Phe	Lys	Asn	Glu	Ala	Arg	Asp	Thr	Pro	Glu	Tyr	130	135	140	
Lys	His	Tyr	Asn	Thr	Gln	Gln	Leu	Gln	Ala	Gln	Val	Thr	Leu	Asn	Val	145	150	155	160
Phe	Asn	Gly	Phe	Ser	Asn	Val	Asn	Asn	Val	Lys	Glu	Lys	Ser	Ala	Thr	165	170	175	
Thr	Asp	Pro	Leu	Trp	Leu	Ile										180			

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

1066

(A) NAME/KEY: misc_feature
(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506

```

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
1      5      10      15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
      20      25      30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
      35      40      45
Ala Asp His Thr Leu Ile Gly Gly Gly Ala Gly Gln Ile Leu Asp Pro
      50      55      60
Glu Met Ile Glu Asn Ala Leu His Ser Val Lys Asn Pro Lys His Thr
      65      70      75      80
Ile Phe Leu Ser Ala Val Gly Lys Pro Phe Lys Gln Ile Asp Ala Met
      85      90      95
Arg Leu Ala Gln Lys Lys His Val Val Leu Val Cys Gly Arg Tyr Glu
      100     105     110
Gly Phe Asp Glu Arg Ser Ile Glu Leu Gly Ala Asp Glu Val Phe Cys
      115     120     125
Ile Gly Asp Phe Ile Leu Thr Gly Gly Glu Leu Gly Ala Leu Cys Leu
      130     135     140
Ile Asp Ser Ile Ala Arg His Ile Gln Gly Val Leu Gly Asn Ala Gln
145     150     155     160
Ser Leu Glu Asn Glu Ser Phe Glu Asn Asn Tyr Leu Glu Thr Pro Asn
      165     170     175
Phe Ala Asn Ala Val Phe Lys Ser Lys Glu Ile Asn Lys Ile Pro Ala
      180     185     190
Pro Leu Glu Tyr Ser Lys Gly Asn His Ala Lys Ile Lys Gln Leu Lys
      195     200     205
Leu Asp Leu Ser Lys Leu Arg Thr Lys Phe Tyr Arg Leu Asp Leu Phe
      210     215     220
Lys Gln His Lys Ser
225

```

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507

```

Arg Glu Gln Trp Phe His Phe Arg Ser Thr Pro Pro Thr Val Val Leu
1      5      10      15
Met Ala Gly Leu Gln Gly Ser Gly Lys Thr Thr Thr Thr Ala Lys Leu
      20      25      30
Ala His Tyr Leu Lys Thr Lys Asn Lys Lys Val Leu Leu Cys Ala Cys
      35      40      45
Asp Leu Gln Arg Leu Ala Ala Val Glu Gln Leu Lys Val Leu Gly Glu
      50      55      60

```

SUBSTITUTE SHEET (RULE 26)

1067

Gln Val Gly Val Glu Val Phe His Glu Glu Asn Lys Ser Val Lys Glu
 65 70 75 80
 Ile Ala Asn Asn Ala Leu Lys Arg Ala Lys Glu Ala Gln Phe Asp Val
 85 90 95
 Leu Ile Val Asp Ser Ala Gly Arg Leu Ala Ile Asp Lys Glu Leu Met
 100 105 110
 Gln Glu Leu Lys Glu Val Lys Glu Val Leu Asn Pro His Glu Val Leu
 115 120 125
 Tyr Val Ala Asp Ala Leu Ser Gly Gln Asp Gly Val Lys Ser Ala Asn
 130 135 140
 Thr Phe Asn Glu Glu Ile Gly Val Ser Gly Val Val Leu Ser Lys Phe
 145 150 155 160
 Asp Ser Asp Ser Lys Gly Gly Ile Ala Leu Gly Ile Thr Tyr Gln Leu
 165 170 175
 Gly Leu Pro Leu Arg Phe Ile Gly Ser Gly Glu Lys Ile Pro Asp Leu
 180 185 190
 Asp Val Phe Met Pro Glu Arg Ile Val Gly Arg Leu Met Gly Ala Gly
 195 200 205
 Asp Ile Ile Ser Leu Ala Glu Lys Thr Ala Ser Val Leu Asn Pro Asn
 210 215 220
 Glu Ala Lys Asp Leu Ser Lys Lys Leu Lys Lys Gly Gln Phe Thr Phe
 225 230 235 240
 Asn Asp Phe Leu Asn Gln Ile Glu Lys Val Lys Lys Leu Gly Ser Met
 245 250 255
 Ser Ser Leu Ile Ser Met Ile Pro Gly Leu Gly Asn Met Ala Ser Ala
 260 265 270
 Leu Lys Asp Thr Asp Leu Glu Ser Ser Leu Glu Val Lys Lys Ile Lys
 275 280 285
 Ala Met Val Asn Ser Met Thr Lys Lys Glu Arg Glu Asn Pro Glu Ile
 290 295 300
 Leu Asn Gly Ser Arg Arg Lys Arg Ile Ala Leu Gly Ser Gly Leu Glu
 305 310 315 320
 Val Ser Glu Ile Asn Arg Ile Ile Lys Arg Phe Asp Gln Ala Ser Lys
 325 330 335
 Met Ala Lys Arg Leu Thr Asn Lys Lys Gly Ile Ser Asp Leu Met Asn
 340 345 350
 Leu Met Ser Gln Ala Lys Asn Gln Thr Pro Pro Lys Met Arg
 355 360 365

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508

Arg Lys Ala Met Asn Thr His Leu Lys Gln Leu Ile Glu Ile Ser His
 1 5 10 15
 Leu Asp Lys Glu Ile Asp Ser Leu Glu Pro Leu Ile Arg Glu Lys Arg
 20 25 30
 Lys Asp Leu Asp Lys Ala Leu Asn Asp Lys Glu Ala Lys Asn Lys Ala

SUBSTITUTE SHEET (RULE 26)

1068

```

      35              40              45
Ile Leu Asn Leu Glu Glu Glu Lys Leu Ala Leu Lys Leu Gln Val Ser
  50              55              60
Lys Asn Glu Gln Thr Leu Gln Asp Thr Asn Ala Lys Ile Ala Ser Ile
  65              70              75              80
Gln Lys Lys Met Ser Glu Ile Lys Ser Glu Arg Glu Leu Arg Ser Leu
      85              90              95
Asn Ile Glu Glu Asp Ile Ala Lys Glu Arg Ser Asn Gln Ala Asn Arg
      100              105              110
Glu Ile Glu Asn Leu Gln Asn Glu Ile Lys His Lys Ser Glu Lys Gln
      115              120              125
Glu Val Leu Lys Lys Glu Met Leu Glu Leu Glu Lys Leu Ala Leu Glu
      130              135              140
Leu Glu Asn Leu Val Glu Asn Glu Val Lys Asn Ile Lys Glu Thr Gln
      145              150              155              160
Gln Ile Ile Phe Lys Lys Lys Glu Glu Leu Val Glu Lys Thr Glu Pro
      165              170              175
Lys Ile Tyr Ser Phe Tyr Glu Arg Ile Arg Arg Trp Ala Lys Asn Thr
      180              185              190
Ser Ile Val Thr Ile Lys Lys Gln Ala Cys Gly Gly Cys Phe Ile Arg
      195              200              205
Leu Asn Asp Lys Ile Tyr Ala Glu Val Leu Thr Ser Gly Asp Met Ile
      210              215              220
Thr Cys Pro Tyr Cys Gly Arg Ile Leu Tyr Ala Glu Ser Thr His Glu
      225              230              235              240
Ser Asn Ala Gln Pro Pro Lys Glu Ser Gln Pro Lys Glu Ser Gln Glu
      245              250              255
Glu Ser Gln Glu Glu Ser Gln Glu Glu Ser Gln Glu Ser Val
      260              265              270

```

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509

```

Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
  1              5              10              15
Asp Val Ile Lys Lys Val Lys Thr Pro Lys Gly Gly Ile Glu Val Leu
      20              25              30
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
      35              40              45
Ala Thr Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
      50              55              60
Ile Val His Pro Ile Cys Val Ala Ser Val Val Ala Phe Cys Gly Gly
      65              70              75              80
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
      85              90              95
Thr Pro Cys Glu Ile Glu Thr Ile Glu Arg Glu Phe Gly Gln Asp Val
      100              105              110

```

1069

Ala	Asn	Leu	Val	Asp	Ala	Leu	Thr	Lys	Ile	Thr	Glu	Ile	Arg	Lys	Glu
	115						120					125			
Glu	Leu	Gly	Val	Ser	Ser	Gln	Asp	Pro	Arg	Met	Val	Val	Ser	Ala	Leu
	130					135					140				
Thr	Phe	Arg	Lys	Ile	Leu	Ile	Ser	Ala	Ile	Gln	Asp	Pro	Arg	Ala	Leu
	145				150					155					160
Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	His	Asn	Met	Leu	Thr	Leu	Asp	Ala
				165					170					175	
Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Glu	Thr	Leu	Ala	Val
		180						185					190		
Tyr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	Lys	Asn	Glu
	195						200					205			
Leu	Glu	Asp	Lys	Ser	Phe	Tyr	Tyr	Ile	Tyr	Pro	Glu	Glu	Tyr	Lys	Asn
	210					215					220				
Ile	Lys	Glu	Tyr	Leu	His	Lys	Asn	Lys	Gln	Ser	Leu	Leu	Leu	Lys	Leu
	225				230					235					240
Asn	Ala	Phe	Ala	Ser	Lys	Leu	Glu	Lys	Lys	Leu	Phe	Asp	Ser	Gly	Phe
				245					250					255	
Ser	His	Ser	Asp	Phe	Lys	Leu	Val	Thr	Arg	Val	Lys	Arg	Pro	Tyr	Ser
		260						265					270		
Ile	Tyr	Leu	Lys	Met	Gln	Arg	Lys	Gly	Ala	Val	Asn	Ile	Asp	Glu	Ile
	275					280						285			
Leu	Asp	Leu	Leu	Ala	Ile	Arg	Ile	Leu	Leu	Lys	Asn	Pro	Ile	Asp	Cys
	290					295					300				
Tyr	Lys	Val	Leu	Gly	Ile	Ile	His	Leu	Asn	Phe	Lys	Pro	Ile	Val	Ser
	305				310					315					320
Arg	Phe	Lys	Asp	Tyr	Ile	Ala	Leu	Pro	Lys	Glu	Asn	Gly	Tyr	Lys	Thr
				325					330					335	
Ile	His	Thr	Thr	Ile	Phe	Asp	Glu	Ser	Ser	Val	Tyr	Glu	Val	Gln	Ile
		340					345						350		
Arg	Thr	Phe	Asp	Met	His	Met	Gly	Ala	Glu	Tyr	Gly	Asn	Ser	Ala	His
		355					360					365			
Trp	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Asp	His	Glu	Glu	His	His	Glu	Gly
	370					375					380				
Met	Arg	Trp	Leu	Gln	Asn	Phe	Lys	Tyr	His	Asp	Ser	Asp	Leu	Lys	Asn
	385				390					395					400
Asp	Pro	Lys	Glu	Phe	Tyr	Glu	Leu	Ala	Lys	Asn	Asp	Leu	Tyr	Arg	Glu
				405					410					415	
Asp	Ile	Val	Val	Phe	Ser	Pro	His	Gly	Asp	Thr	Tyr	Thr	Leu	Pro	Val
		420						425					430		
Gly	Ala	Ile	Ala	Leu	Asp	Phe	Ala	Tyr	Met	Val	His	Ser	Asp	Leu	Gly
	435						440					445			
Asp	Lys	Ala	Thr	Asp	Ala	Tyr	Ile	Asn	Ser	Lys	Lys	Ala	Leu	Leu	Asn
	450					455					460				
Gln	Glu	Leu	Arg	Ser	Gly	Asp	Val	Val	Lys	Ile	Ile	Lys	Gly	Asp	Lys
	465				470					475					480
Val	Ile	Pro	Arg	Phe	Ile	Trp	Met	Asp	Gln	Leu	Lys	Thr	Ser	Lys	Ala
				485					490					495	
Lys	Asn	His	Leu	Arg	Ile	Gln	Arg	Arg	Asn	Arg	Leu	Lys	Glu	Ile	Asp
		500					505						510		
Thr	Lys	Ser	Met	Ile	Asn	Ile	Leu	Ser	Thr	Phe	Phe	Gly	Arg	Ser	Val
		515					520					525			
Phe	Glu	Asp	Ala	Asp	Leu	Lys	Asp	Tyr	Lys	Asn	Phe	Glu	Glu	Lys	Leu
	530					535					540				
Thr	Asp	Cys	Gly	Val	Glu	Thr	Thr	Leu	Thr	Glu	Ala	Met	Lys	Ser	Phe
	545				550					555					560
Glu	Asn	Leu	Gly	Gln	Thr	His									
				565											

(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

1070

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510

```

Val Thr Ile Lys Ser Phe Ile Asn Gly Leu Arg Arg Asp His Ala Gly
1      5      10      15
Lys Asp Lys Lys Gln Ala Gly Phe Gly Glu Ile Phe Trp Gly Ser Val
20      25      30
Ser Trp Gly Gln Pro Val Trp Ile Asp Ile His Val Leu Asp His Ile
35      40      45
Ala Lys Glu Ile Arg Ser Leu Val Glu Asn Asp Ile Glu Val Gly Ile
50      55      60
Val Ile Gly Gly Gly Asn Ile Ile Arg Gly Val Ser Ala Ala Gln Gly
65      70      75      80
Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr Met Gly Met Leu Ala Thr
85      90      95
Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His Ile Gly Leu
100     105     110
Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile Cys Glu Ser
115     120     125
Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly Arg Val Val
130     135     140
Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr Asp Thr Ala
145     150     155     160
Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile Ile Lys Ala
165     170     175
Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys Phe Lys Asp
180     185     190
Ala Lys Asn Trp Thr Leu
195

```

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511

```

Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Glu Thr Asn
1      5      10      15

```

1071

```

Thr Asp Asp Leu Ser Pro Ala Ser Asp Ala Phe Thr Arg Ser Asp Ile
      20      25      30
Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Glu Asn Tyr Glu
      35      40      45
Gln Arg Ile Glu Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
      50      55      60
Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
      65      70      75      80
Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
      85      90      95
Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
      100      105      110
Thr Cys Glu Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
      115      120      125
Leu Lys Glu Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Glu Ile
      130      135      140
Thr Leu Asn Asp Lys Val Val Ser Thr Phe Lys Leu Glu Pro Glu Thr
      145      150      155      160
Leu Leu Asp Glu Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
      165      170      175
Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Leu Gly Glu Ser
      180      185      190
Glu Ala Phe Lys Lys Pro Ser Ala Pro Lys Ser Asp Ala Lys Gly Tyr
      195      200      205
Thr Leu Ala Gln Lys Ile Val Gly His Ala Cys Gly Val Lys Gly Ile
      210      215      220
Leu Pro Gly Ala Tyr Cys Glu Pro Lys Val Thr Thr Val Gly Ser Gln
      225      230      235      240
Asp Thr Thr Gly Ala Met Thr Arg Asp Glu Val Lys Glu Leu Ala Ser
      245      250      255
Leu Lys Phe Asp Ala Pro Phe Val Leu Gln Ser Phe Cys His Thr Ala
      260      265      270
Ala Tyr Pro Lys Pro Ser Asp Val Ser Leu His Ala Thr Leu Pro Gly
      275      280      285
Phe Ile Thr Gln Arg Gly Gly Val Ala Leu His Pro Gly Asp Gly Val
      290      295      300
Ile His Thr Trp Leu Asn Arg Met Gly Leu Pro Asp Thr Leu Gly Thr
      305      310      315      320
Gly Gly Asp Ser His Thr Arg Phe Pro Leu Gly Ile Ser Phe Arg Gln
      325      330      335
Gly Ala Gly

```

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512

Thr Phe Thr Ile Lys Arg Phe Val Leu Met Lys Ile Lys Ile Gln Lys

SUBSTITUTE SHEET (RULE 26)

1072

```

1           5           10           15
Ile His Pro Asn Ala Leu Ile Pro Lys Tyr Gln Thr Glu Gly Ser Ser
                20           25           30
Gly Phe Asp Leu His Ala Val Glu Glu Val Val Ile Lys Pro His Ser
                35           40           45
Val Gly Leu Val Arg Ile Gly Ile Cys Leu Ser Leu Glu Val Gly Tyr
                50           55           60
Glu Leu Gln Val Arg Thr Arg Ser Gly Leu Ala Leu Asn His Gln Val
        65           70           75           80
Met Val Leu Asn Ser Pro Gly Thr Val Asp Asn Asp Tyr Arg Gly Glu
                85           90           95
Ile Lys Val Ile Leu Ala Asn Leu Ser Asp Lys Asp Phe Lys Val Gln
                100           105           110
Val Gly Asp Arg Ile Ala Gln Gly Val Val Gln Lys Thr Tyr Lys Ala
                115           120           125
Glu Phe Ile Glu Cys Glu Gln Leu Asp Glu Thr Ser Arg Gly Ser Gly
        130           135           140
Gly Phe Gly Ser Thr Gly Val Ser Lys Ala
145           150

```

(2) INFORMATION FOR SEQ ID NO:1513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513

```

Arg Lys Lys Pro Phe Lys Glu Arg Ile Asp Leu Met Asn Lys Pro Phe
1           5           10           15
Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser Gly Cys Asn Met Arg
        20           25           30
Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys Gly Glu Ala Tyr Phe
        35           40           45
Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser Asn Arg Tyr Gly Ala
        50           55           60
Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys Gly Leu Thr Gln Leu
        65           70           75           80
Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser Phe Leu Asn Glu Ser
        85           90           95
Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu Asn Lys Ile Asp Lys
        100           105           110
Lys Thr Ser Lys Ser Arg Ala Ala Lys Thr Glu Glu Thr Glu Leu Lys
        115           120           125
Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys Val Cys His Gln Val
        130           135           140
Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile
145           150           155           160
Pro Leu Glu Thr Phe Ala Leu Ala Arg Ala Leu Lys Gly Ile Phe
        165           170           175

```

SUBSTITUTE SHEET (RULE 26)

1073

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514

```

Gly Met Ser Ile Lys Glu Asn Leu Glu Gln Val Arg Asn Glu Phe Lys
1          5          10          15
Ser Asp Glu Lys Leu Leu Glu Gly Ala Phe Arg Leu Glu Lys Phe Phe
          20          25          30
Lys Arg Tyr Lys Trp Val Leu Leu Phe Ile Val Val Ala Phe Ile Ala
          35          40          45
Tyr Leu Gly Asp Thr Lys Leu Gln Asp Tyr Lys His Glu Gln Thr Arg
          50          55          60
Glu Arg Ile Thr Gln Ile Tyr Asn Glu Val Leu Glu Ser Pro Asn Asn
          65          70          75          80
Ile Ala Leu Gln Lys Arg Leu Lys Glu Val Ala Pro Glu Leu Tyr Asp
          85          90          95
Leu Tyr Gln Phe Ala Arg Ala Ser Glu Arg Asn Asp Ala Asn Glu Phe
          100          105          110
Lys Arg Leu Ser Gln Ser Ser Asn Glu Ile Val Lys Ala Phe Ala Lys
          115          120          125
Tyr Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Leu Glu Lys Ser
          130          135          140
Pro Ile Leu Lys Glu Met Ser Ala Leu Gln Glu Val Asn Leu Leu Tyr
          145          150          155          160
Glu Glu Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser
          165          170          175
Thr Ile Pro Leu Ser Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys
          180          185          190
His Tyr Gly Met Leu Glu Asp Ile Gln Gln Asn Pro Ser Lys Pro Thr
          195          200          205
Asn Leu Lys Lys Glu Thr Ile Gln Gly Thr His
          210          215

```

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

1074

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515

```

Lys Arg Tyr Lys Arg Leu Glu Gln Glu Ile Lys Lys Arg Asp Lys Met
1      5      10      15
Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu Ala
20     25     30
His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met Arg
35     40     45
Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile Leu
50     55     60
Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu Glu
65     70     75     80
Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val Gly
85     90     95
Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu Phe
100    105    110
Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val Pro
115    120    125
Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile Gly
130    135    140
Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe Leu
145    150    155    160
Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val Leu
165    170    175
Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu Ala
180    185    190
Leu Gln Gln Leu Arg Ser
195

```

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516

```

Ser Arg Thr Leu Cys Ala Lys Ile Val Leu Gln Lys Glu Arg Lys Lys
1      5      10      15
Met Glu Ile Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
20     25     30
Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
35     40     45
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
50     55     60
Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
65     70     75     80
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
85     90     95

```

SUBSTITUTE SHEET (RULE 26)

1075

```

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
      100      105      110
Glu Tyr Asp Leu Tyr Lys Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
      115      120      125
Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
      130      135      140
Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys
      145      150      155      160
Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
      165      170      175
Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
      180      185      190
Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asn Phe Asn Ala
      195      200      205
Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
      210      215      220
Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
      225      230      235      240
Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
      245      250      255
Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Asn Gly Asn
      260      265      270
Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
      275      280      285
Tyr Ser Thr Ile Asn Thr Ser Lys Val Gln Gly Glu Val Asp Phe Asn
      290      295      300
His Leu Thr Val Gly Asp Gln Asn Ala Ala Gln Ala Gly Ile Ile Ala
      305      310      315      320
Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
      325      330      335
Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
      340      345      350
Ser Thr Thr Ser Gln Ser Gly Thr Lys Asn Asp Lys Lys Glu Ile Ser
      355      360      365
Gln Asn Asn Asn Ser Asn Thr Glu Val Ile Asn Pro Pro Asn Asn Thr
      370      375      380
Gln Lys Thr Glu Thr Glu Pro Thr Lys Ser Leu Met Gly Leu Leu Leu
      385      390      395      400
Lys Ala Lys Thr Arg Leu Ser
      405

```

(2) INFORMATION FOR SEQ ID NO:1517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517

```

Val Ile Asn Thr Thr Ser Met Leu Lys Lys Ile Phe Leu Thr Asn Ser
1           5           10           15
Leu Gly Ile Leu Cys Ser Arg Ile Phe Gly Phe Leu Arg Asp Leu Met

```

SUBSTITUTE SHEET (RULE 26)

			20						25				30			
Met	Ala	Asn	Ile	Leu	Gly	Ala	Gly	Val	Tyr	Ser	Asp	Ile	Phe	Phe	Val	
		35					40					45				
Ala	Phe	Lys	Leu	Pro	Asn	Leu	Phe	Arg	Arg	Ile	Phe	Ala	Glu	Gly	Ser	
	50					55					60					
Phe	Ser	Gln	Ser	Phe	Leu	Pro	Ser	Phe	Ile	Arg	Ser	Ser	Ile	Lys	Gly	
65					70					75					80	
Gly	Phe	Ala	Ser	Leu	Val	Gly	Leu	Ile	Phe	Cys	Gly	Val	Leu	Phe	Met	
				85					90					95		
Trp	Cys	Leu	Leu	Val	Ala	Leu	Asn	Pro	Leu	Trp	Leu	Thr	Lys	Leu	Leu	
			100					105						110		
Ala	Tyr	Gly	Phe	Asp	Glu	Glu	Thr	Leu	Lys	Leu	Cys	Thr	Pro	Ile	Val	
		115					120					125				
Ala	Ile	Asn	Phe	Trp	Tyr	Leu	Leu	Val	Phe	Ile	Thr	Thr	Phe	Leu		
	130					135				140						
Gly	Ala	Leu	Leu	Gln	Tyr	Lys	His	Ser	Phe	Phe	Ala	Ser	Ala	Tyr	Ser	
145					150					155					160	
Ala	Ser	Leu	Leu	Asn	Leu	Cys	Met	Ile	Leu	Ala	Leu	Leu	Ile	Ser	Lys	
				165					170					175		
Glu	Lys	Thr	His	Leu	Glu	Ala	Leu	Tyr	Tyr	Leu	Ser	Tyr	Gly	Val	Leu	
			180					185						190		
Leu	Gly	Gly	Val	Ala	Gln	Ile	Leu	Leu	His	Phe	Tyr	Pro	Leu	Val	Lys	
		195					200					205				
Leu	Gly	Leu	Trp	Asp	Leu	Leu	Phe	Lys	Gly	Leu	Leu	Gly	Phe	Lys	Thr	
	210				215					220						
Lys	Asn	Thr	Asn	Lys	Lys	Glu	Tyr	Arg	Leu	Asn	Arg	Ala	Lys	Lys	Asp	
225					230					235					240	
Leu	Lys	Ala	Phe	Phe	Lys	Gln	Phe	Phe	Pro	Ser	Val	Leu	Gly	Asn	Ser	
				245					250					255		
Ser	Ala	Gln	Ile	Ala	Ser	Phe	Leu	Asp	Thr	Thr	Ile	Ala	Ser	Phe	Leu	
			260					265						270		
Ala	Ser	Gly	Ser	Val	Ser	Tyr	Leu	Tyr	Tyr	Ala	Asn	Arg	Val	Phe	Gln	
		275					280					285				
Leu	Pro	Leu	Ala	Leu	Phe	Ala	Ile	Ala	Ile	Ser	Thr	Ala	Leu	Phe	Pro	
	290					295					300					
Ser	Ile	Ala	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Gln	Asp	Leu	Ile	Leu	Gln	
305					310					315					320	
Arg	Leu	Gln	Lys	Ala	Trp	Phe	Phe	Leu	Val	Gly	Val	Leu	Leu	Leu	Cys	
				325					330					335		
Ser	Ile	Gly	Gly	Ile	Met	Leu	Ser	Lys	Glu	Ile	Thr	Glu	Leu	Leu	Phe	
			340					345								

(vi) ORIGINAL SOURCE:

1077

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518

```

Phe Arg Leu Pro Ser Pro Leu Thr Ser Ile Leu Met Arg Leu Asp Tyr
1          5          10          15
Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg Glu Lys Ala Lys Ala
20          25          30
Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys Met Val Val Ser Lys
35          40          45
Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile Glu Leu Ile Ala Pro
50          55          60
Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu Gly Ala Phe Leu Glu
65          70          75          80
Asp His Phe Ile Asp Phe Lys Glu Lys Val Val Leu Asp Val Gly Ala
85          90          95
Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu Lys Gly Ala Lys Lys
100         105         110
Val Leu Cys Val Asp Val Gly Lys Met Gln Leu Asp Glu Ser Leu Lys
115         120         125
Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys Asp Ile Arg Gly Phe
130         135         140
Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile
145         150         155         160
Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro Leu Ser Gly Glu Phe
165         170         175
Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Thr Ile Lys Arg
180         185         190
Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala Ile Leu Asn Ala Leu
195         200         205
Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Thr
210         215         220
Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe
225         230         235         240
Ile His Phe Lys Arg Ala
245

```

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519

```

Arg His Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile
1          5          10          15
Ile Gly Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn

```

SUBSTITUTE SHEET (RULE 26)

1078

[illegible]

SUBSTITUTE SHEET (RULE 26)

1079

Gly Lys Ser Val Gly Val Asn Ala Met Ile Leu Ser Leu Leu Tyr Lys
 545 550 555 560
 Asn Pro Pro Asp Gln Leu Lys Leu Val Met Ile Asp Pro Lys Met Val
 565 570 575
 Glu Phe Ser Ile Tyr Ala Asp Ile Pro His Leu Leu Thr Pro Ile Ile
 580 585 590
 Thr Asp Pro Lys Lys Ala Ile Gly Ala Leu Gln Ser Val Ala Lys Glu
 595 600 605
 Met Glu Arg Arg Tyr Ser Leu Met Ser Glu Tyr Lys Val Lys Thr Ile
 610 615 620
 Asp Ser Tyr Asn Glu Gln Ala Gln Ser Asn Gly Val Glu Ala Phe Pro
 625 630 635 640
 Tyr Leu Ile Val Val Ile Asp Glu Leu Ala Asp Leu Met Met Thr Gly
 645 650 655
 Gly Lys Glu Ala Glu Phe Pro Ile Ala Arg Ile Ala Gln Met Gly Arg
 660 665 670
 Ala Ser Gly Leu His Leu Ile Val Ala Thr Gln Arg Pro Ser Val Asp
 675 680 685
 Val Val Thr Gly Leu Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe
 690 695 700
 Arg Val Gly Thr Lys Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly
 705 710 715 720
 Ala Gln Ser Leu Leu Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly
 725 730 735
 Thr Asn Gly Leu Val Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu
 740 745 750
 Ile Lys Lys Ile Val Asp Phe Ile Lys Ala Gln Lys Glu Val Glu Tyr
 755 760 765
 Asp Lys Asp Phe Leu Leu Glu Ser Arg Met Pro Leu Asp Thr Pro
 770 775 780
 Asn Tyr Gln Gly Asp Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu
 785 790 795 800
 Glu Lys Lys Ile Thr Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile
 805 810 815
 Gly Tyr Asn Gln Ala Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly
 820 825 830
 Phe Leu Ser Pro Arg Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn
 835 840 845
 Phe

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520

Asn Tyr Leu Lys Ile Ser Cys Ser Arg Ile Ala Met Asn Pro Gln Ile
 1 5 10 15
 Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu Leu Ala Ala Ser Ser

1080

			20						25					30			
Gly	Asn	Leu	Val	Glu	Trp	Tyr	Asp	Phe	Tyr	Ala	Tyr	Ala	Phe	Leu	Ala		
	35						40					45					
Pro	Tyr	Phe	Ala	Lys	Glu	Phe	Thr	His	Thr	Asn	Asp	Pro	Thr	Leu	Ala		
	50					55				60							
Leu	Ile	Ser	Ala	Phe	Leu	Val	Phe	Met	Leu	Gly	Phe	Phe	Met	Arg	Pro		
65					70					75					80		
Leu	Gly	Ser	Leu	Phe	Phe	Gly	Lys	Leu	Gly	Asp	Lys	Lys	Gly	Arg	Lys		
				85					90					95			
Thr	Ser	Met	Val	Tyr	Ser	Ile	Ile	Leu	Met	Ala	Leu	Gly	Ser	Phe	Met		
			100					105						110			
Leu	Ala	Leu	Leu	Pro	Thr	Lys	Glu	Ile	Val	Gly	Glu	Trp	Ala	Phe	Leu		
	115						120					125					
Phe	Leu	Leu	Leu	Ala	Arg	Leu	Gln	Gly	Phe	Ser	Val	Gly	Gly	Glu			
	130					135				140							
Tyr	Gly	Val	Val	Ala	Thr	Tyr	Leu	Ser	Glu	Leu	Gly	Lys	Asn	Gly	Lys		
145					150					155					160		
Lys	Gly	Phe	Tyr	Gly	Ser	Phe	Gln	Tyr	Val	Thr	Leu	Val	Gly	Gly	Gln		
				165					170					175			
Leu	Leu	Ala	Ile	Phe	Ser	Leu	Phe	Ile	Val	Glu	Asn	Val	Tyr	Thr	His		
			180					185						190			
Glu	Gln	Ile	Ser	Ala	Phe	Ala	Trp	Arg	Tyr	Leu	Phe	Ala	Leu	Glu	Gly		
	195						200					205					
Ile	Leu	Ala	Leu	Leu	Ser	Leu	Phe	Leu	Arg	Asn	Ile	Met	Glu	Glu	Thr		
	210					215				220							
Met	Asp	Asn	Glu	Ala	Thr	Pro	Gln	Lys	Lys	Thr	Asn	Val	Asn	Asn	Thr		
225					230					235					240		
Lys	Glu	Thr	His	Ile	Lys	Glu	Thr	Gln	Arg	Gly	Ser	Leu	Lys	Glu	Leu		
				245					250					255			
Leu	Asn	His	Lys	Lys	Ala	Leu	Met	Ile	Val	Phe	Gly	Leu	Thr	Met	Gly		
			260					265					270				
Gly	Ser	Leu	Cys	Phe	Tyr	Thr	Phe	Thr	Val	Tyr	Leu	Lys	Ile	Phe	Leu		
	275						280					285					
Thr	Asn	Ser	Ser	Ser	Phe	Ser	Pro	Lys	Glu	Ser	Ser	Phe	Ile	Met	Leu		
	290					295					300						
Leu	Ala	Leu	Ser	Tyr	Phe	Ile	Phe	Leu	Gln	Pro	Leu	Cys	Gly	Met	Leu		
305					310					315					320		
Ala	Asp	Lys	Ile	Lys	Arg	Thr	Gln	Met	Leu	Met	Val	Phe	Ala	Ile	Thr		
				325					330					335			
Gly	Leu	Ile	Val	Thr	Pro												

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

1081

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521

```

Lys Trp Lys Asn Leu Met Gln Leu Ser Asn Ala Asp Leu Glu Arg Leu
1      5      10      15
Lys Ser Met Ala Asn Thr Leu Arg Phe Leu Cys Ala Asp Met Ile Asp
20     25     30
Lys Ala Asn Ser Gly His Pro Gly Val Cys Leu Gly Leu Ala Asp Val
35     40     45
Met Val Val Leu Ser Leu His Leu Asn Leu Asn Pro Thr Asn Pro Lys
50     55     60
Trp Leu Asn Arg Asp Arg Leu Val Phe Ser Gly Gly His Ala Ser Ala
65     70     75     80
Leu Val Tyr Ser Leu Leu His Leu Trp Gly Phe Asp Leu Ser Leu Asp
85     90     95
Asp Leu Lys Arg Phe Arg Gln Leu His Ser Lys Thr Pro Gly His Pro
100    105    110
Glu Leu His His Thr Glu Gly Ile Glu Ile Thr Thr Ala Pro Leu Gly
115    120    125
Gln Gly Phe Ala Asn Ala Val Gly Phe Ser Met Ala Ser Gln Tyr Ala
130    135    140
Gln Thr Leu Leu Asp Lys Glu Ala Ile Ser His Lys Val Tyr Cys Leu
145    150    155    160
Cys Gly Asp Gly Asp Leu Gln Glu Gly Ile Ser Tyr Glu Ser Thr Ser
165    170    175
Leu Ala Gly His Leu Arg Leu Asp Asn Leu Ile Val Ile Tyr Asp Ser
180    185    190
Asn Gln Ile Ser Ile Glu Gly Ala Ile Asn Ile Ser Phe Ser Glu Gln
195    200    205
Val Lys Thr Arg Phe Leu Ala Gln Asn Trp Glu Val Leu Glu Cys Asp
210    215    220
Gly His Asp Tyr Gln Ala Ile His Asn Ala Leu Glu Glu Ala Lys Lys
225    230    235    240
Ser His Lys Pro Thr Leu Leu Ile Ala His Thr Ile Ile Gly Lys Gly
245    250    255
Ala Ile Gly Leu Glu Gly Ser Glu Lys Thr His Gly Ser Pro Leu Ser
260    265    270
Lys Glu Val Leu Lys Gln Ser Lys Glu Asn Ala Gln Ile Asn Pro Asn
275    280    285
Glu Ser Phe Ile Ile Ser Pro Lys Asn Lys Met His Phe Glu Glu Val
290    295    300
Lys Val Arg Gly Ile Ser Leu Glu Ala Leu Trp Glu Lys Ser Leu Ser
305    310    315    320
Pro Lys Thr Lys Glu Lys Ile His Ala Leu Lys Asn Phe Asp Phe Asn
325    330    335
Ala Ile Asn Tyr Pro Ala Phe Lys Lys Gly Glu Ser Leu Ala Thr Arg
340    345    350
Val Ser Asn Gly Met Ile Leu Asn Ala Ile Ala Lys Glu Cys Glu Gly
355    360    365
Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser Asn Asn Thr His Leu
370    375    380
Lys His Ser Gly Asp Phe Pro Leu Gly Gln Asn Leu His Phe Gly Ile
385    390    395    400
Arg Glu His Ala Met Gly Ala Ile Thr Asn Ala Leu Ala Ala Tyr Gly
405    410    415
Leu Phe Val Pro Phe Cys Ala Thr Phe Phe Val Phe Ser Asp Tyr Leu
420    425    430
Met Pro Ser Ile Arg Leu Ser Ala Leu Met Lys Leu Lys Ala Leu Phe

```

SUBSTITUTE SHEET (RULE 26)

1082

```

      435      440      445
Ile Phe Thr His Asp Ser Ile Gly Val Gly Glu Asp Gly Ala Thr His
450      455      460
Gln Pro Ile Glu Gln Leu Ser His Leu Arg Ala Leu Pro His Phe Tyr
465      470      475      480
Ala Phe Arg Pro Ser Asp Ala Phe Glu Asn Lys Ala Cys Met Gln Val
      485      490      495
Ala Leu Ser Leu Asn Ala Pro Ser Ala Leu Ile Leu Ser Arg Gln Asn
      500      505      510
Leu Ser Val Leu Asp Glu Val Ser Lys Glu Gln Val Leu Lys Gly Ala
      515      520      525
Tyr Val Lys His His Ser Lys Asp Pro Ile Ile Thr Leu Val Ala Ser
      530      535      540
Gly Ser Glu Val Ser Leu Ala Leu Glu Ser Ala Lys Ile Leu Glu Arg
545      550      555      560
Glu Asn Ile Pro Thr Gln Val Val Ser Ala Pro Cys Phe Asp Leu Leu
      565      570      575
Val Glu Gln Asp Glu Ser Tyr Phe Lys Glu Leu Phe Lys Gly Lys Val
      580      585      590
Leu Val Ile Glu Ala Ser Arg Ala Ile Glu Trp Tyr Arg Phe Ala Asp
      595      600      605
Lys Ile Ile Gly Met Asp Ser Phe Gly Ser Ser Ala Lys Gly Asp Lys
      610      615      620
Leu Phe Glu Lys Phe Gly Phe Ser Val Glu Asn Ile Thr Ala Gln Ala
625      630      635      640
Lys Arg Leu Leu Asn Ala
      645

```

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522

```

Lys Asp Tyr Cys Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met
1      5      10      15
Ala Thr Gln Phe Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn
      20      25      30
Leu Asn Thr Asn Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe
      35      40      45
Leu Arg Leu Tyr Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln
      50      55      60
Thr Lys Ala Ser Ala Lys Tyr Leu Asn Arg Asn Leu Asn Arg Val Pro
      65      70      75      80
Ile Leu Ser Glu Ile Tyr Thr Asp Arg Ser Leu Gly Ala Phe Glu Gly
      85      90      95
Thr Asn Asn Pro Leu Asp Phe Ala Leu Thr Ser Pro Asn Leu Tyr Phe
      100      105      110
Ala Ile Gln Thr Asn Glu Gly Val Ala Tyr Thr Lys Asp Gly His Phe
      115      120      125

```

SUBSTITUTE SHEET (RULE 26)

1083

```

Ser Val Asp Lys Asp Gly Phe Leu Val Thr Leu Asn Gly Phe Lys Val
130          135          140
Leu Ser Arg Ser Gly Leu Asn Glu Lys Gly Gly Ile Met Leu Met Pro
145          150          155          160
Asn Ala Glu Ile Glu Val Asp Gln Asn Gly Gly Ile Thr Phe Arg Asp
          165          170          175
Asn Glu Ala Gln Ile Gln Ala Gly Ala Leu Ala Leu Val Ser Phe Ser
          180          185          190
Glu Pro Lys Asn Leu Lys Lys Ile Gly Gln Asn Leu Tyr Thr Tyr Gln
          195          200          205
Gly Glu Gly Val His Gln Val Ser Asp Ser Gly Ala Leu Arg Gln Ser
210          215          220
Met Leu Glu Lys Ser Asn Val Asn Ala Val Arg Glu Met Ser Thr Leu
225          230          235          240
Ile Glu Ile Asn Arg Phe Leu Asp Met Tyr Ser Lys Val Leu Lys Thr
          245          250          255
His Gln Asp Asp Met Asn Ala Glu Ala Ile Asn Lys Leu Ala Thr Lys
          260          265          270
Ala

```

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523

```

Gly Met Ile Ala Leu Asn Phe Asn Leu Leu Asp Lys Glu Thr Asn Thr
1          5          10          15
Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu Leu Tyr Lys
          20          25          30
Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr Phe Gly Leu
          35          40          45
Gly Asn Gly Val Phe Tyr Arg Leu Leu Gly Asn Glu Asn Leu Lys
50          55          60
Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe Ile Val Leu
65          70          75          80
Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg Leu Ile Leu
          85          90          95
Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser Leu Phe Asp
          100          105          110
Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp Leu Lys Leu
          115          120          125
Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile Glu Ile Asn
          130          135          140
Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser Val Gly Asn
          145          150          155          160
Asp Ala Lys Asp Ala Leu Ile Gly Ile Lys Gln His Val Ala Asn Leu
          165          170          175
Pro Glu Val Ile Lys Ser Pro Ser Leu Val Asp Phe Val Asn Ala Leu

```

SUBSTITUTE SHEET (RULE 26)

				180					185					190					
Lys	Asn	Arg	Asp	Thr	Ala	Ile	Ile	Val	Ser	Thr	Gly	Pro	Ser	Leu	Asn				
		195					200					205							
Lys	Gln	Leu	Pro	Leu	Leu	Lys	Glu	Ile	Ala	Pro	Tyr	Ala	Thr	Leu	Phe				
		210				215					220								
Cys	Ile	Asp	Ala	Ser	Phe	Pro	Ile	Leu	Ala	Arg	Ala	Gly	Ile	Lys	Pro				
225					230					235					240				
Asp	Ile	Val	Leu	Ser	Leu	Glu	Arg	Val	Asp	Leu	Thr	Ala	Lys	Phe	Tyr				
				245					250					255					
Glu	Glu	Thr	Pro	Leu	Asp	Phe	Gln	Glu	Gly	Val	Ile	Phe	Ala	Leu	Thr				
			260					265						270					
Ser	Ile	Val	His	Lys	Arg	Leu	Ile	Gln	Ala	Ile	Gln	Lys	Gly	Val	Lys				
		275					280							285					
Gln	Phe	Ser	Phe	Arg	Pro	Phe	Gly	Tyr	Thr	Asn	Leu	Phe	Asp	Leu	His				
		290				295					300								
Gln	Tyr	Gly	Tyr	Val	Gly	Ile	Gly	Met	Ser	Ala	Ala	Asn	Met	Ala	Tyr				
305				310						315				320					
Glu	Leu	Val	Val	His	Ser	Arg	Phe	Lys	Arg	Cys	Val	Phe	Ile	Gly	Gln				
				325						330				335					
Asp	Leu	Ser	Phe	Ser	Gln	Ser	Gly	Asn	Ser	His	Ala	Ser	Gly	Ala	Ile				
			340					345						350					
Tyr	Gly	Asp	Arg	Glu	Ile	Lys	Pro	Lys	Lys	Asp	Lys	Asp	Lys	Ile	Phe				
		355					360							365					
Ile	Glu	Lys	Tyr	Gly	Gly	Asn	Gly	Lys	Val	Glu	Thr	Thr	Leu	Val	Trp				
		370				375					380								
Lys	Leu	Phe	Leu	Glu	Phe	Phe	Glu	Lys	Asp	Ile	Phe	Asn	Thr	Pro	Tyr				
385					390					395				400					
Lys	Leu	Glu	Val	Ile	Asn	Ala	Thr	Glu	Gly	Ala	Arg	Ile	Lys	Gly					
				405						410				415					
Thr	Lys	Glu	Met	Pro	Phe	Lys	Glu	Val	Cys	Glu	Lys	Ile	Asp	Lys	Ser				
			420					425						430					
Lys	Pro	Lys	Pro	Pro	Ile	Asn	Leu	Ile	Tyr	Pro	Thr	Gln	Ser	Glu	Gln				
			435				440							445					
Ala	Lys	Asn	Leu	Lys	Ile	Ala	Lys	Lys	Lys	Cys	Glu	Glu	Ile	Ile	Lys				
		450				455					460								
Tyr	Ala	Asn	Glu	Lys	Lys	Thr	Gln	Val	Glu	Glu	Ala	Phe	Leu	Lys	Val				
465					470														

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

1085

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524

```

Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1           5           10           15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Pro Pro Thr Arg Ser Ile Gln
          20           25           30
Gly Leu Gln Asn Ile Gln Gln Asn Ile Pro Pro Gln Val Leu Thr Pro
          35           40           45
Gln Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
          50           55           60
Ser Ser Thr Leu Glu Ala Pro Leu Leu Phe Ser Lys Gln Asn Val Val
65           70           75           80
Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly Lys
          85           90           95
Ile His Asp Gly Ala His Cys Arg Ile Glu Cys Lys Lys Thr Pro Met
          100          105          110
Lys Cys Ile Ala
          115

```

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525

```

Arg Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val
1           5           10           15
Ser His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr
          20           25           30
Gly Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln
          35           40           45
Lys Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu
          50           55           60
Ala Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser
65           70           75           80
Pro Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr
          85           90           95
Gly Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln
          100          105          110
Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu Ile
          115          120          125
Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu Asn
          130          135          140
Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu

```

SUBSTITUTE SHEET (RULE 26)

1086

```

145          150          155          160
Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro Ser
          165          170          175
Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile Leu
          180          185          190
His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg
          195          200          205
Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu Cys
          210          215          220
Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu Trp
225          230          235          240
Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly Ser
          245          250          255
Ala Leu Met Val Phe Leu Asn Ser Leu Ile Phe Met Leu Ala Ala Leu
          260          265          270
Ser Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr
          275          280          285
Thr Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly
290          295          300
Phe Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val
305          310          315          320
Gln Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn
          325          330          335
His Met His Ala Glu Phe Ile Asp Val Tyr Ile His Phe Tyr Ala Leu
          340          345          350
Ile Ala Ile Phe Ile Val Ser Phe Ile Gly Cys Val Phe Lys Leu Ser
          355          360          365
Ser Leu Lys Lys Ala Cys Glu Asn Ala
          370          375

```

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526

```

Thr Leu Lys Gly Ile Val Leu Phe Arg Leu Ile Ser Ala Trp Val Leu
1          5          10          15
Gln Asp Lys Phe Leu Phe Val Val Cys Phe Ile Leu Pro Phe Cys Leu
          20          25          30
Gly Val Leu Gly Thr Gln Ile Phe Lys Gln Glu Thr Pro Arg Gln Leu
          35          40          45
Pro Ile Val Val Val Asp Leu Asp Lys Thr Thr Thr Ser His Gln Val
50          55          60
Ala Phe Glu Leu Gly Ala Thr Ser Ala Val Glu Ile Lys Tyr Gln Val
65          70          75          80
Thr Ser Leu Ser Glu Ala Lys Arg Phe
          85

```

1087

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527

```

Ser Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser
1          5          10          15
Ser Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu
20          25          30
Asn Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys
35          40          45
Leu Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly
50          55          60
Leu His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528

```

Val Arg Arg Gln Thr Met Lys Lys Val Ile Val Ala Leu Gly Val Leu
1          5          10          15
Ala Phe Ala Asn Val Leu Met Ala Thr Asp Val Lys Ala Leu Val Lys
20          25          30
Gly Cys Ala Ala Cys His Gly Val Lys Phe Glu Lys Lys Ala Leu Gly
35          40          45
Lys Ser Lys Ile Val Asn Met Met Ser Glu Lys Glu Ile Glu Glu Asp
50          55          60
Leu Met Ala Phe Lys Ser Gly Ala Asn Lys Asn Pro Val Met Thr Ala
65          70          75          80
Gln Ala Lys Lys Leu Ser Asp Glu Asp Ile Lys Ala Leu Ala Ile Tyr
85          90          95
Ile Pro Thr Leu Lys

```

SUBSTITUTE SHEET (RULE 26)

1088

100

(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529

```

Arg Pro Met Leu His Lys Lys Tyr Arg Pro Asn Val Ala Ala Ile Ile
1           5           10           15
Met Ser Pro Asp Tyr Pro Asn Thr Cys Glu Val Phe Ile Ala Glu Arg
20           25           30
Ile Asp Ile Glu Gly Ala Trp Gln Phe Pro Gln Gly Gly Ile Asp Glu
35           40           45
Gly Glu Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile
50           55           60
Gly Thr Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg Trp Ile Ala
65           70           75           80
Tyr Asp Phe Pro Ser Asn Met Glu His Lys Phe Tyr Ser Phe Asp Gly
85           90           95
Gln Lys Gln Arg Tyr Phe Leu Val Arg Leu Lys His Val Asn Asn Ile
100          105          110
Asp Leu Asn Lys His Thr Pro Glu Phe Arg Ser Tyr Gln Phe Ile Gln
115          120          125
Leu Lys Asp Leu Leu Lys Lys Ile Val Pro Phe Lys Arg Gln Val Tyr
130          135          140
Arg Gln Val Ile Ala Tyr Phe Arg Lys Glu Gly Tyr Leu Gly Cys
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530

1089

```

Cys Met Asn Leu Val Phe Leu Trp Ala Ala Leu Gly Gly Ala Ile Gly
1      5      10      15
Ser Ser Leu Arg Tyr Phe Val Gly Lys Met Met Pro Ser Lys Phe Leu
20      25      30
Met Phe Glu Ser Phe Pro Leu Gly Thr Phe Ser Val Asn Leu Ile Gly
35      40      45
Cys Phe Ile Ile Gly Phe Met Gly His Leu Ala Ala Lys Lys Val Phe
50      55      60
Gly Asp Asp Phe Gly Ile Phe Phe Val Thr Gly Val Leu Gly Gly Phe
65      70      75      80
Thr Thr Phe Ser Ser Tyr Gly Leu Asp Thr Leu Lys Leu Leu Gln Lys
85      90      95
Ser Gln Tyr Leu Glu Ala Ile Ser Tyr Val Leu Gly Thr Asn Leu Leu
100     105     110
Gly Leu Ile Gly Val Ala Ile Gly Trp Phe Leu Ala Lys Asn Phe Val
115     120     125
Gly Val Asn
130

```

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531

```

Tyr Leu Ser Ile Val Val Glu Asp Gln Lys Gly Ile Phe Pro Ile Ala
1      5      10      15
Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu Asp Val Cys
20      25      30
Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile Glu Gly Leu
35      40      45
Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe Gly His Ala
50      55      60
Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu Glu Asn Glu
65      70      75      80
Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met Phe Leu Met
85      90      95
Val Ser Lys Ser Ser Gly Ser Ile Lys Ala Glu His Gly Thr Gly Arg
100     105     110
Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys Ala Tyr Lys
115     120     125
Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly Leu Leu Asn
130     135     140
Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr Lys Asn Leu
145     150     155     160
Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys Met Glu Cys
165     170     175
Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser Leu Thr Pro
180     185     190
Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu Lys Glu Arg

```

SUBSTITUTE SHEET (RULE 26)

1090

```

      195              200              205
Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp Glu Leu Leu
      210              215              220
Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val Cys His Met
225              230              235              240
Cys Ser Thr Leu Cys Pro Leu Gly Ile Asp Thr Gly Ser Ile Ala Leu
      245              250              255
Asn His Tyr Gln Lys Asn Pro Lys Gly Glu Lys Ile Cys Phe Lys Asp
      260              265              270
Ser

```

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532

```

Arg Phe Leu Gln Lys Ser Ala Gln Ile Trp Gly Ile Lys Met Leu Val
1              5              10              15
Glu Ile Glu Asn Leu Thr Lys Thr Tyr Gly Ser Leu Lys Ala Leu Asp
      20              25              30
Asn Ile Ser Leu Lys Leu Pro Lys Gln Gln Phe Ile Gly Leu Leu Gly
      35              40              45
Pro Asn Gly Ala Gly Lys Thr Thr Leu Leu Lys Ile Leu Ala Gly Leu
      50              55              60
Asn Leu Asn Tyr Gln Gly Glu Val Lys Ile Leu Asn Gln Lys Ile Gly
      65              70              75              80
Ile Glu Thr Lys Lys Ser Val Ala Phe Leu Ser Asp Gly Asp Phe Leu
      85              90              95
Asp Pro Lys Leu Thr Pro Leu Lys Ala Ile Ala Phe Tyr Lys Asp Phe
      100              105              110
Phe Ser Asp Phe Asp Glu Ser Lys Ala Leu Asn Leu Leu Lys Arg Phe
      115              120              125
Ser Val Pro Leu Lys Arg Glu Phe Lys Ala Leu Ser Lys Gly Met Arg
      130              135              140
Glu Lys Leu Gln Leu Ile Leu Thr Leu Ser Arg Asn Ala Ser Leu Tyr
      145              150              155              160
Leu Phe Asp Glu Pro Val Ala Gly Ile Asp Pro Ile Ala Arg Glu Glu
      165              170              175
Ile Phe Glu Leu Ile Ala Lys Glu Phe Ser Gln Asn Ala Ser Leu Leu
      180              185              190
Val Ser Thr His Leu Val Val Asp Val Glu Lys Tyr Leu Asp Ser Ala
      195              200              205
Ile Phe Leu Lys Glu Ala Lys Val Val Ala Phe Gly Asp Val Gly Glu
      210              215              220
Leu Lys Lys Gly Tyr Ser Ser Leu Glu Ala Ala Tyr Lys Glu Arg Leu
225              230              235              240
Lys

```

1091

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533

```

Lys Ser Trp Phe Phe Tyr Ala Pro Phe Tyr Gly Leu Trp Cys Leu Lys
1      5      10      15
Thr Pro Ile Ile Gly His Gly Met Lys Lys Lys Ala Lys Val Phe Trp
20      25      30
Cys Cys Phe Lys Met Ile Arg Trp Leu Tyr Leu Ala Val Phe Phe Leu
35      40      45
Leu Ser Val Ser Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys
50      55      60
Gln Asn His Lys Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys
65      70      75      80
Asp Asn Val Ile Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp
85      90      95
Val Tyr Ile Leu Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu
100     105     110
Ala Leu Leu Glu Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu
115     120     125
Val Lys Thr Asp Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile
130     135     140
Ile Phe Pro Phe Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser
145     150     155     160
Ala Asp Ile Ala Ser Gly Lys Asp Gln Lys Tyr Lys Ile Lys Asn Met
165     170     175
Ser Ala Ser Gly Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala
180     185     190
Thr Ser Gly Ser Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn
195     200     205
Pro Lys Ile Tyr Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile
210     215     220
Phe Met Ser Thr Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu
225     230     235     240
Phe Gly Thr Ser His Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr
245     250     255
Leu Ala Pro Lys Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg
260     265     270
Tyr Lys Arg Gly Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Pro
275     280     285

```

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid

1092

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534

```

Ile Val Arg Lys Lys Leu Met Leu Glu Met Ser Leu Gln Ala Leu Asn
1      5      10      15
Thr Gln Asp Ser Ser Val Met Ala Gln Ser Leu Leu Val His Ala Phe
20      25      30
Phe Ala Ala Leu Leu Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu
35      40      45
Phe Lys Glu Lys Asn Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val
50      55      60
Met Pro Ala Ile Tyr Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val
65      70      75      80
Phe Ile Trp Ala Met Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val
85      90      95
Met Leu Leu Gly Leu Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His
100      105      110
Lys Ser Val Lys Phe Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr
115      120      125
Ile Lys Lys Ala Lys Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile
130      135      140
Val Leu Met Gly Ile
145

```

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535

```

Pro Glu Gly Gly Asn Glu Leu Asn Val Phe Glu Pro Val Ile Ala Tyr
1      5      10      15
Lys Leu Phe His Ser Phe Val Ile Leu Gly Cys Ala Ile Glu Thr Leu
20      25      30
Thr Thr Lys Cys Val Glu Gly Ile Thr Ala Asn Glu Lys Ile Cys His
35      40      45
Asp Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Ala Leu Asn Pro His
50      55      60

```

1093

```

Ile Gly Tyr Glu Lys Ser Ala Met Ile Ala Lys Glu Ala Leu Lys Ser
65          70          75          80
Asp Arg Ser Ile Tyr Asp Ile Ala Leu Glu Lys Lys Ile Leu Thr Lys
          85          90          95
Glu Gln Leu Asp Asp Ile Phe Lys Pro Glu Asn Met Leu Ser Pro His
          100          105          110
Ala Phe Lys Lys His Lys Asp
          115

```

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536

```

Lys Arg Leu Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn
1          5          10          15
Asp Phe Leu Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu
          20          25          30
Leu Ser Leu Ala Phe Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser
          35          40          45
Ile Val Asn Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr
          50          55          60
Ala His Ser Gln Gly Phe Phe Ala Gly Val Phe Ala Trp Val Phe Lys
65          70          75          80
Ala Leu Val Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu
          85          90          95
Val Ile Asn Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser
          100          105          110
Tyr Leu His Gln Lys Tyr Tyr Pro His Val Val Leu Glu Phe Gly
          115          120          125
Ser Ile Leu Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met
          130          135          140
Leu Leu Phe Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile
145          150          155          160
Gly Val Phe Gly Val Phe Phe Ser Ile Val Pro His Phe Leu Phe Phe
          165          170          175
Lys Asn Thr Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln
          180          185          190
Ser Tyr Gln Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe
          195          200          205
Ser Phe Phe Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Phe
210          215          220
Ala Thr Leu Leu Gln Thr Leu Met Leu Thr His
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

1094

(A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537

```

Glu Cys Lys Gly Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu
1      5      10      15
Leu Ser Ala Val Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val
20      25      30
Tyr Ile Gly Thr Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn
35      40      45
Ile Tyr Asn Thr Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro
50      55      60
Gly Leu Thr Ala Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp
65      70      75      80
His Ser Lys Tyr Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val
85      90      95
Gly Tyr Lys Lys Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys
100     105     110
Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp
115     120     125
Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val
130     135     140
Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp
145     150     155     160
Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr
165     170     175
Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala
180     185     190
Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro
195     200     205
Tyr Ser Thr Asn Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe
210     215     220
Gly Val Arg Ala Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val
225     230     235     240
Arg Val Pro Leu Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala
245     250     255
Thr Asn Leu Tyr Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly
260     265     270
Tyr Asn Tyr Thr Phe
275

```

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

1095

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538

```

Ala Phe Glu Glu Leu Glu Pro Leu Ser Phe Ser Phe Asn Ser Pro Lys
1      5      10
Gly Ala Cys Glu Ser Cys Leu Gly Leu Gly Thr Lys Phe Ser Leu Asp
      20      25      30
Ile Ser Lys Ile Leu Asp Pro Asn Thr Pro Leu Asn Gln Gly Ala Ile
      35      40      45
Lys Val Ile Phe Gly Tyr Asn Arg Ser Tyr Tyr Ala Gln Met Phe Glu
      50      55      60
Gly Phe Cys Thr Tyr Asn Gly Ile Asp Ser Ala Leu Cys Phe Asn Glu
      65      70      75      80
Leu Asn Lys Glu Gln Gln Asp Ala Leu Leu Tyr Gly Asn Gly Thr Glu
      85      90      95
Ile Ser Phe His Phe Lys Asn Ser Pro Leu Lys Arg Pro Trp Lys Gly
      100      105      110
Ile Ile Gln Ile Ala Tyr Asp Met Phe Lys Glu Gln Lys Asp Leu Ser
      115      120      125
Asp Tyr Met Ser Glu Lys Thr Cys Ser Ser Cys Asn Gly His Arg Leu
      130      135      140
Lys Ala Ser Ser Leu Ser Val Gln Val Ala Gly Leu Lys Met Ala Asp
      145      150      155      160
Phe Leu Thr Lys Pro Ile Glu Glu Val Tyr His Phe Phe Asn Asp Pro
      165      170      175
Thr His Phe Asn Tyr Leu Asn Glu Gln Glu Lys Lys Ile Ala Glu Pro
      180      185      190
Ile Leu Lys Glu Ile Leu Glu Arg Val Phe Phe Leu Tyr Asp Val Gly
      195      200      205
Leu Gly Tyr Leu Thr Leu Gly Arg Asp Ala Arg Thr Ile Ser Gly Gly
      210      215      220
Glu Ser Gln Arg Ile Arg Ile Ala Ser Gln Ile Gly Ser Gly Leu Thr
      225      230      235      240
Gly Val Leu Tyr Val Leu Asp Glu Pro Ser Ile Gly Leu His Glu Lys
      245      250      255
Asp Thr Leu Lys Leu Ile Asn Thr Leu Arg Asn Leu Gln Lys Lys Gly
      260      265      270
Asn Thr Leu Ile Val Val Glu His Asp Lys Glu Thr Ile Lys His Ala
      275      280      285
Asp Phe Val Val Asp Ile Gly Pro Lys Ala Gly Arg His Gly Gly Glu
      290      295      300
Val Val Phe Ser Gly Ser Val Lys Asp Leu Leu Gln Asn Asn His Ser
      305      310      315      320
Thr Ala Leu Tyr Leu Asn Gly Thr Lys Lys Ile Glu Arg Pro Lys Phe
      325      330      335
Glu Pro Pro Lys Glu Lys His Phe Leu Glu Ile Lys Asn Val Asn Ile
      340      345      350
Asn Asn Ile Lys Asn Leu Ser Val Gln Ile Pro Leu Lys Gln Leu Val
      355      360      365
Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Ile Leu Gln
      370      375      380
Thr Leu Leu Pro Thr Ala Gln Thr Leu Leu Asn His Ala Lys Lys Asn
      385      390      395      400
Gln Ser Leu Asn Gly Val Glu Ile Val Gly Leu Glu Tyr Leu Asp Lys
      405      410      415
Val Ile Tyr Leu Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn
      420      425      430
Pro Ala Thr Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala

```

SUBSTITUTE SHEET (RULE 26)

1096

```

      435      440      445
Glu Gln Lys Glu Ala Lys Ile Leu Gly Tyr Ser Thr Ser Arg Phe Ser
  450      455      460
Phe Asn Val Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp
  465      470      475      480
Ile Lys Ile Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp
      485      490      495
Ser Cys Lys Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val
      500      505      510
Lys Gly Lys Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala
      515      520      525
Tyr Glu Phe Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr
      530      535      540
Leu Ile Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr
  545      550      555      560
Thr Leu Ser Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu
      565      570      575
Ser Lys Lys Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr
      580      585      590
Thr Gly Leu His Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His
      595      600      605
Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu
      610      615      620
Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly
  625      630      635      640
Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val
      645      650      655
Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala
      660      665      670
Leu Glu Leu Lys
      675

```

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539

```

Ala Arg Phe Val Lys Ile Thr Ala Asp Tyr Phe Ser Pro Met Glu Asn
  1      5      10      15
Val Phe Tyr Arg Ser Ile Thr Met Thr Leu Leu Leu Leu Ile Tyr
      20      25      30
Pro Phe Lys Pro Tyr Arg Leu Lys Ser Tyr Lys Gln Gly Gly Phe Lys
      35      40      45
Lys Leu Ala Phe Arg Val Val Val Gly Gly Leu Ala Met Leu Ala Phe
      50      55      60
Phe Tyr Asn Ile Glu Lys Ile Ser Leu Ala Thr Ala Asn Ala Phe Ser
  65      70      75      80
Gln Cys Ala Pro Ile Tyr Thr Val Leu Leu Ser Pro Leu Leu Leu Lys
      85      90      95

```

SUBSTITUTE SHEET (RULE 26)

1097

```

Glu Lys Leu Lys Arg Ser Ala Leu Ile Ser Ala Cys Ile Gly Leu Val
      100      105      110
Gly Val Val Leu Ile Ser Asp Pro Ser Val Glu Asn Val Gly Leu Val
      115      120      125
Glu Ile Ile Met Gly Ile Leu Ser Gly Ile Phe Val Ser Leu Ala Tyr
      130      135      140
Ile Thr Leu Arg Asp Leu Arg Glu Tyr Tyr Asp Lys Gln Ala Val Ile
      145      150      155      160
Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly Met Phe
      165      170      175
Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg Lys Glu
      180      185      190
Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu Gly Gln
      195      200      205
Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile Ile Ala
      210      215      220
Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly Leu Tyr
      225      230      235      240
Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val Ala Leu
      245      250      255
Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu Lys Glu
      260      265      270
Leu Lys Lys Ile
      275

```

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540

```

Val Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr
1      5      10      15
Phe Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu
      20      25      30
Ile Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met
      35      40      45
Ser Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr
      50      55      60
Ser Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu
      65      70      75      80
Gly Gln Asn Asp Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val
      85      90      95
Ile Asn Met Phe Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys
      100      105      110
Pro Lys Asp Ala Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly
      115      120      125
Val Asn Leu Phe Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser
      130      135      140
Leu Gly Leu Leu Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro

```

SUBSTITUTE SHEET (RULE 26)

1098

```

145          150          155          160
Tyr Leu Thr Leu Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro
          165          170          175
Leu Leu Leu Gly Val Phe Ala Tyr Ala Leu Arg Lys Arg Tyr Phe Lys
          180          185          190
Ser Ala Ile Phe Ala Leu Val Val Leu Ile Val Asn Thr Ala Leu Phe
          195          200          205
Ser Gly Asp Phe Asn Lys Gly Leu Pro Ser Gly Tyr Phe Ile Asp Thr
          210          215          220
Cys Leu Glu Leu Met Leu Leu Tyr Ser Pro Leu Leu Phe Leu Tyr Tyr
225          230          235          240
Pro Tyr Thr Leu Tyr Lys Ala Leu Leu Asp Lys Lys Pro Ser Leu Leu
          245          250          255
Ala Phe Met Ala Arg Ala Ala Gly Phe Ser Leu Cys Phe
          260          265

```

(2) INFORMATION FOR SEQ ID NO:1541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541

```

Ser Pro Phe Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn
1          5          10          15
Ala Tyr Ser Tyr Asn Ser Asp Ser Leu Phe Leu Tyr Asp Phe Ser Arg
          20          25          30
Pro Phe Ile Lys Asn Ser Gly Ala Ile Leu Asp Ile Gly Ser Gly Cys
          35          40          45
Gly Val Leu Gly Leu Leu Cys Ala Arg Asp Asn Pro Leu Ala Ser Val
50          55          60
His Leu Val Glu Lys Asp Ser Lys Met Ala Phe Cys Ser Gln Lys Asn
65          70          75          80
Ala Leu Lys Phe Pro Asn Ala Gln Val Phe Glu Ser Asp Phe Leu Asp
          85          90          95
Phe Asn Pro Pro Ile Leu Tyr Asp Ala Ile Val Cys Asn Pro Pro Phe
          100          105          110
Tyr Ala Leu Gly Ser Ile Lys Ser Gln Ile Lys Gly His Ala Arg His
          115          120          125
Gln Ser Glu Leu Asp Phe Ala Ser Leu Val Ala Lys Val Lys Lys Cys
130          135          140
Leu Lys Pro Lys Gly Tyr Phe Ile Phe Cys Tyr Glu Ala Leu Ser Leu
145          150          155          160
Cys Leu Val Ile Glu Ser Leu Lys Ser Val Lys Leu Thr Leu Glu Thr
          165          170          175
Leu Arg Phe Val Gln Ser Phe Lys Asp Lys Asn Ala His Leu Met Leu
          180          185          190
Gly Ala Ala Arg Asn Asn Ser Lys Ser Ala Leu Lys Val Leu Pro Pro
          195          200          205
Leu Ile Thr His Asn Ser Lys Asn Gln Ser Asp Asn Thr Lys Glu Val
210          215          220

```

1099

Leu Asn Ile Tyr Gln Ile Cys Asn Thr Tyr Ser Ile Lys Ala Pro Leu
 225 230 235 240
 Asp

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542

Ser Arg Ser Phe Arg Gly Leu Leu Tyr Tyr Asn Lys Ile Asn Leu Ile
 1 5 10 15
 Asn Lys Asp Thr Gly Leu Gln Glu Ile Lys Leu Asp Ile Tyr Ala Thr
 20 25 30
 Leu Val Cys Met Val Leu Val Leu Leu Gly Arg Tyr Val Ile Ser
 35 40 45
 Lys Val Lys Phe Leu Arg Asp Tyr Asp Ile Pro Glu Pro Val Val Gly
 50 55 60
 Gly Val Leu Val Ala Phe Phe Ile Met Leu Ala Arg Gln Phe Tyr His
 65 70 75 80
 Phe Gly Leu Gln Phe Asp Ser Ser Leu Lys Asp Pro Leu Met Leu Thr
 85 90 95
 Phe Phe Ile Thr Ile Gly Leu Ser Ala Asp Phe Lys Ser Leu Gln Lys
 100 105 110
 Gly Gly Lys Met Leu Ala Val Phe Leu Leu Ala Val Ala Gly Phe Val
 115 120 125
 Val Cys Gln Asn Ala Val Gly Ile Ser Ile Ala Ser Leu Leu Gly Val
 130 135 140
 Asn Pro Leu Met Gly Leu Leu Gly Gly Ser Ile Ala Leu Val Gly Gly
 145 150 155 160
 His Gly Thr Ser Ala Ala Trp Ala Asn Phe Thr Gln Pro Pro Tyr
 165 170 175
 His Phe Ser Ser Ser Leu Glu Val Gly Met Ala Cys Ala Thr Phe Gly
 180 185 190
 Leu Val Ser Gly Gly Ile Ile Gly Gly Pro Val Ala Lys Tyr Leu Ile
 195 200 205
 Ser Lys Tyr Lys Leu Glu Pro Lys Asp Thr Lys Glu Lys Asp Thr Leu
 210 215 220
 Glu Gly Val Val Ser Lys Gly Phe Glu Thr Pro Lys Glu Gln Arg Leu
 225 230 235 240
 Ile Thr Ala Ser Ser Phe Val Glu Thr Leu Ala Leu Ile Ala Ile Ala
 245 250 255
 Leu Leu Val Gly Thr Phe Leu Ser His Leu Met Pro Lys Ser Phe Thr
 260 265 270
 Leu Pro Thr Phe Val Trp Cys Leu Phe Val Gly Val Ile Leu Arg Asn
 275 280 285
 Ala Leu Ser Phe Phe Lys Ile His Ser Val Phe Asp Arg Glu Val Ser
 290 295 300
 Val Ile Gly Asn Val Ser Leu Ser Leu Phe Leu Ala Tyr Ala Leu Met

SUBSTITUTE SHEET (RULE 26)

1100

```

305          310          315          320
Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala Val
          325          330          335
Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu Val
          340          345          350
Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys Ala
          355          360          365
Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val Asn
          370          375          380
Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe Ile
385          390          395          400
Val Val Pro Leu Val Gly Ala Phe Phe Val Asp Ile Ile Asn Ala Leu
          405          410          415
Ala Ile Lys Gly Phe Leu Leu Leu Pro Phe Phe Pro Ser
          420          425

```

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543

```

Lys Phe Val Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr
1          5          10          15
Glu Lys Gly Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu
          20          25          30
Ser Glu Asp Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala
          35          40          45
Val Leu Gln Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly
          50          55          60
Ser Gly Asp Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val
65          70          75          80
Gly Arg Phe Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro
          85          90          95
Met Cys Gln Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile
          100          105          110
Lys Ala Trp Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val
          115          120          125
Asp Cys Val Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu
130          135          140
Asp Phe Glu Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp
145          150          155          160
Ile Pro Ser Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Arg Leu
          165          170          175
Arg Arg Ile Arg Leu Ser Ala Trp Ala Leu Ser Ser His Ala Tyr
          180          185          190

```

(2) INFORMATION FOR SEQ ID NO:1544:

1101

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544

```

Asn Ala His Asn Leu Lys Asp Lys Thr Phe Gln Gly Gly Phe Glu Leu
1      5      10      15
Leu Thr Thr Pro Lys Glu Tyr Ser Trp Cys Gly Val Val Leu Ser Leu
20      25      30
Leu Leu Ala Ile Asn Leu Tyr Leu Glu Tyr Leu Asn His Gln Lys Leu
35      40      45
Asp Phe Ser Lys Pro Thr Ser Leu Asn Ala Gln Ile Leu Leu Gln Tyr
50      55      60
Pro Lys Thr Lys Asp Gln Lys Thr Tyr Phe Val Leu Lys Leu Gln Ser
65      70      75      80
Lys Gly Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu
85      90      95
Gln Tyr Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe
100      105      110
Leu Glu Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu
115      120      125
Thr Arg Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser
130      135      140
Ala His Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile
145      150      155      160
Gly Asp Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly
165      170      175
Ile Asn His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser
180      185      190
Ala Ser Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys
195      200      205
Arg Tyr Phe Pro Tyr Arg Asn Ala Phe Tyr Asp Ile Gly Val Leu Val
210      215      220
Trp Val Phe Leu Leu Gly Tyr Leu Leu Leu Leu Asp Phe Leu Pro Ser
225      230      235      240
Phe Phe Arg Ala Phe Leu Met Gly Leu Leu Gly Phe Leu Ala Cys Phe
245      250      255
Phe Gly Val Arg Ile Leu Ser Phe Lys Leu Leu Val Leu Ala Cys Cys
260      265      270
Ile Ala Ile Ala Leu Leu Pro Lys Leu Leu Phe Ser Val Gly Phe Leu
275      280      285
Leu Ser Val Cys Gly Val Trp Tyr Ile Phe Leu Phe Leu Lys His Thr
290      295      300
Gln Ile Phe Phe Lys Asp Ser Ser Phe Phe Lys Arg Ser Phe Gln Ala
305      310      315      320
Ile Ala Leu Ser Val Leu Val Phe Leu Asn Met Leu Ile Val Ala His
325      330      335
Ala Phe Phe Pro Met Phe Ser Pro Tyr Gln Leu Phe Ser Ile Pro Leu
340      345      350
Gly Leu Ile Phe Thr Val Phe Phe Pro Leu Ser Leu Phe Leu His Ala
355      360      365
Val Gly Leu Gly Ser Leu Leu Asp Asn Ile Leu Ser Met Pro Leu Thr

```

SUBSTITUTE SHEET (RULE 26)

1102

```

      370              375              380
Ile Pro Thr Ile Ser Val Ser Ser Pro Leu Trp Leu Leu Gly Ala His
385              390              395              400
Leu Phe Leu Thr Ile Leu Ser Val Arg Phe Phe Lys Val Tyr Leu Ser
      405              410              415
Met Asn Val Leu Ser Met Gly Phe Phe Leu Tyr Cys Cys Tyr Gln Tyr
      420              425              430
Ile Ile Met Pro Ser Leu Ile Val Gly
      435              440

```

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545

```

Glu Ala Phe Lys Ala Asp Thr Thr Ile Ser Met Gly Ala Ile Lys Ser
1              5              10              15
Cys Leu Leu Ser Asp Lys Ala Lys Asp Tyr Ile Gly Glu Leu Lys Val
      20              25              30
Gly His Leu Gly Val Phe Asn Gln Ile Tyr Glu Ile Pro Thr Asp Thr
      35              40              45
Phe Leu Leu Glu Lys Ser Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys
      50              55              60
Asn Ala His Lys Gly Asp Tyr Gly His Ala His Val Leu Leu Gly Lys
      65              70              75              80
His Ser Gly Ala Gly Leu Leu Ser Ala Leu Ser Ala Leu Ser Phe Gly
      85              90              95
Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys Glu Ile Thr Ser Asn
      100              105              110
Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn Phe Pro Lys Lys Leu
      115              120              125
Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn Ile Pro Lys Asp Phe
      130              135              140
Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu Asp Ala Gly Val Phe
      145              150              155              160
Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys Glu Val Ile Leu Thr
      165              170              175
Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys Ser Val Gly Ile Asn
      180              185              190
Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu Glu Ile Ala Arg Asp
      195              200              205
Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu Lys Gly Ala Asn
      210              215              220
Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile Asn Asn Leu Gly Ser
      225              230              235              240
Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val Leu Ala Gly Leu Ile
      245              250              255
Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu Asp Ala Ala Ile Asn
      260              265              270

```

1103

Ala Ser Leu Ala His Ala Leu Ala Gly Leu Glu Phe Lys Asn His Tyr
 275 280 285
 Ala Leu Thr Pro Leu Asp Leu Ile Glu Lys Ile Lys Arg Leu
 290 295 300

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546

Leu Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Val Ala
 1 5 10 15
 Thr Met Leu Ala Val Gly Phe Ser Leu Asp Glu Ile Lys Asn Asp Ile
 20 25 30
 Thr Asn Thr Pro Ala Ser Phe Glu Pro Ser Leu Asp Tyr Ile Val Val
 35 40 45
 Lys Ile Pro Arg Phe Ala Phe Glu Lys Phe Ala Gly Val Ser Ser Thr
 50 55 60
 Leu Gly Thr Ser Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly
 65 70 75 80
 Asn Phe Leu Glu Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn
 85 90 95
 Trp Leu Gly Phe Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys
 100 105 110
 Glu Ile Arg Arg Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala
 115 120 125
 Phe Arg Leu Gly Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile
 130 135 140
 Asp Arg Trp Phe Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu
 145 150 155 160
 Gly Ile Asn Ser Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu
 165 170 175
 Lys Asn Leu Gly Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu
 180 185 190
 Asn Glu Asn Leu Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser
 195 200 205
 Asn Leu Gln Ile Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala
 210 215 220
 Glu Phe Leu Ser Leu Thr Pro Tyr Leu Tyr Ser Thr Tyr Ala Pro Asn
 225 230 235 240
 Pro Leu Pro Pro Ile Gly Asn Lys Gln Glu Lys Gln Glu Lys Lys Ile
 245 250 255
 Leu Ile Ile Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe
 260 265 270
 Asp Tyr Cys Val His Ala Ser Phe Ala Leu Lys Asp Leu Asn Ile
 275 280 285
 Lys Ser Val Met Leu Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr
 290 295 300
 Asp Thr Ser Asp Thr Leu Tyr Phe Glu Pro Ile His Phe Glu Cys Val

SUBSTITUTE SHEET (RULE 26)

1104

```

305          310          315          320
Lys Ser Ile Ile Gln Arg Glu Arg Val Asp Gly Ile Ile Val His Phe
          325          330          335
Gly Gly Gln Thr Pro Leu Lys Leu Ala Lys Asp Leu Ala Lys Met Gln
          340          345          350
Ala Pro Ile Ile Gly Thr Pro Phe Lys Val Ile Asp Ile Ala Glu Asp
          355          360          365
Arg Glu Lys Phe Pro Ser Phe
          370          375

```

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547

```

Arg Pro Val Ile Ser Ala Lys Glu Gly Ser Asp Pro Ser Ser Leu Ala
1          5          10          15
Tyr Asn Thr Ile Glu Ser Ala Ile Ala Lys Asn Ile Asp Glu Val Phe
          20          25          30
Ile Asp Thr Ala Gly Arg Leu His Asn Gln Thr Asn Leu Lys Asn Glu
          35          40          45
Leu Ser Lys Ile Ala His Thr Cys Ser Lys Val Leu Lys Asp Ala Pro
          50          55          60
Phe Tyr Lys Phe Leu Ile Leu Asp Gly Thr Gln Gly Ser Ser Gly Leu
65          70          75          80
Thr Gln Ala Lys Ile Phe His Glu Thr Leu Ala Leu Asp Gly Val Ile
          85          90          95
Met Thr Lys Leu Asp Gly Thr Ser Lys Gly Gly Ala Ile Leu Ser Val
          100          105          110
Leu Tyr Glu Leu Lys Leu Pro Ile Leu Tyr Leu Gly Met Gly Glu Lys
          115          120          125
Glu Asp Asp Leu Ile Ala Phe Asp Glu Glu Arg Phe Ile Glu Asp Leu
          130          135          140
Val Asp Ala Val Phe Val Glu Gln
145          150

```

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

1105

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548

```

Asn Leu Arg Ile Ile Thr Ile Lys Thr Ile Phe Arg Asp Phe Cys Lys
1           5           10           15
Glu Arg Leu Lys Arg Ala Lys Ser Lys Asn Lys Val Arg Asp Lys Leu
20           25           30
Ala Cys Lys Leu Leu Phe Trp Lys Leu Lys Asp Tyr Gln Asn Ile Leu
35           40           45
Leu Tyr Ser Pro Leu Gly His Glu Leu Asp Ile Arg Pro Leu Ile Leu
50           55           60
Lys Leu Arg Gln Lys Asn Lys Arg Val Trp Leu Pro Lys Ser Ile Lys
65           70           75           80
Lys Gly Ala His Phe Ser Lys Glu Gly Phe Thr Ile Ala Pro Phe Arg
85           90           95
Leu Pro Leu Arg Arg Leu Gly Trp Phe Asp Glu Pro Ser Leu Ser Arg
100          105          110
Tyr Tyr Lys Arg Glu Leu Asp Cys Ile Val Val Pro Ile Leu Gly Met
115          120          125
Asp Thr Ser Phe Arg Arg Val Gly Phe Gly Leu Gly Met Tyr Asp Arg
130          135          140
Ser Leu Pro Gln Leu Phe Lys Lys Gln Leu Lys Arg Pro Leu Val Ile
145          150          155          160
Phe Val Ser Arg Glu Leu Ala Leu Ala Asn Gly Ile Leu Thr Asp Ala
165          170          175
Tyr Asp Ile Glu Ala Asn Leu Tyr Met Asn Ala Arg Ile Val Met Lys
180          185          190
Asn Asn Lys Arg Lys His Tyr Glu Gln Arg Val Asn Leu His Phe Ile
195          200          205
Arg Ser Leu Gly Ser Val Phe Asp His Arg Ser Asn His Val Leu Cys
210          215          220
Asp Glu Lys Asp Leu Leu Arg
225          230

```

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549

```

Arg Ile Ile Lys Gly Asn Ile Met Ser Ser Gly Leu Ile Tyr Ile Ser
1           5           10           15
Leu Glu Val Leu Val Ala Cys Leu Ile Thr Ala Leu Ile Met Tyr Tyr
20           25           30
Val Met Lys Lys Ile Tyr Tyr Ala Arg Gly Gln Ala Ile Leu Lys Gly

```

1106

```

      35      40      45
Ala Ser Ala Lys Ala Lys Leu Met Glu Phe Gln Ala Lys Ser Phe Val
  50      55      60
Glu Ala Glu Glu Met Arg Met Lys Ser Gln Glu Cys Lys Leu Gln Gln
  65      70      75      80
Gln Tyr Glu Asn Lys Asn Leu Gln Leu Gln Thr His Phe Asp Lys Lys
      85      90      95
Glu Ala His Leu Lys His Leu Glu Ala Gln His Lys Glu Phe Val Arg
      100      105      110
Asp Glu Lys Arg Tyr Leu Glu Lys Glu Lys Lys Glu Leu Glu Lys Glu
      115      120      125
Arg Gln Ile Leu Glu Gln Glu Arg Glu Asn Phe Lys Lys Gln Arg Ala
      130      135      140
Ile Cys Lys Glu Ala Gln Ala Lys Ala Leu Asp Ala Met Leu Asn Tyr
      145      150      155      160
Met Ala Tyr Thr Lys Asp Glu Ile Lys Ser Met Ile Leu Glu Gln Leu
      165      170      175
Glu Gln Glu Leu Glu Ala Gln Lys Ser Ala Leu Ile Arg Arg Tyr Glu
      180      185      190
Glu Glu Ala Phe Ile Met Cys Leu
      195      200

```

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550

```

Ile Arg Ser Ser Asn Asp Thr Gln Thr Thr Gln Thr Pro Trp His Ser
1      5      10      15
Asn Thr Arg Arg Pro Lys Pro Thr Pro Lys Pro Ile Lys Lys Glu Ala
      20      25      30
Lys Lys Ala Lys Glu Lys Thr Thr Lys His Ala His Ser Lys His Ala
      35      40      45
His Ser Pro Leu Asn Glu Arg Ser Ala Lys Lys Glu Ile Pro Lys Lys
      50      55      60
Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu
      65      70      75      80
Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile
      85      90      95
Pro Lys Lys Glu Ala Glu Asn Glu Ser Lys Asn Gln Ile Phe Ile Ala
      100      105      110
Glu Lys Asn Asp Thr Trp Ile Lys Thr Lys Arg Lys Lys His Lys Lys
      115      120      125
Ile Val Leu Asp Ala Gly His Gly Gly Lys Asp Cys Gly Ala Met Ser
      130      135      140
Ala Asn Leu Val Cys Glu Lys Asp Ile Val Leu Glu Val Val Lys Phe
      145      150      155      160
Leu His Lys Glu Leu Lys Lys Arg Gly Tyr Ser Val Leu Leu Thr Arg
      165      170      175

```

SUBSTITUTE SHEET (RULE 26)

1107

```

Asp Lys Asp Ile Tyr Ile Asp Leu Val Ala Arg Thr Glu Leu Ala Asn
      180      185      190
Lys Lys Gly Ala Asp Leu Phe Ile Ser Val His Ala Asn Ser Ile Pro
      195      200      205
Lys Arg Ser Thr Ser Asn Ala His Gly Ile Glu Thr Tyr Phe Leu Ser
      210      215      220
Thr Ala Arg Ser Glu Arg Ala Arg Lys Val Ala Glu Gln Glu Asn Lys
      225      230      235      240
Asp Asp Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn
      245      250      255
Ser Leu Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp
      260      265      270
Val Gln Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val
      275      280      285
Val Asp Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala
      290      295      300
Leu Met Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile
      305      310      315      320
Glu Ser Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys
      325      330      335
Gly Ile Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
      340      345      350

```

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551

```

Arg Val Ser Met Asn Val Lys Lys Lys Gly Lys Pro Gln Ser Gly Lys
1      5      10      15
Ile Asp Arg Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr
      20      25      30
Phe Leu Ser Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro
      35      40      45
Ile Pro Gly Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met
      50      55      60
Ser Lys Thr Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys
      65      70      75      80
Leu Ala Arg Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser
      85      90      95
Ile Arg Gln Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu
      100      105      110
Arg Tyr Phe His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu
      115      120      125
Leu Glu Arg Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val
      130      135      140
Asn Asn Lys Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn
      145      150      155      160
Lys Gln Glu Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly Trp Asn

```

SUBSTITUTE SHEET (RULE 26)

1108

165 170 175
 Phe Val Thr Ser Arg Gly Lys Thr Glu Ile
 180 185

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) . ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature
(B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552

Lys 1	Arg	Asp	Gln	Met 5	Ala	Glu	Glu	Glu	Lys 10	Thr	Glu	Leu	Pro	Ser 15	Ala
Lys	Lys	Ile	Gln 20	Lys	Ala	Arg	Glu	Glu 25	Gly	Asn	Val	Pro	Lys 30	Ser	Met
Glu	Val	Val 35	Gly	Phe	Leu	Gly	Leu 40	Leu	Ala	Gly	Leu	Met 45	Ser	Ile	Phe
Val	Phe	Phe 50	Ile	Trp	Trp	Val 55	Asp	Gly	Phe	Ser	Glu	Met 60	Tyr	Arg	His
Val 65	Leu	Lys	Asp	Phe 70	Ser	Leu	Asp	Phe	Ser	Lys 75	Glu	Ser	Val	Gln	Glu 80
Leu	Phe	Asn	Gln 85	Leu	Ala	Lys	Asp	Thr	Phe 90	Leu	Leu	Leu	Leu	Pro 95	Val
Leu	Ile	Ile 100	Leu	Met	Val	Val	Ala	Phe 105	Leu	Ser	Asn	Val	Leu	Gln 110	Phe
Gly	Trp	Leu 115	Phe	Ala	Pro	Lys	Val 120	Ile	Glu	Pro	Lys	Phe 125	Ser	Lys	Ile
Asn	Pro	Ile 130	Asn	Gly	Val	Lys	Asn 135	Leu	Phe	Ser	Leu	Lys 140	Lys	Ile	Leu
Asp 145	Gly	Ser	Leu	Ile 150	Thr	Leu	Lys	Val	Phe	Leu	Ala	Phe 155	Phe	Leu	Gly 160
Phe	Phe	Ile 165	Phe	Ser	Leu	Phe	Leu	Gly 170	Glu	Leu	Asn	His 175	Ala	Ala	Leu 180
Leu	Asn	Leu 185	Gln	Gly	Gln	Leu	Leu	Trp 190	Phe	Lys	Ser	Lys 195	Ala	Leu	Trp 200
Leu	Ile	Ser 205	Ser	Leu	Leu	Phe	Leu 210	Phe	Phe	Val	Leu	Ala 215	Phe	Val	Asp 220
Leu	Ile	Ile 225	Lys	Arg	Arg	Gln	Tyr 230	Thr	Asn	Ser	Leu	Lys 235	Met	Thr	Lys 240
Gln 245	Glu	Val	Lys	Asp	Glu	Tyr	Lys 250	Gln	Gln	Glu	Gly	Asn 255	Pro	Glu	Ile 260
Lys	Ala	Lys 265	Ile	Arg	Gln	Met	Met 270	Val	Lys 275	Asn	Ala	Thr 280	Asn	Lys 285	Met 290
Met	Gln	Glu 295	Ile	Pro	Lys	Ser	Asn 300	Val	Val	Val	Thr	Asn 305	Pro	Thr	His 310
Tyr	Ala	Val 315	Ala	Leu	Lys	Phe	Asp 320	Glu	Glu	His	Pro	Val 325	Pro	Val	Val 330
Val	Ala	Lys 335	Gly	Thr	Asp	Tyr	Leu 340	Ala	Ile	Arg	Ile	Lys 345	Gly	Ile	Ala 350
Arg 355	Glu	His	Asp	Ile 360	Glu	Ile	Ile 365	Glu	Asn	Lys	Thr	Leu 370	Ala	Arg	Glu 375

1109

```

Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro Glu Glu Leu Phe
          325          330          335
Glu Ala Val Ala Ile Val Phe Ala Gln Val Ala Lys Leu Glu Gln Glu
          340          345          350
Arg Gln Lys Gln Lys Ile Ile Lys Pro Leu
          355          360

```

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553

```

Glu Asn Thr Met Gln Asp Leu Gln His Phe Lys Asn Asp Ile Thr Leu
1          5          10          15
Ile Leu Ser Lys Asp Arg Leu Asp Thr Tyr Asp Ser Leu Glu Gln Tyr
          20          25          30
Lys Glu Asn Lys Leu Ile Ser Phe Ile Thr Pro Lys Ile Ser Asn
          35          40          45
Leu Glu Ile Tyr Leu Arg Asn Ala Leu Asp Tyr Cys Leu Thr Gln Ile
          50          55          60
Lys Gly Ser Glu Trp Val Phe Asn Glu Asn Ser Leu Thr Asp Leu Ile
65          70          75          80
Asn Glu Gln Lys Glu Lys Lys Lys Glu Ile Thr His Ser Leu Ile Leu
          85          90          95
Ser Lys Met Ser Leu Gly Ala Val Val Arg Leu Ile Phe Cys Tyr Lys
          100          105          110
Leu Glu Gly Val Ile Leu Asp Leu Arg Ala Tyr Arg Leu Arg Ala Tyr
          115          120          125
Tyr His Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu
130          135          140
Leu Tyr Asn Tyr Ile Lys Ala His Ile Ala Leu Asn Leu Leu Trp Thr
145          150          155          160
Ile Arg Asn Arg Thr Tyr His Trp Glu Asn Leu Leu Lys Ile Gln Pro
          165          170          175
Asn Asn Arg Pro Gln
          180

```

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

1110

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554

```

Ala Asn Gly Cys Glu Lys Arg Ile Phe Met Leu Leu Cys Ala Gly Arg
 1           5           10           15
Asn Glu Thr Leu Lys Lys Ala Val Pro Ile Gly Val Gly Leu Ile Glu
      20           25           30
Ser Ala Ile Asn Leu Thr Arg Met Cys Leu Lys Asn Pro Asp Thr Glu
      35           40           45
Ser Leu Ile Phe Ile Gly Ser Ala Gly Ser Tyr Ser Pro Glu Thr Glu
      50           55           60
Ile Leu Ser Val Phe Glu Ser Ile Glu Gly Tyr Gln Ile Glu Glu Ser
      65           70           75           80
Phe Ser His Leu Asn Ser Tyr Thr Pro Leu Asp Asn Phe Ile His Ile
      85           90           95
Glu Thr Lys Glu Gln Ala Leu Phe Glu Arg Val Arg Val Asn Ser Ser
      100          105          110
Asn Tyr Ile His Thr Ser Glu Met Phe Ala Lys Lys Met Val Gln Lys
      115          120          125
Gly Val Leu Leu Glu Asn Met Glu Phe Phe Ser Val Leu Ser Val Ala
      130          135          140
Lys Ile Phe Ser Leu Lys Ala Lys Gly Ile Phe Cys Val Ser Asn His
      145          150          155          160
Val Gly Leu Asn Ala His Lys Glu Phe Lys Glu Asn His Ala Lys Val
      165          170          175
Lys Gln Ile Leu Glu Asn Ile Ile Asp Ser Leu Ile Val
      180          185

```

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555

```

Phe Val Leu Ala Cys Asn Arg Leu Leu Ala Arg Thr Leu Lys Ser Glu
 1           5           10           15
Tyr Arg Ile Cys Gly Phe Ala Lys Asn His Pro Phe Ser Gly Pro Phe
      20           25           30
Glu Ser Gly Gly Val Trp Phe Cys Gly Tyr Ser Thr Phe Arg Leu Asn
      35           40           45
Arg Phe Ser Gly His Tyr Cys Cys Lys Trp Arg Arg Asn Gly Ile Gln
      50           55           60
Ser Val Val Asp Glu Thr Lys Pro Phe Thr His Ser Lys Asn Gly Arg
      65           70           75           80

```

1111

Lys Arg Gly Phe Ser Leu Phe Gln Ala Ile Gln Pro Ser Val Phe Asp
 85 90 95
 Arg Ser Thr Leu Ala Asn Gln Ser Asp His Arg Tyr Phe His Leu Phe
 100 105 110
 Val Gly Tyr Phe Phe Glu Trp Val Pro Lys Asn Arg Phe Lys Glu Ser
 115 120 125
 Val Gln Cys Leu Arg Gly Gly Asp Leu Tyr Cys Asn His Gln His Ala
 130 135 140
 Gln Tyr Phe Lys Leu Glu Phe Asn Phe Arg Lys Lys Arg Ala Gly Tyr
 145 150 155 160
 Lys Arg Arg Tyr Asn Phe His Ala Val Phe Phe Gly Gly His Cys Arg
 165 170 175
 His Ala Arg Glu Thr Phe Phe Arg Gln Ser Ile Lys Leu Leu Arg Leu
 180 185 190
 Leu Arg Phe Ser Glu Lys Arg Lys Thr Lys Arg Ser Lys Asp Lys Glu
 195 200 205
 Arg Arg Lys Asp Cys Arg Lys Thr Arg Asn Gln Ala Arg Ser His Arg
 210 215 220
 Ala Lys Ser Gln Ser Arg His Arg Lys Arg Ser His Phe Arg Arg Glu
 225 230 235 240
 Lys Leu Pro Lys Ser Arg Ala Lys Ile Arg Arg Arg Lys Ala Ser Phe
 245 250 255
 Lys Arg Lys Glu Lys Asn Ser His Gln Lys Gly Tyr Gly Ile Thr Lys
 260 265 270
 Ser Glu Arg Thr Ser Arg Lys Arg Lys Arg Ala Arg Lys Lys Lys Ser
 275 280 285
 Phe Arg Asn Glu Glu
 290

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556

Gly Glu Thr Thr Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala
 1 5 10 15
 Ile Leu Cys Leu Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val
 20 25 30
 Val Lys Gln Lys Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile
 35 40 45
 Glu Lys Tyr Ser Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro
 50 55 60
 Phe Met Val Gln Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp
 65 70 75 80
 Asn Lys Gln Val Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys
 85 90 95
 Ile Thr Leu Ile Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr
 100 105 110
 Phe Gln Ala Asn Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro

SUBSTITUTE SHEET (RULE 26)

1112

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      115      120      125
Thr Leu Asn Gln Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp
 130      135      140
Asn Pro Asn Asn Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly
145      150      155      160
Ser Gln Pro Met Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp
      165      170      175
Val Ser Gly Ala Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu
      180      185      190
Lys Ala Gln Leu Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln
      195      200      205
Asp Lys Glu Gln Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile
      210      215      220
Leu Glu Thr Leu Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val
225      230      235      240
Ile Ser Ser Glu Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys
      245      250      255
Glu Glu Glu Val Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr
      260      265      270
Leu Arg Asn Gln Ile Arg Ser Leu Leu Ser Gly Lys
      275      280

```

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557

```

Ser Tyr Cys Gln Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe
 1      5      10      15
Leu Leu Leu Ser Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys
      20      25      30
Gln Leu Asp Asn Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn
      35      40      45
Leu Asp Glu Ile Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile
      50      55      60
Gly Gln Glu Asp Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg
      65      70      75      80
Gly Asp Leu Ala Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe
      85      90      95
Phe Ile Ser Glu Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu
      100      105      110
Leu Leu Leu Thr Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala
      115      120      125
Glu Gln Gln Cys Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu
      130      135      140
Gly Lys Leu Lys Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu
145      150      155      160
Glu Thr Ser Leu Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser
      165      170      175

```


1113

```

Leu Ile Thr Ala Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn
      180      185      190
Phe Ile Lys Gly Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe
      195      200      205
Leu Asn Tyr Leu Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln
      210      215      220
Ser Lys Arg Gln Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val
      225      230      235      240
Lys

```

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558

```

Ile Asn Lys Asn Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile
1      5      10      15
Ile Ser Phe Phe Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu
      20      25      30
Pro Ile Val Ser Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu
      35      40      45
Ile Pro Ser Tyr Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr
      50      55      60
Gly Tyr Thr Ser Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln
      65      70      75      80
Gly Val Ile Glu Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala
      85      90      95
Ser Asn Leu Val Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser
      100      105      110
Ala Trp Ala Ser Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro
      115      120      125
Ser Ser Gly Cys Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile
      130      135      140
Asp Val Ser Met Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln
      145      150      155      160
Asn Phe Thr Lys Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu
      165      170      175
Leu Gln Ile Ile Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr
      180      185      190
Ala Asp Gly Leu Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys
      195      200      205
Leu Gln Asn Asn Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser
      210      215      220
Val Val Lys Gly Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val
      225      230      235      240
Asn Leu Pro Asp Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val
      245      250      255
Ser Tyr Leu Ile Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe

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1114

```

      260      265      270
Met Lys Leu Arg Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe
      275      280      285
Glu Tyr Met Arg Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val
      290      295      300
Ser Phe Ile Ala Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr
      305      310      315      320
Ser Ile Tyr Phe Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu
      325      330      335
Phe Trp Ala Leu Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu
      340      345      350
Pro Ala Val Arg Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser
      355      360      365
Leu Leu Gln Gly Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe
      370      375      380
Met Gln Val Thr Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro
      385      390      395      400
Leu Ile Ala Gly Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys
      405      410      415
Leu Ile Val Leu Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile
      420      425      430
Trp Phe Ile Asn Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu
      435      440      445
Leu Phe Gly Val Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro
      450      455      460
Ser Val Ala Ile Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser
      465      470      475      480
Thr Ile Ala Ser Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu
      485      490      495
Thr Ile Ile Glu Ser Val Asn Ala Ile Val Asn Thr Ile Phe Ser Ser
      500      505      510
Val Ser Met Asp Gly Ser Arg Met Asp Arg Glu Arg Asp Ala Leu Met
      515      520      525
Val Gly Arg Val Gly Gly Ser Met Phe Lys Gly
      530      535

```

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559

```

Leu His Arg Ile Ile Ser Cys Asp Ser Ala Trp Arg Thr Asn Leu Val
1      5      10      15
Val Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln
      20      25      30
Lys Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro
      35      40      45
Gln Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Lys Lys Arg
      50      55      60

```

SUBSTITUTE SHEET (RULE 26)

1115

```

Glu Glu Ala Lys Arg Gln Arg Glu Leu Ile Lys Gln Glu Asn Leu Asn
65          70          75          80
Thr Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile
          85          90          95
Ile Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp
          100         105         110
Gln Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg
          115         120         125
Asn Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg
          130         135         140
Ser Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr
145          150         155         160
Tyr Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val
          165         170         175
Gln Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn
          180         185         190
Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu
          195         200         205
Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys
          210         215         220
Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr
225          230         235         240
Gly Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
          245         250         255

```

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560

```

Thr Ser Ser Phe Lys Thr Lys Met Lys Arg Pro Ile Ser Lys Leu Lys
1          5          10          15
Gln Asn Phe Leu Gln Phe Lys His Ser Phe Asn Lys His Leu Asp Lys
          20          25          30
Tyr Ser Leu Tyr Tyr Arg Leu Phe Asn Ile Ser Ser Ile Val Ile Gly
          35          40          45
Phe Leu Ile Ala Leu Phe Ser Tyr Gly Ala Gly Val Ile Leu Val Tyr
          50          55          60
Pro Ile Leu Phe Leu Phe Ala Leu Ile Ile Lys Pro Ser Phe Phe Tyr
65          70          75          80
Tyr Thr Thr Tyr Leu Leu Leu Val Ser Leu Ser Ile Ile Ser Lys
          85          90          95
Tyr Tyr Leu Leu Ser His Ala Asn Phe Thr Met Lys Leu Ile Met Leu
          100         105         110
Met Thr Gln Trp Gln Asn Trp Phe Leu
          115         120

```

(2) INFORMATION FOR SEQ ID NO:1561:

SUBSTITUTE SHEET (RULE 26)

1116

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561

```

Val Cys Tyr Cys Glu Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro
1      5      10      15
Asn Lys Gln Glu Leu Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly
      20      25      30
Lys Ile Leu Ala Ser Leu Leu Gly Gly Thr Asn Leu Phe Thr Gly
      35      40      45
Leu Ser Ser Asp Leu Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu
      50      55      60
Met Leu Met Met Gly Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu
65      70      75      80
Pro Met Asp Asn Ile Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly
      85      90      95
Phe Asp Ser Ile Lys Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe
      100     105     110
Gly Ser Ser Lys Ser Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln
      115     120     125
Val Arg Leu
      130

```

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562

```

Glu Glu Leu Leu Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys
1      5      10      15
Phe Cys Leu Gly Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala
      20      25      30
Leu Asp Ile Lys Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys
      35      40      45

```

1117

```

Lys Ile Ala Tyr Leu Gly Asp Glu Lys Pro Ile Thr Ile Trp Thr Ser
 50          55          60
Leu Asp Asn Val Thr Val Ile Gln Leu Glu Lys Asp Glu Thr Ile Ser
65          70          75          80
Tyr Ile Thr Thr Gly Phe Asn Lys Gly Trp Ser Ile Val Pro Asn Ser
          85          90          95
Asn His Ile Phe Ile Gln Pro Lys Ser Val Lys Ser Asn Leu Met Phe
          100          105          110
Glu Lys Glu Ala Val Asn Phe Ala Leu Met Thr Arg Asp Tyr Gln Glu
          115          120          125
Phe Leu Lys Thr Lys Lys Leu Ile Val Asp Ala Pro Asp Pro Lys Glu
          130          135          140
Leu Glu Glu Gln Lys Lys Ala Leu Glu Lys Glu Lys Glu Ala Lys Glu
145          150          155          160
Gln Ala Gln Lys Ala Gln Lys Asp Lys Arg Glu Lys Arg Lys Glu Glu
          165          170          175
Arg Ala Lys Asn Arg Ala Asn Leu Glu Asn Leu Thr Asn Ala Met Ser
          180          185          190
Asn Pro Gln Asn Leu Ser Asn Asn Lys Asn Leu Ser Glu Leu Ile Lys
          195          200          205
Gln Gln Arg Glu Asn Glu Leu Asp Gln Met Glu Arg Leu Glu Asp Met
          210          215          220
Gln Glu Gln Ala Gln Ala Asn Ala Leu Lys Gln Ile Glu Glu Leu Asn
225          230          235          240
Lys Lys Gln Ala Glu Glu Ala Val Arg Gln Arg Ala Lys Asp Lys Ile
          245          250          255
Ser Ile Lys Thr Asp Lys Ser Gln Lys Ser Pro Glu Asp Asn Ser Ile
          260          265          270
Glu Leu Ser Pro Ala Ile Ala Leu Gly Gly Leu Ile Leu Leu Cys Gly
          275          280          285
Pro Ile Lys Pro Cys Ile Asn Ser Phe
          290          295

```

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563

```

Ser Cys Arg Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu
 1          5          10          15
Asn Leu Val Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn
          20          25          30
Lys Ala Asn Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu
          35          40          45
Asn Val Ala Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys
          50          55          60
Thr Asp Ile Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys
65          70          75          80
Ile Val Lys Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val

```

1118

85								90				95			
Val	Asp	Ser	Ala	Thr	Ser	Lys	Phe	Val	Ser	Leu	Leu	Phe	Gly	Tyr	Ser
100								105				110			
Lys	Asn	Ser	Leu	Arg	Asp	Arg	Lys	Asp	Gln	Leu	Met	Gln	Tyr	Cys	Asp
115								120				125			
Val	Ser	Phe	Gln	Thr	Gln	Ala	Met	Arg	Met	Phe	Asn	Glu	Asn	Ile	Arg
130								135				140			
Gln	Phe	Val	Asp	Lys	Val	Arg	Ala	Glu	Ala	Ile	Ile	Ser	Ser	Asn	Ile
145								150				155			
Gln	Arg	Glu	Lys	Val	Lys	Asn	Ser	Pro	Leu	Thr	Arg	Leu	Thr	Phe	Phe
165								170				175			
Ile	Thr	Ile	Lys	Ile	Thr	Pro	Asp	Thr	Met	Glu	Asn	Tyr	Glu	Tyr	Ile
180								185				190			
Thr	Lys	Lys	Gln	Val	Thr	Ile	Tyr	Tyr	Asp	Phe	Ala	Arg	Gly	Asn	Ser
195								200				205			
Ser	Gln	Glu	Asn	Leu	Ile	Ile	Asn	Pro	Phe	Gly	Phe	Lys	Val	Phe	Asp
210								215				220			
Ile	Gln	Ile	Thr	Asp	Leu	Gln	Asn	Glu	Gln	Thr	Val	Ser	Glu	Ile	Leu
225								230				235			
Arg	Lys	Ile	Lys	Glu	Val	Glu	Ser	Lys	Asn	Lys	Ala	Leu	Asn	Lys	
245								250				255			

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564

Lys	Arg	Leu	Ile	Gln	Arg	Asp	Glu	Thr	Ile	Ala	Thr	Gln	Arg	Glu	Asn
1				5					10					15	
Gly	Ile	Ile	Ser	Lys	Gln	Phe	Leu	Asn	Leu	Ile	Leu	Glu	Arg	Ser	Phe
			20					25					30		
Met	Asn	Asp	Thr	Thr	Glu	His	His	Gly	Ser	Asn	Pro	Leu	Asn	Ala	Pro
		35					40					45			
Pro	Pro	Ser	Asn	Ser	Gln	Ser	Asn	Asp	Leu	Leu	Asn	Leu	Leu	Asp	Ser
		50				55					60				
Leu	Tyr	Pro	Lys	Gly	Ser	Leu	Gly	Glu	Gln	Arg	Phe	His	Glu	Ala	Leu
65					70					75					80
Lys	Asn	Gln	Glu	Glu	Leu	Lys	Asn	Ile	Leu	Ile	Glu	Ile	Glu	Lys	Leu
				85					90					95	
Pro	Gln	Glu	Lys	Arg	Tyr	Glu	Leu	Leu	Met	Gln	Ile	Gly	Gln	Ala	Lys
			100					105					110		
Gln	Arg	Ile	Met	Glu	Ala	Tyr	Ala	His	Ser	Phe	Leu	Gly	Tyr	Ile	Gly
		115					120					125			
Gly	Leu	Glu	His	Leu	Leu	Gly	Leu	Cys	Met	Gly	Gly	Ile	Phe	Val	Leu
		130				135					140				
Phe	Ala	Ile	Tyr	Phe	Val	Phe	Leu	Arg	Thr	Ser	Lys	Asn	Thr	Glu	Leu
145					150					155					160
Val	Glu	Ser	Leu	Lys	Thr	Lys	Leu	Lys	Leu	Gln	Tyr	Phe	Tyr	Tyr	Ala
				165					170					175	

1119

```

Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser
      180      185      190
Ile Tyr Glu Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val
      195      200      205
Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile
      210      215      220
Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu
      225      230      235      240
Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565

```

Gly Tyr Lys Asn Tyr Lys Met Leu Ala Lys Ile Val Phe Ser Ser Leu
1      5      10      15
Val Ala Phe Gly Val Leu Ser Ala Asn Val Glu Gln Phe Gly Ser Phe
      20      25      30
Phe Asn Glu Ile Lys Lys Glu Gln Glu Val Ala Ala Lys Glu Asp
      35      40      45
Ala Leu Lys Ala Arg Lys Lys Leu Leu Asn Asn Thr His Asp Phe Leu
      50      55      60
Glu Asp Leu Val Phe Arg Lys Gln Lys Ile Lys Glu Leu Val Asp Tyr
      65      70      75      80
Arg Ala Lys Val Leu Asp Leu Glu Asn Lys Tyr Lys Lys Glu Lys
      85      90      95
Glu Ala Leu Glu Lys Glu Thr Arg Gly Lys Ile Leu Thr Ala Lys Ser
      100      105      110
Lys Ala Tyr Gly Asp Leu Glu Gln Ala Leu Lys Asp Asn Pro Leu Tyr
      115      120      125
Lys Lys Leu Leu Pro Asn Pro Tyr Ala Tyr Val Leu Asn Gln Glu Thr
      130      135      140
Phe Thr Gln Glu Asp Lys Glu Arg Leu Ser Tyr Tyr Tyr Pro Gln Val
      145      150      155      160
Lys Thr Ser Ser Ile Phe Lys Lys Thr Thr Ala Thr Thr Lys Asp Lys
      165      170      175
Ala Gln Ala Leu Leu Gln Met Gly Val Phe Ser Leu Asp Glu Glu Gln
      180      185      190
Asn Lys Lys Ala Ser Arg Leu Ala Leu Ser Tyr Lys Gln Ala Ile Glu
      195      200      205
Glu Tyr Ser Asn Asn Ile Ser Asn Leu Leu Ser Arg Lys Glu Leu Asp
      210      215      220
Asn Ile Asp Tyr Tyr Leu Gln Leu Glu Arg Asn Lys Phe Asp Ser Lys
      225      230      235      240
Ala Lys Asp Ile Ala Gln Lys Ala Thr Asn Thr Leu Ile Phe Asn Ser
      245      250      255
Glu Arg Leu Ala Phe Ser Met Ala Ile Asp Lys Ile Asn Glu Lys Tyr

```

SUBSTITUTE SHEET (RULE 26)

1120

260 265 270
 Leu Arg Gly Tyr Glu Ala Phe Ser Asn Leu Leu Lys Asn Val Lys Asp
 275 280 285
 Asp Val Glu Leu Asn Thr Leu Thr Lys Asn Phe Thr Asn Gln Lys Leu
 290 295 300
 Ser Phe Ala Gln Lys Gln Lys Leu Cys Leu Leu Val Leu Asp Ser Phe
 305 310 315 320
 Asn Phe Asp Thr Gln Ser Lys Lys Ser Ile Leu Lys Lys Thr Asn Glu
 325 330 335
 Tyr Asn Ile Phe Val Asp Ser Asp Pro Met Met Ser Asp Lys Thr Thr
 340 345 350
 Met Gln Lys Glu His Tyr Lys Ile Phe Asn Phe Phe Lys Thr Val Val
 355 360 365
 Ser Ala Tyr Arg Asn Asn Val Ala Lys Asn Asn Pro Phe Glu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566

Lys Phe Ser Glu Val Tyr Phe Ile Met Lys Thr Lys Ala Gly Phe Val
 1 5 10 15
 Ala Leu Ile Gly Lys Pro Asn Ala Gly Lys Ser Thr Leu Leu Asn Thr
 20 25 30
 Leu Leu Asn Ala His Leu Ala Leu Val Ser His Lys Ala Asn Ala Thr
 35 40 45
 Arg Lys Leu Met Lys Cys Ile Val Pro Phe Lys Asp Lys Glu Gly Tyr
 50 55 60
 Glu Ser Gln Ile Ile Phe Leu Asp Thr Pro Gly Leu His His Gln Glu
 65 70 75 80
 Lys Leu Leu Asn Gln Cys Met Leu Ser Gln Ala Leu Lys Ala Met Gly
 85 90 95
 Asp Ala Glu Leu Arg Val Phe Leu Ala Ser Val His Asp Asp Leu Lys
 100 105 110
 Gly Tyr Glu Glu Phe Leu Ser Leu Cys Gln Lys Pro His Ile Leu Ala
 115 120 125
 Leu Ser Lys Ile Asp Thr Ala Thr His Lys Gln Val Leu Gln Lys Leu
 130 135 140
 Gln Glu Tyr Gln Lys Tyr Ser Ser Gln Phe Leu Ala Leu Val Pro Leu
 145 150 155 160
 Ser Ala Lys Lys Ser Gln Asn Leu Asn Ala Leu Leu Glu Cys Ile Ser
 165 170 175
 Lys His Leu Ser Pro Ser Ala Trp Leu Phe Glu Lys Asp Leu Met Ser
 180 185 190
 Asp Glu Lys Met Arg Asp Ile Tyr Lys Glu Ile Ile Arg Glu Ser Leu
 195 200 205
 Phe Asp Phe Leu Ser Asp Glu Ile Pro Tyr Glu Ser Asp Val Met Ile
 210 215 220

SUBSTITUTE SHEET (RULE 26)

1121

```

Asp Lys Phe Ile Glu Glu Glu Arg Ile Asp Lys Val Tyr Ala Arg Ile
225          230          235          240
Ile Val Glu Lys Glu Ser Gln Lys Lys Ile Val Ile Gly Lys Asn Gly
          245          250          255
Val Asn Ile Lys Arg Ile Gly Thr Asn Ala Arg Leu Lys Met Gln Glu
          260          265          270
Val Gly Glu Lys Lys Val Phe Leu Asn Leu Gln Val Ile Ala Gln Lys
          275          280          285
Ser Trp Ser Lys Glu Glu Lys Ser Leu Gln Lys Leu Gly Tyr Ile Tyr
290          295          300
Gln Arg Asn Arg Asp
305

```

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567

```

Phe Leu Ser Leu Ser Leu Ile Glu Arg Asp Leu Lys Thr Met Ala Lys
1          5          10          15
Ile Leu Lys Pro Asn Leu Asp Arg Asp Glu Leu Asn Thr Leu Tyr Lys
          20          25          30
Ala Asn Leu Ala Tyr Ala Lys Asn Thr His Glu His Tyr Phe Lys Phe
          35          40          45
Lys Lys Asp Val Asp Tyr Lys Leu Phe Asn Pro Ser Ile Met His Glu
          50          55          60
Gln Cys Ser Ile Ser Phe Val Gly Gly Gln Gly Ala Lys Arg Leu Leu
          65          70          75          80
Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn Lys Ile Ala
          85          90          95
Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val Ala Arg Thr
          100          105          110
Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe Ile Glu Val
          115          120          125
Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys Asp Tyr Arg
          130          135          140
Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr Val Met Tyr
          145          150          155          160
Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg Tyr Gly Phe
          165          170          175
Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys Glu Ser Leu
          180          185          190
Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu Lys Thr Leu
          195          200          205
Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn Lys Cys Ile
          210          215          220
Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu Val Leu Asn
          225          230          235          240
Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr Ser Ile Leu

```

SUBSTITUTE SHEET (RULE 26)

1122

```

                245                250                255
Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile Lys Lys Ser
                260                265                270
Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp Tyr Arg Leu
                275                280                285
Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys Gln Lys Ser
                290                295                300
Gln Asn Ser Leu Thr Leu Tyr Asn Phe Ile Pro Leu Ile Phe Lys Leu
305                310                315                320
Ala Gln Ile Lys His Tyr Lys Gln Tyr Gly Thr Gly Leu His Leu Phe
                325                330                335
Arg His Ser Phe Ala Thr Leu Ile Tyr Gln Glu Thr Gln Asp Leu Val
                340                345                350
Leu Thr Ser Arg Ala Leu Gly His Ser Ser Leu Leu Ser Thr Lys Ile
                355                360                365
Tyr Ile His Thr Thr Gln Glu His Asn Lys Lys Val Ala Leu Val Phe
370                375                380
Asp Ser Leu Ile Glu Asn Lys Lys
385                390

```

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568

```

Lys Arg Lys Glu His Cys Met Lys Asn Leu Arg His Phe Arg Lys Leu
1      5      10      15
Ile Ala Phe Leu Gly Phe Ser Pro Leu Leu Gln Ala Asp Met Thr
20     25     30
Thr Phe Phe Asn Ser Ile Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys
35     40     45
Gly Ile Leu Met Val Ile Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys
50     55     60
Asn Leu Asp Arg Trp Lys Glu Ile Leu Met Thr Val Leu Ala Leu Lys
65     70     75     80
Glu Val Pro Met Gln Leu Val Ala Ile Ser Val Ser Asn Leu Lys Glu
85     90     95
Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Phe Leu
100    105    110
Leu Ser Gly Phe Val Pro Phe Ile Met Ile Pro Trp Leu Asp Ile Leu
115    120    125
Asn Ser Phe Val Leu Tyr Val Cys Phe Leu Leu Ile Phe Ser Ile Ala
130    135    140
Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile Leu Ile Ala His Ser Lys
145    150    155    160
Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala
165    170

```

1123

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569

```

Lys Ser Arg Asn Phe Ser Tyr Asn Gln Thr Glu Lys Ile Trp Glu Asn
1          5          10          15
His Phe Asn Leu Phe Ser Val Gly Ile Gly Met Ala Glu Glu Gln Glu
20          25          30
Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser Lys Ala Leu Leu Phe Val
35          40          45
Ile Ile Gly Ser Val Leu Val Met Leu Leu Leu Val Gly Val Ile Ile
50          55          60
Met Leu Leu Met Gly Asn Lys Glu Glu Ser Lys Glu Asn Ala Ser Lys
65          70          75          80
Asn Thr Gln Glu Val Gln Ala Asn Pro Met Ala Asn Lys Asn Gln Glu
85          90          95
Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr Leu Val Leu Gly Pro Leu
100         105         110
Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn Leu Val Ser Gln Asn Gly
115         120         125
Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu Glu Leu Ser Asn Glu Lys
130         135         140
Leu Leu Asn Glu Val Lys Val Lys Asp Thr Ala Ile Lys Asp Thr Ile
145         150         155         160
Ile Glu Ile Leu Ser Ser Lys Ser Val Glu Glu Val Val Thr Asn Lys
165         170         175
Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys Ser His Leu Asn Ser Phe
180         185         190
Leu Ile Asp Gly Phe Ile Lys Asn Val Phe Phe Thr Asp Phe Ile Ile
195         200         205
Gln

```

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

1124

(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570

```

Gly Ser Met Met Thr Glu Met Glu Leu Lys Leu Ile Lys Ile Asp Thr
1      5      10      15
Ser His Tyr Phe Glu Lys Lys Pro Gly Leu Gly Glu Arg Met Asp Tyr
      20      25      30
Ala Gly Arg Cys Tyr Tyr Asn Lys Phe Gln Arg Val Asn Ala Met Leu
      35      40      45
Thr Ser Ser Leu Ile Gln Lys His Leu Lys Arg Glu Ile Glu Ile Ala
      50      55      60
His Asn Leu Ile Leu Arg Asn Asp Lys Val Glu Asn Ile Val Phe Asp
      65      70      75      80
Tyr Asn Gly Arg Asn Pro Glu Arg Phe Tyr His Lys Ala Gln Leu Leu
      85      90      95
Leu Arg Glu Glu Gly Phe Met Asn Phe Thr Ala Tyr Asn Thr Lys Thr
      100     105     110
Pro Gly His Leu His Leu Tyr Val His Lys Gly His Thr Glu Leu Gly
      115     120     125
Glu Gly Glu Arg Leu Ile Lys Thr Leu Ser Met Lys Leu Ala Gln Gly
      130     135     140
Leu Pro Lys Glu Trp Arg Val Phe Pro Ser Asn Glu Trp Pro Lys Glu
      145     150     155     160
Phe Asn Ile Leu Ala Leu Pro Tyr Glu Val Phe Ala Lys Glu Arg Gly
      165     170     175
Ser Ser Trp Ala Lys His Leu
      180

```

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571

```

Pro Phe Leu Lys Gly Phe Leu Met Ser Glu Lys Glu Arg Leu Asn Glu
1      5      10      15
Val Ile Leu Glu Glu Asn Asn Gly Ser Gly Thr Lys Lys Val Phe
      20      25      30
Leu Ile Val Ala Ile Ala Ile Ile Ile Leu Ala Val Leu Leu Met Val
      35      40      45
Phe Trp Lys Ser Thr Arg Val Ala Pro Lys Glu Thr Phe Leu Gln Thr
      50      55      60
Asp Ser Gly Met Gln Lys Ile Gly Asn Thr Lys Asp Glu Lys Lys Asp
      65      70      75      80
Asp Glu Phe Glu Ser Leu Asn Met Asp Ser Pro Lys Gln Glu Asp Lys
      85      90      95
Leu Asp Lys Val Val Asp Asn Ile Lys Lys Gln Glu Ser Glu Asn Ser
      100     105     110

```

1125

```

Met Pro Ile Gln Thr Asp Gln Ala Gln Met Glu Met Lys Thr Thr Glu
  115          120          125
Glu Lys Gln Glu Ser Gln Lys Glu Leu Lys Ala Val Glu Pro Ile Pro
  130          135          140
Met Ser Thr Gln Lys Glu Ser Gln Ala Val Ala Lys Lys Glu Thr Pro
  145          150          155          160
His Lys Lys Pro Lys Val Ala Pro Lys Asp Lys Glu Ala His Lys Asp
          165          170          175
Lys Ala Lys His Ala Ala Lys Glu Pro Lys Val Lys Lys Glu Ala Arg
          180          185          190
Lys Glu Val Ser Lys Lys Ala Asn Ser Lys Thr Asn Leu Thr Lys Gly
          195          200          205
His Tyr Leu Gln Val Gly Val Phe Ala His Thr Pro Asn Lys Ala Phe
          210          215          220
Leu Gln Glu Phe Asn Gln Phe Pro His Lys Ile Glu Asp Arg Gly Ala
  225          230          235          240
Thr Lys Arg Tyr Leu Ile Gly Pro Tyr Lys Ser Lys Gln Glu Ala Leu
          245          250          255
Met His Ala Asp Glu Val Ser Lys Lys Met Thr Lys Pro Val Val Ile
          260          265          270
Glu Val Arg
          275

```

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572

```

Ser Arg Leu Gln Lys Ala Ile Ile Lys Arg Val Glu Met Leu Glu Lys
  1          5          10          15
Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu Leu Ala Pro Leu
          20          25          30
Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly Tyr Val Phe Met
          35          40          45
Lys Glu Leu Trp His Met Leu Ser His Leu Asp Thr Ile Ser Glu Thr
          50          55          60
Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu Leu Phe Met Ala
          65          70          75          80
Gly Leu Val Leu Met Val Leu Leu Ala Ser Tyr Glu Ser Phe Val Ser
          85          90          95
Lys Leu Asp Lys Val Asp Ala Ser Glu Ile Thr Trp Leu Lys His Thr
          100          105          110
Asp Phe Asn Ala Leu Lys Leu Lys Val Ser Leu Ser Ile Val Ala Ile
          115          120          125
Ser Ala Ile Phe Leu Leu Lys Arg Tyr Met Ser Leu Glu Asp Val Leu
          130          135          140
Ser Ser Ile Pro Lys Asp Thr Pro Leu Ser His Asn Pro Ile Phe Trp
          145          150          155          160
Gln Val Val Ile His Leu Val Phe Val Cys Ser Ala Leu Leu Thr Ala

```

SUBSTITUTE SHEET (RULE 26)

1126

165 170 175
Val Thr Asn Asn Ile Ala Phe Ser Gln Lys Glu Arg His
180 185

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573

Gly Leu Asn Tyr Ile Asp Leu Ala Leu Leu Val Val Val Val Ala Phe
1 5 10 15
Gly Ile Arg Gly Phe Tyr His Gly Phe Val Ser Glu Ile Ala Ala Thr
20 25 30
Leu Gly Ile Val Leu Gly Val Tyr Leu Ala Ser Arg Tyr Ser Val Ala
35 40 45
Val Gly Asn Leu Phe Ser Glu His Leu Tyr Asp Leu Arg Asn Glu Thr
50 55 60
Met Thr Asn Leu Ile Gly Phe Leu Leu Val Leu Ala Ser Ile Trp Val
65 70 75 80
Phe Phe Leu Ala Leu Gly Val Leu Leu Gly Lys Met Leu Val Phe Ser
85 90 95
Gly Leu Gly Ile Ile Asp Lys Ala Leu Gly Phe Ile Phe Ser Cys Leu
100 105 110
Lys Thr Phe Leu Val Leu Ser Phe Ile Leu Tyr Ala Leu Ser Lys Met
115 120 125
Asp Leu Met Lys Asp Ala Asn Ala Tyr Leu Gln Glu Lys Ser Ala Ile
130 135 140
Phe Pro Thr Met Lys Ser Val Ala Ser Lys Ile Met Arg Leu Asp Gly
145 150 155 160
Val Lys His Val Glu Lys Asn Leu Lys Asp Asn Leu Glu Glu Met Ser
165 170 175
Asp Glu Val Lys Asn Lys Gly Ser Ile Asp Asn Ala Lys Glu Ser Phe
180 185 190
Asn Lys Ala Thr Asp Lys Gly Val Glu Ala Leu Lys Glu Lys Ala Lys
195 200 205
Asp Leu Pro Lys Asn Met Leu Glu Pro Lys His Asn Lys Pro Asn Gln
210 215 220
Thr Pro Pro Ile Pro Thr Pro Ser Asn Lys Glu Pro Leu
225 230 235

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1127

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574

```

Ser Leu Trp Val Glu Asn Pro Ile Leu Ser His Ser Gln Val Tyr
1      5      10      15
Ser Pro Pro Arg Cys Trp Val Phe Lys Thr Pro Arg Asn Ser Ala Phe
20     25     30
Ala Leu Gly Phe Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu
35     40     45
Arg Leu Ser His Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val
50     55     60
Leu Val Ala Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Leu Tyr Phe
65     70     75     80
Glu Asn Pro Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile
85     90     95
His Pro Phe Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr
100    105    110
Ser Val Phe Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala
115    120    125
Cys Ile Phe Leu Ser Ala Gln Asn Leu Lys Lys Tyr Arg Met Ile Gly
130    135    140
Val Leu Leu Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser
145    150    155    160
Asp Leu Lys Glu Val Gly Asn Ile Glu Leu Val Ser Thr Arg Thr Pro
165    170    175
Gln Asp Leu Lys Phe Asp Ser Asn Tyr Leu Asn Asn Ile Glu Asn Asn
180    185    190
Ile Leu Lys Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile
195    200    205
Val Phe Pro Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe
210    215    220
Lys Thr Gln Leu Glu Asp Leu Ser Ala Lys Ile Ala Ile Leu Ile Gly
225    230    235    240
Thr Leu Arg Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe
245    250    255
Ser Lys Lys Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe
260    265    270
Gly Glu Ile Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys
275    280    285
Leu Phe Phe Gly Glu Ser Ala Tyr Leu Tyr Arg Asn Ala Pro His Phe
290    295    300
Ser Asp Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr
305    310    315    320
Glu Gly Thr Ser Lys Pro Ala Tyr Ser Ser Pro Ser Lys Val Phe
325    330    335
Ile Leu Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr
340    345    350
Leu Gln Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile
355    360    365
Ile Leu His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser
370    375    380
Leu Leu Gly Asp Ile Leu Phe Arg Lys Arg Ser
385    390    395

```

(2) INFORMATION FOR SEQ ID NO:1575:

SUBSTITUTE SHEET (RULE 26)

1128

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575

Glu	Thr	Ile	Met	Ile	Lys	Ala	Ile	Asp	Ile	Ser	His	Ala	Phe	Glu	Lys
1			5					10						15	
Pro	Leu	Tyr	Asn	Gly	Val	Asn	Leu	Arg	Ile	Lys	Pro	Lys	Glu	Ser	Leu
			20					25					30		
Ala	Ile	Leu	Gly	Val	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Ser	His
		35				40						45			
Leu	Ala	Thr	Met	Leu	Lys	Pro	Asp	Ser	Gly	Thr	Val	Ser	Leu	Leu	Glu
		50				55				60					
His	Gln	Asp	Ile	Tyr	Ala	Leu	Asn	Ser	Lys	Lys	Leu	Leu	Glu	Leu	Arg
65				70					75					80	
Arg	Leu	Lys	Val	Gly	Ile	Val	Phe	Gln	Ser	His	Tyr	Leu	Phe	Lys	Gly
			85					90						95	
Phe	Ser	Ala	Leu	Glu	Asn	Leu	Gln	Val	Ala	Ser	Ile	Leu	Ala	Lys	Gln
		100					105					110			
Glu	Ile	Asn	His	Ser	Leu	Leu	Glu	Gln	Leu	Gly	Ile	Ala	His	Thr	Leu
		115					120					125			
Lys	Gln	Gly	Val	Gly	Glu	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg	Leu	Ser
		130				135					140				
Ile	Ala	Arg	Val	Leu	Ser	Lys	Lys	Pro	Gln	Ile	Ile	Ile	Ala	Asp	Glu
145				150					155					160	
Pro	Thr	Gly	Asn	Leu	Asp	Thr	Thr	Ser	Ala	Asn	Gln	Val	Ile	Ser	Met
			165					170						175	
Leu	Gln	Asn	Tyr	Ile	Thr	Glu	Asn	Glu	Gly	Ala	Leu	Val	Leu	Ala	Thr
		180					185						190		
His	Asp	Glu	His	Leu	Ala	Phe	Thr	Cys	Ser	Gln	Val	Tyr	Arg	Leu	Glu
		195				200						205			
Lys	Glu	Ser	Leu	Ile	Lys	Glu	Lys								
		210				215									

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature

1129

(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576

```

Ser Leu Ala Pro Lys Leu Lys Ala Phe Phe Lys Val Ala Leu Ser Cys
1           5           10           15
Lys Ala Val Ile Lys Ile Thr Gly Val Glu Ile Lys Lys Ser Phe Leu
          20           25           30
Met Arg Leu Asn Asn Ser Lys Leu Phe Ile Ser Gly Thr Cys Thr Ser
          35           40           45
Lys Ser Lys Arg Leu Lys Arg Ser Thr Glu Ser Leu Ser
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577

```

Phe Ala Leu His Lys Lys Val Leu Leu Ala Leu Thr Ala Ser Leu Ile
1           5           10           15
Cys Gln Glu Ser Leu Phe Ala Lys Asp Lys Asp Tyr Thr Leu Gly Lys
          20           25           30
Val Ser Thr Ala Gly Lys Lys Asp Arg Ser Asp Tyr Ser Gly Gln Val
          35           40           45
Asn Leu Gly Tyr Ser Gly Ile Thr Ala Pro Lys Ser Trp Gln Asp Glu
          50           55           60
Glu Val Lys Lys Tyr Thr Gly Ser Arg Thr Val Ile Ser Asn Lys Ala
          65           70           75           80
Leu Thr Gln Gln Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val
          85           90           95
Pro Gly Leu Gln Ile Arg Asn Ala Thr Gly Val Gly Ala Met Pro Thr
          100          105          110
Ile Gln Ile Arg Gly Phe Gly Ala Gly Gly Ser Gly His Ser Asp Ala
          115          120          125
Thr Leu Met Leu Val Asn Gly Ile Pro Val Tyr Met Ala Pro Tyr Ala
          130          135          140
His Ile Glu Leu Asp Ile Phe Pro Val Thr Phe Gln Ala Ile Asp Arg
          145          150          155          160
Ile Asp Val Ile Lys Gly Gly Gly Ser Val Gln Tyr Gly Pro Asn Thr
          165          170          175
Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys Pro Ile Pro Asn Gln Trp
          180          185          190
Glu Asn Gln Ala Ala Glu Arg Ile Thr Tyr Trp Ala Lys Ala Arg Asn
          195          200          205
Ala Gly Phe Ala Ala Pro Pro Asp Lys Thr Gly Asp Pro Ser Phe Ile
          210          215          220
Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn Thr Tyr Val Arg Ser Gly
          225          230          235          240
Gly Met Ile Asn Lys His Val Gly Ile Gln Ala Gln Ala Asn Trp Val

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SUBSTITUTE SHEET (RULE 26)

1130

				245					250					255	
Arg	Gly	Gln	Gly	Phe	Arg	Asp	Asn	Ser	Pro	Ser	Ser	Ile	Ser	Asn	Tyr
			260					265					270		
Trp	Leu	Asp	Gly	Val	Tyr	Asp	Ile	Asn	Glu	Ser	Asn	Gly	Ile	Lys	Ala
		275				280						285			
Tyr	Tyr	Gln	Tyr	Tyr	Asp	Phe	Ala	Ile	Ala	Gln	Pro				
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578

Val	Ser	Ile	Leu	Val	Ile	Ile	Glu	Pro	Tyr	Thr	Phe	Tyr	Lys	Arg	Glu
1			5					10					15		
Glu	Ser	Val	Met	Leu	Gly	Ser	Val	Lys	Lys	Ala	Val	Phe	Arg	Val	Leu
		20						25				30			
Cys	Leu	Gly	Ala	Leu	Cys	Leu	Cys	Gly	Gly	Leu	Met	Ala	Glu	Gln	Asp
		35				40					45				
Pro	Lys	Glu	Leu	Ile	Phe	Ser	Gly	Ile	Thr	Ile	Tyr	Thr	Asp	Lys	Asn
	50				55					60					
Phe	Thr	Arg	Ala	Lys	Lys	Tyr	Phe	Glu	Lys	Ala	Cys	Lys	Ser	Asn	Asp
65				70				75					80		
Ala	Asp	Gly	Cys	Ala	Ile	Leu	Arg	Glu	Val	Tyr	Ser	Ser	Gly	Lys	Ala
			85					90					95		
Ile	Ala	Arg	Glu	Asn	Ala	Arg	Glu	Ser	Ile	Glu	Lys	Ala	Leu	Glu	His
			100				105						110		
Thr	Ala	Thr	Ala	Lys	Val	Cys	Lys	Leu	Asn	Asp	Ala	Glu	Lys	Cys	Lys
		115				120						125			
Asp	Leu	Ala	Glu	Phe	Tyr	Phe	Asn	Val	Asn	Asp	Leu	Lys	Asn	Ala	Leu
	130				135					140					
Glu	Tyr	Tyr	Ser	Lys	Ser	Cys	Lys	Leu	Asn	Asn	Val	Glu	Gly	Cys	Met
145				150					155					160	
Leu	Ser	Ala	Thr	Phe	Tyr	Asn	Asp	Met	Ile	Lys	Gly	Leu	Lys	Lys	Asp
		165						170					175		
Lys	Lys	Asp	Leu	Glu	Tyr	Tyr	Ser	Lys	Ala	Cys	Glu	Leu	Asn	Asn	Gly
		180					185						190		
Gly	Gly	Cys	Ser	Lys	Leu	Gly	Gly	Asp	Tyr	Phe	Phe	Gly	Glu	Gly	Val
	195					200						205			
Thr	Lys	Asp	Phe	Lys	Lys	Ala	Phe	Glu	Tyr	Ser	Ala	Lys	Ala	Cys	Glu
	210				215						220				
Leu	Asn	Asp	Ala	Lys	Gly	Cys	Tyr	Ala	Leu	Ala	Ala	Phe	Tyr	Asn	Glu
225				230					235					240	
Gly	Lys	Gly	Val	Ala	Lys	Asp	Glu	Lys	Gln	Thr	Thr	Glu	Asn	Leu	Glu
		245					250						255		
Lys	Ser	Cys	Lys	Leu	Gly	Leu	Lys	Glu	Ala	Cys	Asp	Ile	Leu	Lys	Glu
		260					265						270		
Gln	Lys	Gln													
		275													

1131

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579

```

Thr Arg Lys Ser Ser Ala Ser Met Ser Glu Asn Glu Lys His Pro His
1      5      10      15
Arg Val Leu Gln Leu Ile Lys Ser Ser Gly Ile Thr Pro Gly Ile Val
      20      25      30
Leu Asn Pro His Thr His Glu Glu Ser Ile Lys Tyr Leu Leu Glu Ser
      35      40      45
Val Gly Leu Val Leu Leu Met Ser Val Asn Pro Gly Phe Gly Gly Gln
      50      55      60
Lys Phe Leu Asp Leu Val Leu Glu Lys Cys Leu Lys Val Lys Glu Leu
      65      70      75      80
Ile Lys Arg Tyr Asn Pro Ser Cys Leu Leu Glu Val Asp Gly Gly Val
      85      90      95
Asn Asp Lys Asn Ile Phe Glu Leu Gln Gln Ala Gly Val Asp Val Val
      100     105     110
Val Ser Gly Ser Tyr Ile Phe Glu Ser Lys Asp Arg Lys Leu Ala Ile
      115     120     125
Glu Gly Leu Gln Asn Val Arg Gln Pro Leu Ala
      130     135

```

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580

```

Lys Leu Leu Arg Val Leu His Lys Met Ile Lys Lys Ala Ala Lys Thr
1      5      10      15
Pro Phe Phe Lys Ile Leu Phe Gln Ala Leu Ser Tyr Asn Ile Arg Met

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SUBSTITUTE SHEET (RULE 26)

1132

```

      20      25      30
Lys Asp Leu Asn Lys Thr Ile Gly Val Phe Val Arg Pro Thr His His
      35      40      45
Gln Asn Ala Leu Phe Lys Glu Leu Glu Gln Ala Lys Glu Trp Val Leu
      50      55      60
Thr Leu Leu Glu Asp Glu Gly Phe Glu Ser Phe Met Ile Asp Ser Leu
      65      70      75      80
Asp Gly Ala Lys Asp Ala Gln Leu Ile Lys Lys Ala Tyr Ala Phe Leu
      85      90      95
Cys Leu Gly Gly Asp Gly Thr Ile Leu Gly Ala Leu Arg Met Thr His
      100      105      110
Ala His Asn Lys Pro Cys Phe Gly Val Arg Ile Gly Asn Leu Gly Phe
      115      120      125
Leu Ser Ala Val Glu Leu Asn Gly Leu Lys Asp Phe Leu Gln Asp Leu
      130      135      140
Lys Gln Asn Arg Ile Lys Leu Glu Glu His Leu Ala Leu Glu Gly Arg
      145      150      155      160
Ile Gly Asn Thr Ser Phe Tyr Ala Ile Asn Glu Ile Val Ile Ala Lys
      165      170      175
Lys Lys Ala Leu Gly Val Leu Asp Ile Lys Ala Cys Ala Gly His Thr
      180      185      190
Pro Phe Asn Thr Tyr Lys Gly Asp Gly Leu Ile Ile Ala Thr Pro Leu
      195      200      205
Gly Ser Thr Ala Tyr Asn Leu Ser Ala His Gly Pro Ile Val His Ala
      210      215      220
Leu Ser Gln Ser Tyr Ile Leu Thr Pro Leu Cys Asp Phe Ser Leu Thr
      225      230      235      240
Gln Arg Pro Leu Val Leu Gly Ala Glu Phe Cys Leu Ser Phe Cys Ala
      245      250      255
His Glu Asp Ala Leu Val Val Ile Asp Gly Gln Ala Thr Tyr Asp Leu
      260      265      270
Lys Ala Asn Gln Pro Leu Tyr Ile Gln Lys Ser Pro Thr Thr Thr Lys
      275      280      285
Leu Leu Gln Lys Asn Ser Arg Asp Tyr Phe Lys Val Leu Lys Glu Lys
      290      295      300
Leu Leu Trp Gly Glu Ser Pro Asn Lys Lys Arg
      305      310      315

```

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581

```

Arg Tyr Asn Thr Pro Met Gln Lys Lys Ile Phe Leu Leu Glu Asp Asp
1      5      10      15
Tyr Leu Leu Ser Glu Ser Ile Lys Glu Phe Leu Glu His Leu Gly Tyr
      20      25      30
Glu Val Phe Cys Ala Phe Asn Gly Lys Glu Ala His Glu Arg Leu Ser
      35      40      45

```

SUBSTITUTE SHEET (RULE 26)

1133

Val Glu Arg Phe Asn Leu Leu Leu Asp Val Gln Val Pro Glu Met
 50 55 60
 Asn Ser Leu Glu Leu Phe Lys Arg Ile Lys Asn Asp Phe Leu Ile Ser
 65 70 75 80
 Thr Pro Val Ile Phe Ile Thr Ala Leu Gln Asp Asn Ala Thr Leu Lys
 85 90 95
 Asn Ala Phe Asn Leu Gly Ala Ser Asp Tyr Leu Lys Lys Pro Phe Asp
 100 105 110
 Leu Asp Glu Leu Glu Ala Arg Ile Lys Arg Phe Phe Asn Asp Asp Pro
 115 120 125
 Ile Glu Ile Met Pro Asn Ile Phe Tyr His Gln His Ala Leu Asn Val
 130 135 140
 Lys Gly Lys Lys Glu Ile Leu Ala Pro Lys Thr Ala Gln Leu Leu Glu
 145 150 155 160
 Tyr Phe Leu Glu His Lys Gly Gln Ile Ile Ser Ser Gln Ala Leu Glu
 165 170 175
 Asn Asn Leu Trp Glu Gln Ala Ile Asp Asp Ser Thr Leu Arg Thr Tyr
 180 185 190
 Ile Lys Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His
 195 200 205
 Lys Gly Val Gly Tyr Arg Phe Asn Pro Leu
 210 215

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582

Cys Gly Ala Asn Arg Ser Lys Gly Arg Gly Gly Phe Ser Ser Lys Cys
 1 5 10 15
 Ala Gly Ala Asn Ser Gly Tyr Ser Asn Glu Ala Tyr Glu Ser Val Gly
 20 25 30
 Ala Lys Ile Val Asp Ser Lys Thr Ala Trp Gly Gln Asp Leu Val Val
 35 40 45
 Lys Cys Lys Glu Pro Leu Glu His Glu Tyr Pro Leu Leu Lys Glu Lys
 50 55 60
 Ala Thr Leu Phe Ser Tyr Leu Asp Leu Ala Tyr Gln Lys Ser Leu Cys
 65 70 75 80
 Glu Met Phe Ile Asn Lys Lys Ile Thr Ser Ile Cys Thr Glu Thr Ile
 85 90 95
 Ala Gly Pro Lys Asn Asp Tyr Pro Ile Leu Ala Pro Met Ser Val Val
 100 105 110
 Ala Gly Arg Leu Ala Ala His Leu Val Gln His Tyr Leu Leu Ala Leu
 115 120 125
 Glu His Val Lys Gly Phe Met Gly Lys Gly Val Met Leu Gly Gly Leu
 130 135 140
 Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val Val
 145 150 155 160
 Gly Met Glu Ser Ala Lys Val Leu Ser Gln Met Gly Ala Lys Val Thr

1134

```

      165      170      175
Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr His
      180      185      190
Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile Gln
      195      200      205
Ala Leu Asn Gly Ala Val Gly Leu Val Gly Ala Val Leu Val Thr Ala
      210      215      220
Ser Gln Thr Pro Lys Val Ile Leu Arg Arg His Leu Lys Tyr Met Gln
      225      230      235
Thr Gln Gly Val Val Ile Asp Val Ala Cys Ser Leu Gly Gly Cys Ile
      245      250      255
Arg Ala Ile Arg Gln Ala Ser His Ser Asn Pro Val Tyr Val Glu Glu
      260      265      270
Ser Leu Leu His Tyr Gly Val Pro Asn Met Pro Gly Ile Val Ala Lys
      275      280      285
Thr Ser Ser Thr Ala Tyr Ser His Ala Ser Val Pro Tyr Leu Leu Tyr
      290      295      300
Tyr Leu Glu His Gly Leu Lys Gly Phe Leu Thr Ala Asn Thr Lys Ile
      305      310      315
Val Ala Asn Thr Leu Gly Gly Leu Ser Ala Tyr Asn Gly Tyr Ile Thr
      325      330      335
Gln Glu Gly Ile Ala Lys Ala Phe Asn Leu Ala Phe Lys Ser Pro Leu
      340      345      350
Glu Ile Leu Lys Glu Leu
      355

```

(2) INFORMATION FOR SEQ ID NO:1583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583

```

Lys Gly Lys Arg Val Lys Asn Met Arg Asp Phe Asn Asn Ile Gln Ile
1      5      10      15
Thr Arg Leu Lys Val Arg Gln Asn Ala Val Phe Glu Lys Leu Asp Leu
      20      25      30
Glu Phe Lys Asp Gly Leu Ser Ala Ile Ser Gly Ala Ser Gly Val Gly
      35      40      45
Lys Ser Val Leu Ile Ala Ser Leu Leu Gly Ala Phe Gly Leu Lys Glu
      50      55      60
Ser Asn Ala Ser Asn Ile Glu Val Glu Leu Ile Ala Pro Phe Leu Asp
      65      70      75      80
Thr Glu Glu Tyr Gly Ile Phe Arg Glu Asp Glu His Glu Pro Leu Val
      85      90      95
Ile Ser Val Ile Lys Lys Glu Lys Thr Arg Tyr Phe Leu Asn Gln Thr
      100      105      110
Ser Leu Ser Lys Asn Thr Leu Lys Ala Leu Leu Lys Gly Leu Ile Lys
      115      120      125
Arg Leu Ser Asn Asp Arg Phe Ser Gln Asn Glu Leu Asn Asp Ile Leu
      130      135      140

```

SUBSTITUTE SHEET (RULE 26)

1135

Met Leu Ser Leu Leu Asp Gly Tyr Ile Gln Asn Lys Asn Arg Arg Leu
 145 150 155 160
 Ala Pro Phe

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584

Ser Asn His Lys Arg Val Phe Met Asp Tyr Lys Arg Phe Lys Gly Lys
 1 5 10 15
 His Ala Asn Ile Val Ile Glu Ile Ile Ser Leu Leu Glu Lys Gly Val
 20 25 30
 Lys Lys Ala Gln Glu Ile Leu Glu Lys Pro Asp Ala Gly Ser Tyr Thr
 35 40 45
 Gln Leu Glu Asn Ser Ser Gly Asp Thr Pro Ile Lys Ala Asp Leu Ala
 50 55 60
 Leu Asp Lys Phe Leu Glu Thr Phe Leu Ser Leu Glu Asn Val Lys
 65 70 75 80
 Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu Asn Gly
 85 90 95
 Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val Met Glu
 100 105 110
 Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys Asp Tyr
 115 120 125
 Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly His Lys
 130 135 140
 Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala Phe Tyr
 145 150 155 160
 Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn Lys Gly
 165 170 175
 Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu Gly Leu
 180 185 190
 Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu Arg Tyr
 195 200 205
 Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys Lys Gly
 210 215 220
 Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe Glu Val
 225 230 235 240
 Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala Phe Tyr
 245 250 255
 Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val Glu Ser
 260 265 270
 Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu Ala Gln
 275 280 285
 Ile Leu Glu Lys His Leu Lys Gly Glu
 290 295

SUBSTITUTE SHEET (RULE 26)

1136

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585

```

Thr Phe Leu Ile Ile Phe Trp Val Phe Phe Leu Arg Ile Lys His Tyr
1      5      10      15
Val Lys Glu Leu Ser Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala
20      25      30
Leu Ile Ile Ser Met Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val
35      40      45
Phe Leu Gly Ala Gly Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp
50      55      60
Ile Asn Ser Gln Lys Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp
65      70      75      80
Ala Leu Leu Gly Tyr Gln Phe Phe Phe Glu Lys His Phe Gly Leu Arg
85      90      95
Leu Tyr Gly Phe Phe Asp Tyr Ala His Ala Asn Ser Ile Lys Leu Lys
100     105     110
Asn Pro Asn Tyr Asn Ser Glu Ala Ala Gln Val Ala Ser Gln Ile Leu
115     120     125
Gly Lys Gln Glu Ile Asn Arg Leu Thr Asn Ile Ala Asp Pro Arg Thr
130     135     140
Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp Val Met Val
145     150     155     160
Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe Gly Gly Ile
165     170     175
Gln Leu Ala Gly Asn Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly
180     185     190
Ile Leu Val Glu Gln Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln
195     200     205
Phe Leu Phe Asn Val Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser
210     215     220
Ile Glu Ala Gly Val Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile
225     230     235     240
Thr Ala Lys Asn Leu Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr
245     250     255
Val Asn Tyr Val Phe Thr Phe
260

```

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1137

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586

```

Trp Ile Asp Ala Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly Tyr Thr
1      5      10      15
Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu Leu Val
20      25      30
Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser Leu
35      40      45
Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser Lys
50      55      60
Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu His
65      70      75      80
Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile Thr
85      90      95
Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu Gln
100     105     110
Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser Glu
115     120     125
Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu Gln Phe
130     135     140
Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu Leu Leu
145     150     155     160
Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Gly Val Ser Glu Glu Ala
165     170     175
Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile Val Glu
180     185     190
Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala Arg Ile
195     200     205
Asp Val Val Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser Asn Phe
210     215     220
Glu Ala Leu Gly Thr Ile His Ile Asn Phe
225     230

```

(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587

```

Lys Lys Lys Thr Leu Asn Ile Ser Gln Leu Gly Lys Thr Met His Val

```

SUBSTITUTE SHEET (RULE 26)

1138

```

1           5           10           15
Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu Ser Leu Leu
20           25           30
Lys Glu Ile Ala Ser Lys Gln Gln Gln Ser Leu Lys Ile Leu Gly Thr
35           40           45
His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu Lys His Phe
50           55           60
Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr Asp Leu Lys
65           70           75           80
Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp Leu Leu Lys
85           90           95
Ala Ile Lys Lys His Gln Ile Lys Arg Leu Ile Leu Glu Lys Gln Asp
100          105          110
Phe Arg Ser Phe Leu Leu Ser Gln Phe Val Ser Ile Thr Thr Pro Asn
115          120          125
Lys Glu Ile Lys Asn Val Tyr Gln Asn Arg Gln Glu Leu Phe Ser Gln
130          135          140
Ile Tyr Gly His Val Phe Asp Asn Pro Pro Tyr Pro Met Ser Leu Lys
145          150          155          160
Asn Pro Lys Lys Ile Leu Ile Asn Pro Phe Thr Arg Glu Asn Asp Arg
165          170          175
Asn Ile Ser Leu Glu His Leu Lys Ile Val Leu Lys Leu Leu Lys Pro
180          185          190
Phe Cys Val Thr Leu Leu Asp Phe Glu Glu Arg Tyr Ala Phe Leu Lys
195          200          205
Asp Arg Val Ala His Tyr Arg Ala Lys Thr Ser Leu Glu Glu Val Lys
210          215          220
Asn Leu Ile Leu Glu Ser Asp Leu Tyr Ile Gly Gly Asp Ser Phe Leu
225          230          235          240
Ile His Leu Ala Tyr Tyr Leu Lys Lys Asn Tyr Phe Ile Phe Phe Tyr
245          250          255
Arg Asp Asn Asp Asp Phe Met Pro Pro Asn Ser Gly Asn Glu Asn Phe
260          265          270
Leu Lys Ala His Lys Ser His Phe Ile Glu Gln Asp Leu Ala Lys Lys
275          280          285
Phe Arg His Leu Gly Leu Leu
290          295

```

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588

```

Asn Thr Gln Arg Gln Thr Leu Pro Leu Val Lys Ser Arg Pro His Pro
1           5           10           15
Leu Val Lys Ile Tyr Leu Lys Gln Met Cys Gly Met Gly Phe Ile Gly
20           25           30
Phe Lys Thr Lys Leu Thr Gln Thr Lys Ala Phe Ile Ile Leu Ile Pro
35           40           45

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1139

Ile Phe Gln Asp Arg Ala Val Lys Ala Ala Thr Arg Ser Ala Pro Ile
 50 55 60
 Gln Leu Ile Cys
 65

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589

Thr Leu Ile Ser Ile Phe Ser Ala Ser Gln Ala Asp Phe Gly Gly Asn
 1 5 10 15
 Thr Thr Ile Asp Thr Ala Ser Phe Asn Phe Asp Ser Ala Ser Ser Leu
 20 25 30
 Asn Phe Asn Asn Leu Thr Ala Asn Gly Ala Leu Asn Phe Asn Gly Tyr
 35 40 45
 Ala Pro Ser Leu Thr Lys Ala Leu Met Asn Val Ser Gly Gln Phe Val
 50 55 60
 Leu Gly Asn Asn Gly Asp Ile Asn Leu Ser Asp Ile Asn Ile Phe Asp
 65 70 75 80
 Asn Ile Thr Lys Ser Val Thr Tyr Asn Ile Leu Asn Ala Gln Lys Gly
 85 90 95
 Ile Thr Gly Ile Ser Gly Ala Asn Gly Tyr Glu Lys Ile Leu Phe Tyr
 100 105 110
 Gly Met Lys Ile Gln Asn Ala Thr Tyr Ser Asp Asn Asn Ile Gln
 115 120 125
 Thr Trp Ser Phe Ile Asn Pro Leu Asn Ser Ser Gln Ile Ile Gln Glu
 130 135 140
 Ser Ile Lys Asn Gly Asp Leu Thr Ile Glu Val Leu Asn Asn Pro Asn
 145 150 155 160
 Ser Ala Ser Asn Thr Ile Phe Asn Ile Ala Pro Glu Leu Tyr Asn Tyr
 165 170 175
 Gln Asp Ser Lys Gln Asn Pro Thr Gly Tyr Ser Tyr Asp Tyr Ser Asp
 180 185 190
 Asn Gln Ala Gly Thr Tyr Tyr Leu Thr Ser Asn Ile Lys Gly Leu Phe
 195 200 205
 Thr Pro Lys Gly Ser Gln Thr Pro Gln Thr Pro Gly Thr Tyr Ser Pro
 210 215 220
 Phe Asn Gln Pro Leu Asn Ser Leu Asn Ile Tyr Asn Lys Gly Phe Ser
 225 230 235 240
 Ser Glu Asn Leu Lys Thr Leu Leu Gly Ile Leu Ser Gln Asn Ser Ala
 245 250 255
 Thr Leu Lys Glu Met Ile Glu Ser Asn Gln Leu Asp Asn Ile Thr Asn
 260 265 270
 Ile Asn Glu Val Leu Gln Leu Leu Asp Lys Ile Lys Ile Thr Gln Ala
 275 280 285
 Gln Lys Gln Ala Leu Leu Glu Thr Ile Asn His Leu Thr Asp Asn Ile
 290 295 300
 Asn Gln Thr Phe Asn Asn Gly Asn Leu Val Ile Gly Ala Thr Gln Asp

SUBSTITUTE SHEET (RULE 26)

1140

305				310				315			320
Asn	Val	Thr	Asn	Ser	Thr	Ser	Ser	Ile	Trp	Phe	Gly
				325					330		Gly
Ser	Ser	Pro	Cys	Ala	Leu	Asp	Ser	Ala	Thr	Cys	Ser
				340				345			335
Thr	Tyr	Leu	Gly	Gln	Leu	Leu	Gly	Ser	Thr	Ser	Pro
				355			360				350
Ile	Asn	Ala	Asp	Phe	Lys	Ala	Lys	Ser	Ile	Tyr	Ile
				370			375				365
Gly	Ser	Ser	Asn	Ala	Phe	Glu	Ser	Gly	Gly	Ser	Ala
385					390				395		Asp
Gln	Ser	Ala	Asn	Asn	Leu	Val	Leu	Asn	Lys	Ala	Asn
				405					410		Ile
Ala	Thr	Asp	Asn	Ile	Phe	Asn	Leu	Leu	Gly	Gln	Glu
				420				425			430
Ile	Phe	Asn	Gln	Gly	Asn	Leu	Ala	Asn	Val	Leu	Ser
				435			440				445
Glu	Lys	Ile	Lys	Gln	Ala	Gly	Gly	Leu	Gly	Asn	Phe
450					455						Ile
Leu	Ser	Pro	Leu	Ser	Lys	Glu	Leu	Pro	Ala	Ser	Leu
465					470				475		Gln
Leu	Gly	Gln	Leu	Ile	Gly	Gln	Asn	Asn	Leu	Asp	Asp
				485					490		Leu
Ser	Gly	Val	Met	Asn	Glu	Ile	Gln	Asn	Ile	Ile	Ser
				500				505			Gln
Ile	Phe	Gly	Asn	Phe	Val	Thr	Pro	Ser	Ile	Ile	Glu
				515			520				Asn
Lys	Gln	Ser	Leu	Lys	Ser	Met	Leu	Asp	Asp	Lys	Gly
530					535						Leu
Ile	Gly	Gly	Tyr	Ile	Asp	Ala	Ser	Glu	Leu	Ser	Ser
545					550				555		Ile
Ile	Leu	Lys	Asp	Ile	Thr	Asn	Pro	Pro	Thr	Ser	Leu
				565					570		Gln
Gly	Val	Val	Ala	Asn	Asp	Leu	Leu	Asn	Glu	Phe	Leu
				580				585			Gly
Val	Lys	Lys	Leu	Glu	Ser	Gln	Gly	Leu	Val	Ser	Asn
				595			600				Ile
Val	Ile	Ser	Gln	Gly	Gly	Leu	Ser	Gly	Val	Tyr	Asn
610					615						Gln
Ser	Val	Leu	Pro	Pro	Ser	Leu	Gln	Asn	Ala	Leu	Lys
625					630				635		Glu
Gly	Thr	Leu	Leu	Ser	Pro	Arg	Gly	Leu	His	Asp	Phe
				645					650		Trp
Tyr	Phe	Asn	Phe	Leu	Ser	Asn	Gly	Tyr	Val	Phe	Val
				660				665			Asn
Phe	Ser	Asn	Ala	Thr	Gly	Gly	Ser	Leu	Asn	Phe	Val
				675				680			Ala
Ile	Ile	Phe	Asn	Gly	Asp	Asn	Thr	Ile	Asp	Phe	Ser
690					695						Lys
Ala	Leu	Ile	Phe	Ala	Ser	Asn	Gly	Val	Ser	Asn	Ile
705					710				715		Asn
Leu	Asn	Ala	Thr	Asn	Gly	Leu	Ser	Leu	Asn	Ala	Gly
				725					730		Leu
Ser	Val	Gln	Lys	Gly	Glu	Ile	Cys	Ile	Asn	Leu	Ala
				740				745			Asn
Thr	Lys	Asn	Ser	Ser	Pro	Ala	Asn	Ser	Ser	Val	Thr
				755				760			Pro
Ser	Leu	Ser	Val	His	Ala	Asn	Asn	Phe	Thr	Phe	Leu
770					775						Gly
Ser	Asn	Gly	Ala	Ile	Asp	Leu	Ser	Gln	Val	Thr	Asn
785					790				795		Asn
Gly	Thr	Leu	Asn	Leu	Asn	Glu	Asn	Ala	Thr	Leu	Gln
				805					810		Ala
Thr	Ile	Thr	Asn	Ala	Phe	Asn	Asn	Ala	Ser	Asn	Ser
				820				825			Thr
											Ala
											Asn
											Ile

1141

Asp Gly Asn Phe Thr Leu Asn Gln Gln Ala Thr Leu Ser Thr Asn Ala
 835 840 845
 Ser Gly Leu Asn Val Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val
 850 855 860
 Phe Asn Leu Ser His Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly
 865 870 875 880
 Thr Ala Thr Ile Met Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala
 885 890 895
 Ser Ser Pro Glu Val Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala
 900 905 910
 Ile Tyr Tyr Gly Tyr Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp
 915 920 925
 Asn Tyr Leu Lys Leu Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met
 930 935 940
 Val Met Thr Asp Asn Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val
 945 950 955 960
 Lys Asp Gly Gly Leu Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr
 965 970 975
 Ile Tyr Thr Ser Ile Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn
 980 985 990
 Asp Pro Ile Asn Asn Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala
 995 1000 1005
 Gln Ile Gln Gly Val Gln Ser Val Asp Ser Ile Asp Gln Ala Gly Gly
 1010 1015 1020
 Asn Gln Ala Ile Asn Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser
 1025 1030 1035 1040
 Pro Leu Phe Ala Pro Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu
 1045 1050 1055
 Thr Thr Ile Ala Gly Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn
 1060 1065 1070
 Pro Asn Phe Lys Asn Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr
 1075 1080 1085
 Thr Gln Gln Met Ser Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe
 1090 1095 1100
 Ala Arg Ser Asp Phe Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg
 1105 1110 1115 1120
 Phe Ala Asp Ala Ile Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser
 1125 1130 1135
 Gln Arg Asn Arg Val Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly
 1140 1145 1150
 Ala Ser Phe Ile Ser Gly Gly Thr Gly Thr Leu Tyr Gly Ile Asn Val
 1155 1160 1165
 Gly Tyr Asp Arg Phe Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala
 1170 1175 1180
 Tyr Gly Tyr Ser Gly Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser
 1185 1190 1195 1200
 Asn Val Asn Val Gly Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu
 1205 1210 1215
 Leu Thr Met Ser Leu Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile
 1220 1225 1230
 Asn Ser Tyr Asp Pro Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr
 1235 1240 1245
 Asp Thr Trp Thr Thr Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met
 1250 1255 1260
 Phe Lys Asp Lys Ser Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr
 1265 1270 1275 1280
 Tyr Tyr Ile Gly Leu Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile
 1285 1290 1295
 Tyr Asn Gln Phe Arg Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu
 1300 1305 1310
 Thr Ile Asn Phe Ala Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser
 1315 1320 1325
 Tyr Tyr Phe Val Ile Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser
 1330 1335 1340
 Met Gly Asp Lys Met Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr

SUBSTITUTE SHEET (RULE 26)

1142

1345 1350 1355 1360
 Arg Asp Gly Gly Arg Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly
 1365 1370 1375
 Glu Ile Arg Leu Phe Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala
 1380 1385 1390
 Arg Phe Gly Leu Asp Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly
 1395 1400 1405
 Met Arg Tyr Ala Phe
 1410

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590

Arg Asp Asn Met Glu Leu Ile Leu Gly Ser Gln Ser Ser Ala Arg Ala
 1 5 10 15
 Asn Leu Leu Lys Glu His Gly Ile Lys Phe Glu Gln Lys Ala Leu Tyr
 20 25 30
 Phe Asp Glu Glu Ser Leu Lys Thr Thr Asp Pro Arg Glu Phe Val Tyr
 35 40 45
 Leu Ala Cys Lys Gly Lys Leu Glu Lys Ala Lys Glu Leu Leu Ala Asn
 50 55 60
 Asn Cys Ala Ile Val Val Ala Asp Ser Val Val Ser Val Gly Asn Arg
 65 70 75 80
 Met Gln Arg Lys Ala Lys Asn Lys Arg Glu Ala Leu Glu Phe Leu Lys
 85 90 95
 Arg Gln Asn Gly Asn Glu Ile Glu Val Leu Thr Cys Ser Ala Leu Ile
 100 105 110
 Ser Pro Val Leu Glu Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu
 115 120 125
 Lys Ala Phe Asp Cys Ser Glu Ile Glu Lys Tyr Leu Glu Ser Gly Leu
 130 135 140
 Trp Gln Gly Ser Ala Gly Cys Val Arg Leu Glu Asp Phe His Lys Pro
 145 150 155 160
 Tyr Ile Lys Ser Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn
 165 170 175
 Val Glu Gly Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu
 180 185 190
 Leu

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

1143

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591

```

Arg Met Ala Leu Phe Gly Ser Lys Ser Lys Met Leu Glu Thr Tyr Ala
1           5           10           15
Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu Pro Lys
20           25           30
Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala Lys Pro
35           40           45
Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val Gly Tyr
50           55           60
Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile His Ala
65           70           75           80
Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His Asp Phe
85           90           95
Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu Arg Gln
100          105          110
Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu Leu Ala
115          120          125
His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile Thr Gln
130          135          140
Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn Leu Leu
145          150          155          160
Ser Phe Lys Thr Leu Tyr Pro Phe
165

```

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592

```

Asn Asp Asp Glu Asn Lys Val Ile Glu Leu Lys Thr Arg Asn Asn Met
1           5           10           15
Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu Arg
20           25           30
Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu Phe
35           40           45
Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala Pro

```

SUBSTITUTE SHEET (RULE 26)

1144

```

      50      55      60
Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile Phe
65      70      75      80
Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly Leu
      85      90      95
Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro Lys
      100      105      110
Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu Leu
      115      120      125
Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn Asp
      130      135      140
Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Asp Leu Glu Leu Asp
145      150      155      160
Ser Gly Asp Ile Leu Glu Ser Ala Ser Phe Leu Arg Glu Asp Tyr Leu
      165      170      175
Asp Leu Asp Ala Leu Ser Leu Lys Leu Ala Arg Met Gly Ala Thr Leu
      180      185      190
Leu Leu Ser Thr Leu Lys Asn Phe His Ser Ile Thr Arg Lys Pro Gln
      195      200      205
Asp His Met Gln Ala Ser Phe Cys Lys Lys Ile Ala Lys Ala Asp Gly
      210      215      220
Leu Val Gly Phe Lys Asp Ala Lys Asn Leu Phe Leu Lys Ser Leu Ala
225      230      235      240
Phe Lys Ser Trp Pro Glu Ile Phe Leu Glu Asn Ser Leu Lys Leu Leu
      245      250      255
Glu Val Glu Leu Val Glu Asn Glu Lys Ser His Lys Glu Gly Glu Ile
      260      265      270
Leu Ala Ile Asp Glu Arg Gly Val Leu Val Gly Cys Leu Lys Gly Ser
      275      280      285
Val Arg Ile Ala Arg Leu Gln Ala Val Gly Lys Lys Pro Leu Lys Ala
      290      295      300
Lys Asp Tyr Leu Asn Gly Arg Arg Leu Lys Val Gly Gly Ile Leu Thr
305      310      315      320

```

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593

```

Lys Ser Thr Arg Lys Thr Ile Met Glu Ala Gln Leu Arg Phe Thr Gly
1      5      10      15
Val Gly Gly Gln Gly Val Leu Leu Ala Gly Glu Ile Leu Ala Glu Ala
      20      25      30
Lys Ile Val Ser Gly Gly Tyr Gly Thr Lys Thr Ser Thr Tyr Thr Ser
      35      40      45
Gln Val Arg Gly Gly Pro Thr Lys Val Asp Ile Leu Leu Asp Lys Asp
      50      55      60
Glu Ile Ile Phe Pro Tyr Ala Lys Glu Gly Glu Ile Asp Phe Met Leu
65      70      75      80

```


1145

```

Ser Val Ala Gln Ile Ser Tyr Asn Gln Phe Lys Ser Asp Ile Lys Lys
      85          90          95
Gly Gly Ile Val Val Ile Asp Pro Asn Leu Val Thr Pro Thr Lys Glu
      100        105        110
Asp Glu Glu Lys Tyr Gln Leu Tyr Lys Ile Pro Ile Ile Ser Ile Ala
      115        120        125
Lys Asp Glu Val Gly Asn Ile Ile Thr Gln Ser Val Val Ala Leu Ala
      130        135        140
Ile Thr Val Glu Leu Thr Lys Cys Val Glu Glu Asn Ile Val Leu Asp
145          150        155        160
Thr Met Leu Lys Lys Val Pro Cys Lys Ser Arg
      165          170

```

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594

```

Ala Cys Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile Leu His Ile
1      5      10      15
Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser Leu Gly Ile
      20      25      30
Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu Glu Val Phe
      35      40      45
Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln Ser Phe Ile
      50      55      60
Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln Lys His Glu
65      70      75      80
Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala Gly Ile Ala
      85      90      95
Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His Lys Arg Asn
      100     105     110
Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu Leu Gln Lys
      115     120     125
Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr Tyr Val Tyr
      130     135     140
Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val Val Glu Gly
145     150     155     160
Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu Glu Val Lys
      165     170     175
Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr Leu Tyr Ser
      180     185     190
Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu Asp Asn Tyr
      195     200     205
Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile Ala Ile Val
      210     215     220
Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile Gln Lys Ala
225     230     235     240
Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu Arg Ile Leu

```

1146

```

                245                250                255
Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro Lys Pro Val
      260      265      270
Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr Ser Pro Glu
      275      280      285
Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Tyr Gln Lys Asp
      290      295      300
Val Ser Ser Cys Glu Lys His Arg Ser Lys Ala Tyr Glu Lys Ile Val
      305      310      315
Glu Gly Ala Val Gly Tyr Ala Ser Tyr Phe Lys Glu Ser Gln Ile Ser
      325      330      335
Leu Asp Ile His Asp Val Ile Glu Trp Val Asn Phe Phe Ile Asp Asn
      340      345      350
Pro Ser Ile Gln Asp Gln Glu Gln Phe Arg Gln Ile Tyr Phe Leu Pro
      355      360      365
Asp Ala Thr His Lys Asn Ala Leu Pro Leu Phe Cys Asn Asp Val Ser
      370      375      380
Leu Leu Ser Cys Ile Leu Lys Pro Ser Gln Ser Tyr Ser Val Leu Lys
      385      390      395
Arg Ser Leu Arg Thr Asn Lys Gln Glu Arg Leu Phe Lys Ile Leu Ser
      405      410      415
Leu Ile Lys Lys Ile Tyr Gly Lys Leu Lys Lys Lys
      420      425

```

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595

```

Gly Leu Leu Ala Cys Leu Leu Val Leu Leu Asn Leu Lys Ile Thr Pro
1      5      10      15
Asn Leu Met Trp Pro Leu Asp Ile Ile Val Val Val Ala Trp Val Leu
      20      25      30
Trp Gly Val Asn Met Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr
      35      40      45
Ile Tyr Val Ser Leu Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala
      50      55      60
Val Met Tyr Ile Phe Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala
      65      70      75      80
Asp Met Gly Ser Val Trp His Ser Ile Ser Met Tyr Ser Gly Ser Asn
      85      90      95
Asp Ala Leu Ile Gln Trp Trp Trp Gly His Asn Ala Val Ala Phe Val
      100      105      110
Phe Thr Ser Gly Val Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu
      115      120      125
Ser Gly Gln Pro Ile Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp
      130      135      140
Ser Leu Met Phe Val Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr
      145      150      155      160

```

SUBSTITUTE SHEET (RULE 26)

1147

Ser Thr Val Pro Asp Trp Val Gln Thr Leu Ser Ser Val Phe Ser Val
 165 170 175
 Val Leu Ile Leu Pro Ser Trp Gly Thr Ala Ile Asn Met Leu Leu Thr
 180 185 190
 Met Arg Gly Gln Trp His Gln Leu Lys Glu Ser Pro Leu Ile Lys Phe
 195 200 205
 Leu Val Leu Ala Ser Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser
 210 215 220
 Ile Gln Ala Ile Lys Ser Val Asn Ala Leu Ala His Phe Thr Asp Trp
 225 230 235 240
 Ile Ile Gly His Val His Asp Gly Val Leu Gly Trp Val Gly Phe Thr
 245 250 255
 Leu Ile Ala Ser Met Tyr His Met Thr Pro Arg Leu Phe Lys Arg Glu
 260 265 270
 Ile Tyr Ser Gly Arg Leu Val Asp Phe Gln Phe Trp Ile Met Thr Leu
 275 280 285
 Gly Ile Val Leu Tyr Phe Ser Ser Met Trp Ile Ala Gly Ile Thr Gln
 290 295 300
 Gly Met Met Trp Arg Asp Val Asp Gln Tyr Gly Asn Leu Thr Tyr Gln
 305 310 315 320
 Phe Ile Asp Thr Val Lys Ala Leu Ile Pro Tyr Tyr Asn Ile Arg Gly
 325 330 335
 Val Gly Gly Leu Met Tyr Phe Ile Gly Phe Ile Ile Phe Ala Tyr Asn
 340 345 350
 Ile Phe Met Thr Ile Thr Ala Gly Lys Lys Leu Glu Arg Glu Pro Asn
 355 360 365
 Tyr Ala Thr Pro Met Ala Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596

Gly Phe Asp Asp Asp Met Glu Ile Arg Asn Ile Lys Glu Phe Glu Lys
 1 5 10 15
 Ala Ser Lys Lys Leu Gln Lys Asp Thr Leu Lys Ile Ala Leu Ala Leu
 20 25 30
 Leu Phe Leu Ile Gly Ala Ala Leu Leu Ala Leu Ile Phe Gly Gln Ala
 35 40 45
 Asn Ser Lys Gly Leu Leu Leu Ile Phe Ala Ala Val Ile Gly Gly Tyr
 50 55 60
 Met Ala Met Asn Ile Gly Ala Asn Asp Val Ser Asn Asn Val Gly Pro
 65 70 75 80
 Ser Val Gly Ser Lys Ala Ile Ser Met Gly Gly Ala Ile Leu Ile Ala
 85 90 95
 Ala Val Cys Glu Met Leu Gly Ala Ile Ile Ala Gly Gly Glu Val Val
 100 105 110
 Ser Thr Ile Lys Gly Arg Ile Val Ser Pro Glu Phe Ile Asn Asp Ala

SUBSTITUTE SHEET (RULE 26)

1148

```

      115      120      125
His Val Phe Ile Asn Val Met Leu Ala Ser Leu Leu Ser Gly Ala Leu
130      135      140
Trp Leu His Val Ala Thr Leu Ile Gly Ala Pro Val Ser Thr Ser His
145      150      155      160
Ser Val Val Gly Gly Ile Met Gly Ala Gly Met Ala Ala Ala Gly Met
      165      170      175
Ser Ala Ile Asn Trp His Phe Leu Ser Gly Ile Val Ala Ser Trp Val
      180      185      190
Ile Ser Pro Leu Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu
      195      200      205
Ile Lys Lys Thr Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu
      210      215      220
Lys Val Val Pro Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp
      225      230      235      240
Tyr Leu Ile Val Lys Val Leu Lys Arg Leu Tyr Ala Val Gly Phe Glu
      245      250      255
Ile Gln Leu Ala Cys Gly Cys Val Leu Ala Leu Leu Ile Phe Ile Leu
      260      265      270
Phe Lys Arg Phe Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His
      275      280      285
Glu Ser Val Asn Glu Leu Phe Asn Val Pro Leu Ile Phe
      290      295      300

```

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597

```

Arg Met Lys Leu Lys Lys Thr Leu Thr Tyr Gln His His Ala Tyr Ser
1      5      10      15
Phe Leu Ser Asp Asn Thr Asn Glu Val Leu Glu Asn Pro Lys Glu Ile
      20      25      30
Leu Phe Val Lys Thr Pro Leu Asn Glu Lys Tyr Ala Pro Leu Ile Ala
      35      40      45
Glu Lys Asn Leu Ala Ile Leu Asp Phe Asn Glu Leu Lys Asn Tyr Phe
      50      55      60
Asp Phe Lys Ile Lys Ile Val Gly Ile Thr Gly Thr Asn Gly Lys Thr
      65      70      75      80
Thr Thr Ala Ser Leu Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys
      85      90      95
Thr Ala Leu Leu Gly Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile
      100      105      110
Lys Glu Lys Gly Leu Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp
      115      120      125
Leu Glu Glu Ala Ile Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val
      130      135      140
Ser Ser His Ala Ile Val Gln Lys Arg Ile Ala Gly Leu Asp Phe Ala
      145      150      155      160

```

SUBSTITUTE SHEET (RULE 26)

1149

```

Leu Lys Ile Leu Thr Asn Ile Thr Ser Asp His Leu Asp Phe His Gln
      165      170      175
Asn Ile Glu Asn Tyr Arg Asp Ala Lys Asn Ser Phe Phe Lys Asp Glu
      180      185      190
Gly Leu Lys Val Ile Asn Arg Asp Glu Thr Asn Ala Leu Phe Asn Pro
      195      200      205
Ile Asn Ala Arg Thr Tyr Ala Leu Asp Lys Lys Ala His Leu Asn Val
      210      215      220
Gln Ala Phe Ser Leu Asn Pro Ser Ile Ser Ala Ser Leu Cys Tyr Gln
      225      230      235
His Asp Leu Arg Asp Pro Asn Leu Lys Glu Thr Ala Leu Ile His Ser
      245      250      255
Pro Leu Leu Gly Arg Tyr Asn Leu Tyr Asn Ile Leu Ala Gly Val Leu
      260      265      270
Gly Val Lys Leu Leu Thr Gln Leu Pro Leu Glu Thr Ile Ala Pro Leu
      275      280      285
Leu Glu Asn Phe Tyr Gly Val Lys Gly Arg Leu Glu Ile Val His Ser
      290      295      300
Lys Pro Leu Val Val Val Asp Phe Ala His Thr Thr Asp Gly Met Gln
      305      310      315
Gln Val Phe Glu Ser Phe Lys Asn Gln Lys Ile Thr Ala Leu Phe Gly
      325      330      335
Ala Gly Gly Asp Arg Asp Lys Thr Lys Arg Pro Lys Met Gly Ala Ile
      340      345      350
Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser Asp Asn Pro Arg
      355      360      365
Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu Lys Gly Ile Asn
      370      375      380
Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys Lys Ala Ile Leu
      385      390      395
Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu Leu Ile Leu Gly
      405      410      415
Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys Thr Ile Phe Phe
      420      425      430

```

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598

```

Arg Leu Leu Ser Gln Phe Lys Thr Arg Ile Asn Met Gln Glu Phe Ser
1      5      10      15
Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn Asp Phe Leu
      20      25      30
Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser Asn Pro Ser
      35      40      45
Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Gln Asp Glu Ile
      50      55      60
Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu Thr Leu Ala

```

SUBSTITUTE SHEET (RULE 26)

1150

```

65          70          75          80
Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro Leu Tyr Glu
      85          90          95
Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp Pro Phe Leu
      100         105         110
Glu Asp Asp Ala Ile Lys Ser Ile Asp Glu Ala Lys Arg Leu Phe Lys
      115         120         125
Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala Ser Glu Ser
      130         135         140
Ala Phe Glu Val Ile Ser Ala Leu Ala Gln Ala Ser Ile Pro Ile Asn
      145         150         155         160
Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile Ala Gln Ile
      165         170         175
Leu Ala Lys Glu Ala Arg Lys Arg Ala Val Ile Ser Val Phe Val Ser
      180         185         190
Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Gln Asn Leu Gln Ala
      195         200         205
Gln Ser Gly Ile Met Asn Ala Thr Glu Cys Tyr Tyr Gln Ile Asn Gln
      210         215         220
His Ala Asn Lys Leu Ile Ser Thr Leu Phe Ala Ser Thr Gly Val Lys
      225         230         235         240
Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu Cys Phe Lys
      245         250         255
Asn Ser Ile Asn Thr Ala Pro Leu Asp Ala Leu Asn Ala Tyr Leu Leu
      260         265         270
Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Ile Thr Glu Ile Glu
      275         280         285
Ala Phe Lys Lys Glu Leu Lys Thr His Asn Ile Asp Leu Glu Asn Thr
      290         295         300
Ala Gln Lys Leu Leu Lys Glu Gly Leu Ile Ala Phe Lys Gln Ser Phe
      305         310         315         320
Glu Lys Leu Leu Ser Ser Phe
      325

```

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599

```

Gly Phe Lys Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys
1          5          10          15
Tyr Phe Leu Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile
      20          25          30
Asp Ser Leu Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile
      35          40          45
Ile Leu Phe Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu
      50          55          60
Pro Ile Ser Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

1151

```

Lys Ser Asn Gln Tyr Thr Ala Leu Leu Ser Ile Gly Phe Ser Lys Cys
      85          90          95
Gln Ile Leu Ser Pro Ile Phe Leu Ile Ser Leu Phe Phe Thr Ala Val
      100        105        110
Tyr Val Gly Leu Asn Ala Thr Pro Phe Val Tyr Met Glu Glu Lys Thr
      115        120        125
Gln Asn Leu Ile Tyr Lys Asp Asn Ser Leu Ser Val Ser Glu His Leu
      130        135        140
Leu Val Lys Tyr Asn Asp Asp Tyr Val Tyr Phe Asp Lys Ile Asn Pro
      145        150        155        160
Leu Leu Gln Lys Ala Gln Asn Ile Lys Val Phe Arg Leu Lys Asp Lys
      165        170        175
Thr Leu Glu Ser Tyr Ala Glu Ala Lys Glu Ala Phe Phe Glu Asp Lys
      180        185        190
Tyr Trp Ile Leu His Asp Thr Thr Ile Tyr Glu Met Pro Leu Ser Phe
      195        200        205
Glu Leu Gly Ala Asn Ala Leu Asn Thr Thr His Leu Glu Thr Phe Lys
      210        215        220
Thr Leu Lys Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn
      225        230        235        240
Lys Pro Ala Val Ser Ile Thr Asp Ala Leu Leu Ser Leu His Ala Leu
      245        250        255
Val Arg Gln Asn Ala Asp Thr Lys Lys Val Arg Ser Phe Leu Tyr Val
      260        265        270
Phe Ala Ile Leu Pro Phe Phe Val Pro Phe Leu Ser Val Leu Ile Ala
      275        280        285
Tyr Phe Ser Pro Ser Leu Ala Arg Tyr Glu Asn Leu Ala Leu Leu Gly
      290        295        300
Leu Lys Phe Ile Ile Ile Thr Leu Val Val Trp Gly Leu Phe Phe Ala
      305        310        315        320
Leu Gly Lys Phe Ser Ile Ser Gly Ile Leu Ile Pro Glu Ile Gly Val
      325        330        335
Leu Ser Pro Phe Phe Val Phe Leu Ala Leu Ser Leu Trp Tyr Phe Lys
      340        345        350
Lys Leu Asn Lys Arg Leu
      355

```

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600

```

Lys Arg Arg Val Val Lys Phe Tyr Thr Tyr Ser Gly Glu Thr Ala Ala
1      5      10      15
Glu Ala Leu Lys Ile Ala Gln Ser His His Gly Val Asp Thr Leu Val
      20      25      30
Phe Lys Thr Gln Glu Ile Arg Lys Lys Thr Leu Thr Ser Ser Gly Leu
      35      40      45
Tyr Glu Ile Val Val Ala Val Glu Glu Glu Glu Asn Lys Lys Ala Pro

```

SUBSTITUTE SHEET (RULE 26)

1152

50	55	60
Leu Ile Pro Glu Ser	Leu Tyr Asp Glu Glu	Leu Asn Glu Glu Asp Val
65	70	75
Val Met Gln Leu Ser	Thr Val Glu Glu Met Arg Lys Leu Ala Gly	80
85	90	95
Val Ser Ser Asn Gln Arg Asn Tyr Thr	Phe Ser Lys Asn Lys Thr Leu	
100	105	110
Leu Glu Lys Asp Ala Pro Leu Glu Asp Thr	Pro Leu Glu Ala Asn Lys	
115	120	125
Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp	Glu Ala Asn His Lys Lys	
130	135	140
Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu Glu Ile Lys Asp Ile		
145	150	155
Asn Ala Gln Leu Ser Lys Ile Arg Asp Ser	Leu Lys Leu Ile Gln Asn	
165	170	175
Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Val	Asn Ile Pro Gln Glu	
180	185	190
Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly Met Lys Ser Ser		
195	200	205
His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu Met Pro Leu Arg		
210	215	220
Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe Arg Glu Val Leu		
225	230	235
Arg Lys Ile Ile Leu Cys Arg Pro Glu Asp Leu Asn Leu Arg Gln Lys		
245	250	255
Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr		
260	265	270
Leu Ala Lys Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr		
275	280	285
Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu		
290	295	300
Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val		
305	310	315
Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys		
325	330	335
Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu		
340	345	350
Lys Ile Ala Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp		
355	360	365
Val Ser Leu Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp		
370	375	380
Ile Tyr Asp Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr		
385	390	395
Lys Leu Asp Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His		
405	410	415
Glu Ser Gln Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro		
420	425	430
Met Asp Leu Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu		
435	440	445
Asp Gly Phe Ser Asn Pro Asn Lys Glu Gln Ala		
450	455	

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

1153

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601

```

Ile Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu
1      5      10      15
Val Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile
20     25     30
Ile Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg
35     40     45
Val Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met
50     55     60
Ala Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val
65     70     75     80
Glu Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu
85     90     95
Met Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro
100    105    110
Met Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro
115    120    125
Met Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn
130    135    140
Arg Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg
145    150    155    160
Gln Val Met Gln Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met
165    170    175
Tyr Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile
180    185    190
Val Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile
195    200    205
Gly His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile
210    215    220
Glu Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu
225    230    235    240
Thr Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser
245    250    255
Gly Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser
260    265    270
Leu Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn
275    280    285
Lys Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Lys Arg
290    295    300
Tyr Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile
305    310    315    320
Lys Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu
325    330    335
Met Leu Glu Glu Gln Arg Arg Gly Lys Val Gly Asp Ile Met Lys Ile
340    345    350
Glu Glu Glu
355

```

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602

Gly Thr Ser Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn
 1 5 10 15
 Ala Lys Asn Pro Lys Ser Phe Phe Asp Asn Lys Gly Asn Thr Lys Phe
 20 25 30
 Ile Ala Ile Thr Ser Gly Lys Gly Gly Val Gly Lys Ser Asn Ile Ser
 35 40 45
 Ala Asn Leu Ala Tyr Ser Leu Tyr Lys Lys Gly Tyr Lys Val Gly Val
 50 55 60
 Phe Asp Ala Asp Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val
 65 70 75 80
 Lys Thr His Lys Asn Ile Leu His Ala Leu Lys Gly Glu Ala Lys Leu
 85 90 95
 Gln Glu Ile Ile Cys Glu Ile Glu Pro Gly Leu Cys Leu Ile Pro Gly
 100 105 110
 Asp Ser Gly Glu Glu Ile Leu Lys Tyr Ile Ser Gly Ala Glu Ala Leu
 115 120 125
 Asp Arg Phe Val Asp Glu Glu Gly Val Leu Ser Ser Leu Asp Tyr Ile
 130 135 140
 Val Ile Asp Thr Gly Ala Gly Ile Gly Ala Thr Thr Gln Ala Phe Leu
 145 150 155 160
 Asn Ala Ser Asp Cys Val Val Ile Val Thr Thr Pro Asp Pro Ser Ala
 165 170 175
 Ile Thr Asp Ala Tyr Ala Cys Ile Lys Ile Asn Ser Lys Asn Lys Asp
 180 185 190
 Glu Leu Phe Leu Ile Ala Asn Met Val Ala Gln Pro Lys Glu Gly Arg
 195 200 205
 Ala Thr Tyr Glu Arg Leu Phe Lys Val Ala Lys Asn Asn Ile Ala Ser
 210 215 220
 Leu Glu Leu His Tyr Leu Gly Ala Ile Glu Asn Ser Ser Leu Leu Lys
 225 230 235 240
 Arg Tyr Val Arg Glu Arg Lys Ile Leu Arg Lys Ile Ala Pro Asn Asp
 245 250 255
 Leu Phe Ser Gln Ser Ile Asp Gln Ile Ala Ser Leu Leu Val Ser Lys
 260 265 270
 Leu Glu Thr Gly Thr Leu Glu Ile Pro Lys Glu Gly Leu Lys Ser Phe
 275 280 285
 Phe Lys Arg Leu Leu Lys Tyr Leu Gly
 290 295

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1155

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603

```

Ile Ser Glu Phe Asn His Arg Ser Ala Pro Leu Ile Ile Asn Tyr Val
1      5      10
Asn Thr Ile Phe Lys Lys Ala Tyr Gln Asn Ser Pro Thr Ala Tyr Leu
20     25     30
Glu Gln Lys Tyr Pro Lys Thr Ser Asn Asn Lys His Val Thr Glu Gly
35     40     45
Tyr Val Lys Val Ser Leu Val Ala Asp Glu Lys Glu Leu Leu Leu Glu
50     55     60
Gln Ile Leu Gln Glu Ala Gln Asn Leu Leu Glu His Arg Ile Asp Pro
65     70     75     80
Lys Asp Ile Thr Ile Leu Cys Ala Thr Asn Lys Asp Ala Leu Glu Ile
85     90     95
Lys Asn Tyr Leu Gln Glu Tyr Leu Ser Ala Ile Arg Pro Ser Thr Glu
100    105    110
Ser Ser Ala Lys Leu Ser Gln Leu Val Glu Ser Lys Ile Ile Lys Asn
115    120    125
Ala Leu Glu Tyr Ala Leu Ala Glu Glu Pro Tyr Lys Pro Phe Tyr Lys
130    135    140
His Ser Val Leu Lys Leu Ala Gly Tyr Leu His Asp Asp Val Ile Ala
145    150    155    160
Leu Pro Gly Phe Asn Pro Lys Lys Glu Ser Val Ala Ser Phe Val Trp
165    170    175
Lys Ile Met Glu Gln Phe Lys Leu Tyr Glu Glu Pro Ala Gln Ser Cys
180    185    190
Leu Glu Leu Ala Val Gly Cys Glu Asp Ala Asp Gly Phe Leu Glu Lys
195    200    205
Leu Glu Ala Lys Glu Ile Ala Ser Phe Asn Pro Lys Gly Ala Gln Ile
210    215    220
Met Thr Ile His Lys Ser Lys Gly Met Gln Phe Pro Tyr Val Ile Val
225    230    235    240
Cys Glu Arg Leu Gly Asn Pro Asn Ser Ser His Ala Asn Gln Leu Leu
245    250    255
Glu Glu Tyr Asp Gly Thr Glu Leu Ala Arg Leu Tyr Tyr Arg Met Lys
260    265    270
Asn Arg Glu Val Val Asp Lys Asp Tyr Ala Arg Ala Leu Asp Lys Glu
275    280    285
Glu Ala Ala Lys Asp His Glu Glu Ile Asn Val Tyr Tyr Val Ala Phe
290    295    300
Thr Arg Ala Glu Leu Gly Leu Ile Val Val Ala Lys Asp Lys Lys Glu
305    310    315    320
Ser Lys Lys Glu Ser Lys Asn Lys Lys Met His Glu Gln Leu Glu Leu
325    330    335
Ala Pro Leu Glu Glu Gly Glu Ile Ala Pro Val Ile Ser Pro Gln Lys
340    345    350
Glu Pro Leu Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu
355    360    365
Gln Val Gln Glu Ile Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn
370    375    380
Asn Asp Gln Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu
385    390    395    400
Glu Tyr Gln Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr
405    410    415
Leu Asn Tyr His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu
420    425    430
Glu Ser Leu Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe
435    440    445
Lys Asn His Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val
450    455    460
Val Ser Arg Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr

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1156

```

465          470          475          480
Val Leu Asp Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala
          485          490          495
Gln Val Ser His Tyr Ala Glu Phe Leu Arg Thr Gln Ala Pro His Phe
          500          505          510
Lys Ile Gln Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys
          515          520          525
Leu Trp Val
          530

```

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604

```

Leu Ser Thr Ala Tyr Gln Ala Val Glu Leu His Trp Phe Leu Lys Ala
1          5          10          15
Val Leu Val Leu Glu Arg Ser Pro Ser Ser Pro Glu Ile Lys Gly Ile
          20          25          30
Trp Asp Arg Asp Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp
          35          40          45
Val Ser Tyr Asp Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val
          50          55          60
Ile Phe Ser Ser Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr
65          70          75          80
Leu Asn Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val
          85          90          95
Tyr Gly Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile
          100          105          110
Asp Leu Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr
          115          120          125
Asn Thr Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly
          130          135          140
Val Thr Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp
145          150          155          160
Glu Phe Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr
          165          170          175
Glu Leu Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp
          180          185          190
Phe Phe Asp Phe Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser
          195          200          205
Phe Phe Tyr Asn Ala Pro Thr Thr Thr Ala Asn Phe Lys Asp Tyr Gly
          210          215          220
Val Val Gly Ala Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly
225          230          235          240
Leu Gln Ile Glu Trp Ile Ser Pro Met Gly Pro Trp Cys
          245          250

```

SUBSTITUTE SHEET (RULE 26)

1157

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605

Ala	Arg	Ile	Met	Leu	Asp	Lys	Arg	Ile	Lys	Thr	Leu	Leu	Leu	Phe	Phe
1				5					10					15	
Gly	Leu	Asn	Met	Val	Cys	Leu	Ser	Val	Ser	Phe	Thr	Asn	Lys	Pro	His
			20					25					30		
Leu	Cys	Phe	Trp	Phe	Leu	Val	Leu	Gly	Cys	Tyr	Leu	Val	Tyr	Glu	Trp
		35				40						45			
Gln	Lys	Lys	Gln	Lys	Lys	Asp	Phe	Gln	Ser	Ala	Lys	Ser	Leu	Lys	Phe
	50				55					60					
Asp	Ser	Val	Ser	Glu	Leu	Glu	Lys	Asp	Leu	Asn	Met	Glu	Val	Thr	Asn
65				70					75					80	
Asp	Glu	Trp	Asp	Thr	His										
				85											

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606

Ser	Arg	Ser	Val	Glu	Met	Asn	Tyr	Pro	Asn	Leu	Pro	Asn	Ser	Ala	Leu
1				5				10					15		
Glu	Ile	Ser	Glu	Gln	Pro	Glu	Val	Lys	Glu	Ile	Thr	Asn	Glu	Leu	Leu
			20					25					30		
Lys	Gln	Leu	Gln	Asn	Ala	Leu	Arg	Ser	Asn	Ala	His	Phe	Ser	Glu	Gln
		35				40					45				
Val	Glu	Leu	Ser	Leu	Lys	Cys	Ile	Val	Arg	Ile	Leu	Glu	Val	Leu	Leu
	50				55				60						
Ser	Leu	Asp	Phe	Phe	Lys	Asn	Ala	Asn	Glu	Ile	Asp	Ser	Ser	Leu	Arg
65				70					75					80	
Asn	Ser	Ile	Glu	Trp	Leu	Thr	Asn	Ala	Gly	Glu	Ser	Leu	Lys	Leu	Lys

1158

				85					90				95				
Met	Lys	Glu	Tyr	Glu	Arg	Phe	Phe	Ser	Glu	Phe	Asn	Thr	Ser	Met	His		
			100						105					110			
Ala	Asn	Glu	Gln	Glu	Val	Thr	Asn	Thr	Leu	Asn	Ala	Asn	Ala	Glu	Asn		
			115						120					125			
Ile	Lys	Ser	Glu	Ile	Lys	Lys	Leu	Glu	Asn	Gln	Leu	Ile	Glu	Thr	Thr		
			130				135					140					
Thr	Arg	Leu	Leu	Thr	Ser	Tyr	Gln	Ile	Phe	Leu	Asn	Gln	Ala	Arg	Asp		
					150					155					160		
Asn	Ala	Asn	Asn	Gln	Ile	Thr	Lys	Asn	Lys	Thr	Gln	Ser	Leu	Glu	Ala		
				165					170						175		
Ile	Thr	Gln	Ala	Lys	Asn	Asn	Ala	Asn	Asn	Glu	Ile	Ser	Asn	Thr	Gln		
			180					185						190			
Thr	Gln	Ala	Ile	Thr	Asn	Ile	Thr	Glu	Ala	Lys	Thr	Asn	Ala	Asn	Asn		
			195				200					205					
Glu	Ile	Ser	Asn	Asn	Gln	Thr	Gln	Ala	Ile	Thr	Asn	Ile	Asn	Glu	Ala		
			210			215					220						
Lys	Glu	Ser	Ala	Thr	Thr	Gln	Ile	Asn	Ala	Asn	Lys	Gln	Glu	Ala	Ile		
				230					235					240			
Asn	Asn	Ile	Thr	Gln	Glu	Lys	Thr	Gln	Ala	Thr	Ser	Glu	Ile	Thr	Glu		
				245				250						255			
Ala	Lys	Lys	Thr	Asp	His	Tyr	Gln	Asn	Ile	Asp	Phe	Phe	Glu	Phe	Glu		
			260					265					270				

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607

Gly	Leu	Ser	Val	Leu	Glu	Arg	Tyr	Ala	Asn	Glu	Glu	Met	Lys	Ala	Leu
1				5					10					15	
Trp	Asn	Glu	Gln	Thr	Lys	Phe	Glu	Thr	Tyr	Leu	Glu	Val	Glu	Lys	Ala
			20					25					30		
Val	Val	Arg	Ala	Trp	Asn	Lys	Leu	Gly	Gln	Ile	Gln	Asp	Ser	Asp	Cys
		35				40					45				
Glu	Lys	Ile	Cys	Leu	Lys	Ala	Ala	Phe	Asn	Leu	Glu	Arg	Ile	Lys	Glu
	50				55					60					
Ile	Glu	Lys	Thr	Thr	Lys	His	Asp	Leu	Ile	Ala	Phe	Thr	Thr	Cys	Val
	65				70				75					80	
Ala	Glu	Ser	Leu	Gly	Glu	Glu	Ser	Arg	Phe	Phe	His	Tyr	Gly	Ile	Thr
			85					90					95		
Ser	Ser	Asp	Cys	Ile	Asp	Thr	Ala	Met	Ala	Leu	Leu	Met	Thr	Lys	Ser
		100					105						110		
Leu	Lys	Leu	Ile	Gln	Lys	Gly	Val	Lys	Asn	Leu	Tyr	Glu	Thr	Leu	Lys
		115				120						125			
Asn	Arg	Ala	Leu	Glu	His	Gln	Asp	Thr	Leu	Met	Val	Gly	Arg	Ser	His
	130				135						140				
Gly	Val	Phe	Gly	Glu	Pro	Ile	Thr	Phe	Gly	Leu	Val	Leu	Ala	Leu	Phe
145					150				155						160

SUBSTITUTE SHEET (RULE 26)

1159

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Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu Asp Leu Thr Met Glu
      165      170      175
Phe Ile Ser Val Trp Ala Ile Ser Gly Gly Leu Gly Asn Phe Ala His
      180      185      190
Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly Phe Leu Gly Leu Lys
      195      200      205
Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg Asp Arg Tyr Ala Arg
      210      215      220
Leu Ala Cys Asp Leu Ala Leu Leu Ala Ser Ser Cys Glu Lys Ile Ala
225      230      235      240
Val Asn Ile Arg His Leu Gln Arg Ser Glu Val Tyr Glu Val Glu Glu
      245      250      255
Ala Phe Ser Ala Gly Gln Lys Gly Ser Ser Ala Met Pro His Lys Arg
      260      265      270
Asn Pro Ile Leu Ser Glu Asn Ile Thr Gly Leu Cys Arg Val Ile Arg
      275      280      285
Ser Phe Thr Thr Pro Met Leu Glu Asn Val Ala Leu Trp His Glu Arg
      290      295      300
Asp Met Ser His Ser Ser Val Glu Arg Phe Ala Leu Pro Asp Leu Phe
305      310      315      320
Ile Thr Ser Asp Phe Met Leu Ser Arg Leu Asn Ser Val Ile Glu Asn
      325      330      335
Leu Val Val Tyr Pro Lys Asn Met Leu Lys Asn Leu Ala Leu Ser Gly
      340      345      350
Gly Leu Val Phe Ser Gln Arg Val Leu Leu Glu Leu Pro Lys Lys Gly
      355      360      365
Leu Ser Arg Glu Glu Ser Tyr Ser Ile Val Gln Glu Asn Ala Met Lys
      370      375      380
Ile Trp Glu Val Leu Gln Gly Ala Phe Lys Asn Ala Asp Glu Asn
385      390      395      400
Leu Phe Leu Asn Ala Leu Leu Asn Asp Glu Arg Leu Lys Lys Tyr Leu
      405      410      415
Asn Glu Ser Glu Ile Arg Ala Cys Phe Asp Tyr Ser Tyr Tyr Thr Lys
      420      425      430
Asn Val Gly Ala Ile Phe Lys Arg Val Phe Gly
      435      440

```

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608

```

Asn Asp Ser Gly Ser Lys His Phe Ile Leu Pro Phe Leu Thr Leu Leu
1      5      10      15
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
      20      25      30
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
      35      40      45
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys

```

1160

```

      50              55              60
Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
65              70              75              80
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
      85              90              95
Ile

```

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609

```

Met Glu Lys Phe Phe Asn Gln Phe Phe Glu Asn Ile Gly Glu Asp Lys
1              5              10              15
Asn Arg Glu Gly Leu Lys Glu Thr Pro Lys Arg Val Gln Glu Leu Trp
      20              25              30
Lys Phe Leu Tyr Lys Gly Tyr Lys Glu Asp Pro Arg Val Ala Leu Lys
      35              40              45
Ser Ala Tyr Phe Gln Gly Val Cys Asp Glu Met Ile Val Ala Gln Asn
50              55              60
Ile Glu Phe Tyr Ser Thr Cys Glu His His Leu Leu Pro Phe Phe Gly
65              70              75              80
Asn Ile Ser Val Gly Tyr Ile Pro Lys Glu Lys Ile Val Gly Ile Ser
      85              90              95
Ala Ile Ala Lys Leu Ile Glu Ile Tyr Ser Lys Arg Leu Gln Ile Gln
      100              105              110
Glu Arg Leu Thr Thr Gln Ile Ala Glu Thr Phe Asp Glu Ile Ile Glu
      115              120              125
Pro Arg Gly Val Ile Val Val Cys Glu Ala Lys His Leu Cys Met Ser
130              135              140
Met Gln Gly Val Gln Lys Gln Asn Ala Ile Ile Lys Thr Ser Val Leu
145              150              155              160
Arg Gly Leu Phe Lys Lys Asp Pro Lys Thr Arg Ala Glu Phe Met Gln
      165              170              175
Leu Leu Lys Ser
      180

```

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

1161

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610

```

Val Ile Ile Leu Gly Met Ser Asn Pro Asn Leu Ser Phe Tyr Cys Asn
1      5      10      15
Glu Cys Glu Arg Phe Glu Ser Phe Leu Lys Asn His Tyr Leu His Leu
20      25      30
Glu Gly Phe His Pro Tyr Leu Glu Lys Ala Phe Phe Glu Met Val Leu
35      40      45
Asn Gly Gly Lys Arg Phe Arg Pro Lys Leu Phe Leu Ala Val Leu Cys
50      55      60
Ser Leu Val Gly Lys Lys Asp Tyr Ser Asn Gln Gln Thr Glu Tyr Phe
65      70      75      80
Lys Ile Ala Leu Ser Ile Glu Cys Leu His Thr Tyr Ser Leu Ile His
85      90      95
Asp Asp Leu Pro Cys Met Asp Asn Ala Ile Leu Arg Arg Asn His Pro
100     105     110
Thr Leu His Ala Lys Tyr Asp Glu Thr Thr Ala Val Leu Ile Gly Asp
115     120     125
Ala Leu Asn Thr Tyr Ser Phe Glu Leu Leu Ser Asn Ser Leu Leu Glu
130     135     140
Ser Arg Ile Ile Val Glu Leu Val Lys Ile Leu Ser Ala Asn Gly Gly
145     150     155     160
Ile Lys Gly Met Ile Leu Gly Gln Ala Leu Asp Cys Tyr Phe Glu Asn
165     170     175
Thr Pro Leu Asn Leu Glu Gln Leu Thr Phe Leu His Glu His Lys Thr
180     185     190
Ala Lys Leu Ile Ser Ala Ser Leu Ile Met Gly Leu Val Ala Ser Gly
195     200     205
Ile Asn Asp Glu Glu Leu Leu Lys Trp Leu Gln Ala Phe Gly Leu Lys
210     215     220
Met Gly Leu Cys Phe Gln Val Leu Asp Asp Ile Ile Asp Val Thr Gln
225     230     235     240
Asp Glu Lys Glu Ser Gly Lys Thr Thr His Leu Asp Ser Ala Lys Asn
245     250     255
Ser Phe Val Asn Leu Leu Gly Leu Lys Lys Ala Ser Gly Tyr Ala Gln
260     265     270
Thr Leu Lys Thr Glu Ile Leu Asn Asp Leu Asn Ala Leu Glu Pro Thr
275     280     285
Tyr Leu Ser Leu Gln Glu Asn Leu Asn Ala Leu Leu Asn Thr Leu Phe
290     295     300
Lys Gly Lys Thr
305

```

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

1162

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611

```

Leu Leu Asn Thr Ser Lys Lys Lys Arg Asn Leu Asn Trp Asn Phe Thr
1      5      10      15
Cys Leu Lys Gly Val Met Arg Ala Arg Cys Ser Lys Lys Ser Ser Met
      20      25      30
Arg Lys Glu Lys Ile Met Thr Asn Phe Glu Lys Ile Ile Ala Gln Asn
      35      40      45
Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe Ala
      50      55      60
Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp Leu
      65      70      75      80
Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr Ile
      85      90      95
Thr Ile Val Met Phe Val Val Ala Phe Val Ile Ile Leu Val Cys Ile
      100      105      110
Gln Asn Phe Ser Ser Ile Met Leu Ser Gly Asp Glu Tyr Lys Leu Ile
      115      120      125
Asp Pro Ser Lys Val Leu Ser Ser Lys Glu Asn Gln Ile His Arg Leu
      130      135      140
Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu His Phe Glu Pro Lys Leu
      145      150      155      160
Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala Phe Ala Ser Gly Trp Asp
      165      170      175
Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser Ala Leu Ile Glu Arg Leu
      180      185      190
Asp Arg Asp Glu Leu Lys Ala Val Ile Ala His Glu Leu Ser His Ile
      195      200      205
Arg His Asn Asp Ile Arg Leu Thr Met Cys Val Gly Ile Leu Ser Asn
      210      215      220
Ile Met Leu Leu Val Ala Asn Phe Ser Val Tyr Phe Phe Met Gly Asn
      225      230      235      240
Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg Met Ile Leu Trp Val Leu
      245      250      255
Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu Gln Met Tyr Leu Ser
      260      265      270
Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly Ala Ala Phe Leu Met His
      275      280      285
Asp Asn Lys Pro Met Ile Arg Ala Leu Gln Lys Ile Ser Asn Asp Tyr
      290      295      300
Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys Asn Ser Thr Arg Ser Ala
      305      310      315      320
Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser Thr His Pro Ser Ile Lys
      325      330      335
Asn Arg Ile Gln Ser Leu Arg Lys Arg Val Ile
      340      345

```

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

1163

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612

```

Thr Gln Pro His Lys Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg
1          5          10          15
Leu Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg
20          25          30
Leu Asn Lys Lys Leu Asn Lys Ser Lys Lys Lys Lys Ile Ser Leu Asn
35          40          45
Lys Thr Val Ser Arg Pro Phe Lys Thr Ile Lys Lys Pro Pro Gln Pro
50          55          60
Pro
65

```

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613

```

Gly Val Asn Met Leu Ile Leu Gly His Pro Leu Ile Pro Ser Ala Arg
1          5          10          15
Phe Val Phe Ile Lys Asn Thr Asp Ala Ile His Ser Ser Ala Asn Asn
20          25          30
Asp Ile Val Cys Phe Glu Ala Asn Pro Lys Asn Leu Glu Leu Ala Gln
35          40          45
Tyr Cys Cys Glu Asn Gly Val His Phe Ser Val Ile Phe Leu Ser His
50          55          60
Lys Ile Glu Thr Asp Thr Phe Phe Leu Phe Asn Ala Phe Lys Pro Leu
65          70          75          80
Tyr Cys Ile Phe Lys Asp Ile Lys Gln Ala Ile Leu Ala Gln Gln His
85          90          95
Ala Thr Asn Tyr Leu Leu Asp Ser Lys Ile Leu Phe Ser Met Asp Phe
100          105          110
Asn Asp Thr Glu Ser Trp Glu Ile Cys Ala Lys Asn Gln Ile Asp Gly
115          120          125
Val Ile Ser Lys Asp Ser Leu Leu Lys
130          135

```

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids
(B) TYPE: amino acid

1164

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614

```

Phe Lys Cys Asn Leu Lys Arg Arg Ser Ala Leu Lys Leu Leu Val Val
1           5           10           15
Asp Asp Ser Ser Thr Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg
20           25           30
Leu Gly Tyr Glu Asp Val Leu Glu Ala Glu His Gly Val Glu Ala Trp
35           40           45
Glu Lys Leu Asp Ala Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp
50           55           60
Asn Met Pro Glu Met Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala
65           70           75           80
Asp Asn Arg Phe Lys Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly
85           90           95
Gly Lys Ala Glu Val Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr
100          105          110
Ile Val Lys Pro Phe Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val
115          120          125
Val Leu Gly Thr Asn Asp
130

```

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615

```

Arg Val Met Ala Val Arg Ile Met Ala Thr Val Trp Thr Asn Ser Cys
1           5           10           15
Lys Glu Phe Gly Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu Val
20           25           30
Val Val Gly Arg Phe Phe Ile Lys Gly Ala Phe Tyr Gly Leu Lys Asn
35           40           45
Gly Val Leu Gly Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser Ala
50           55           60
Phe Val Tyr Ser Leu Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr Phe
65           70           75           80

```

1165

```

Glu Ala Ser Ser Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe Leu
      85                      90                      95
Glu Leu Lys Ala Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu Glu
      100                    105                    110
Ser His Glu Ile His Ser Val Ile Val Val Glu Asn Gly Lys Gln Ile
      115                    120                    125
Glu Lys His Pro Lys Asp Val Ala Ile Gly Ser Val Val Trp Val Pro
      130                    135                    140
Ser Gly Ala Lys Ile Ala Leu Asp Gly Val Leu Leu Asn Ser Ala Ser
      145                    150                    155                    160
Val Asp Ala Ser Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu Gly
      165                    170                    175
Val Asn Asp Pro Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro Phe
      180                    185                    190
Ser Tyr Gln Val Ser Ala Thr Phe Gln Asn Ser Arg Leu Ser Ser Leu
      195                    200                    205
Leu Glu Thr Leu Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu Ser
      210                    215                    220
Ser Ala Asn Lys Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe Leu
      225                    230                    235                    240
Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn Phe
      245                    250                    255
Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys Pro
      260                    265                    270
Cys Ala Phe Ala Arg Leu Arg Pro
      275                    280

```

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616

```

Arg Ala Ser His Lys Leu Pro Leu Arg Val Arg Ser Ala Thr Pro Ile
1      5      10      15
Ala Leu Val Ile Gly Val Phe Lys Asn Pro Leu Ile Val Phe Lys Glu
      20      25      30
Ala Leu Phe Leu Glu Thr Leu Ala Lys Val Lys Lys Ile Phe Ile Asp
      35      40      45
Lys Thr Gly Thr Leu Thr Gln Lys Glu Val Leu Leu Lys Glu Lys Ile
      50      55      60
Ile His Glu Glu Phe Asp Glu Arg Leu Leu Lys Ser Leu Leu Lys Thr
      65      70      75      80
Arg Glu His Leu Ala His Asn Ala Ile Leu Lys Thr Leu Asp Gly Asp
      85      90      95
Glu Val Asp Leu Glu Lys Ile Glu Phe Phe Ala His Gly Leu Lys Ala
      100     105     110
Ser Tyr Gln Asn Glu Thr Leu Leu Val Gly Ser Leu Lys Phe Leu Asn
      115     120     125
Ala Met Gly Val Asp Leu Lys Val Lys Glu Ser Ala Asn Ile Met Val

```

SUBSTITUTE SHEET (RULE 26)

1166

```

      130              135              140
Gly Phe Ala Lys Asn Lys Thr Leu Cys Ala Leu Phe Ile Leu Glu Glu
145              150              155              160
Arg Leu Lys Ala Asn Ala Lys Glu Val Ile Gln Ala Leu Gln Asn Gln
      165              170              175
Gly Leu Glu Leu Glu Ile Leu Ser Gly Asp Asn Glu Ser Ser Val Lys
      180              185              190
Glu Cys Ala Lys
      195

```

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617

```

Thr Pro Thr Lys Ala Pro Lys Ile Val Gln Glu Gln Val Thr Tyr Pro
1      5      10      15
Leu Val Ser Thr Phe Met Ser Ile Ala Asn Ile Asp Thr Val Arg Gly
      20      25      30
Ile Ser Ser Tyr Glu Ser Gly Leu Ile Tyr Ile Ile Phe Lys Asp Gly
      35      40      45
Val Asn Leu Tyr Trp Ala Arg Asp Arg Val Leu Glu Gln Leu Asn Arg
      50      55      60
Val Ser Asn Leu Pro Lys Asp Ala Lys Val Glu Ile Gly Ser Asp Ser
      65      70      75      80
Thr Ser Ile Gly Trp Ala Tyr Gln Tyr Ala Leu Ser Ser Asp Ser Lys
      85      90      95
Asn Leu Ser Asp Leu Lys Val Leu Gln Asp Phe Tyr Tyr Arg Tyr Ala
      100      105      110
Leu Leu Gly Val Asp Gly Val Ser Glu Val Ala Ser Val Gly Gly Phe
      115      120      125
Val Lys Asp Tyr Glu Val Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr
      130      135      140
Asn Leu Ser Leu Glu Gln Val Ala Asn Ala Ile Lys Asn Ser Asn Asn
      145      150      155      160
Asp Thr Gly Gly Gly Val Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile
      165      170      175
Arg Ser His Gly Tyr Ile Gln Ser Leu Asn Asp Leu Glu Glu Ile Val
      180      185      190
Val Lys Lys Glu Gly Ala Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser
      195      200      205
Val Arg Leu Ala Pro Lys Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly
      210      215      220
Asp Lys Glu Val Val Gly Gly Ile Val Met Val Arg Tyr His Ala Asp
      225      230      235      240
Thr Tyr Lys Val Leu Lys Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln
      245      250      255
Ala Ser Asn Pro Asp Val Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu
      260      265      270

```

SUBSTITUTE SHEET (RULE 26)

1167

```

Leu Ile Glu Lys Gly Ile Asp Asn Leu Ile His Thr Leu Ile Glu Glu
275 280 285
Ser Val Ile Val Leu Val Ile Ile Ala Ile Phe Leu Leu His Phe Arg
290 295 300
Ser Ala Leu Val Val Ile Ile Thr Leu Pro Leu Ser Val Cys Ile Ser
305 310 315 320
Phe Leu Leu Met Arg Tyr Phe Asn Ile Glu Ala Ser Ile Met Ser Leu
325 330 335
Gly Gly Ile Ala Ile Ala Ile Arg Ala Met Val Asp Ala Ala Ile Val
340 345 350
Met Val Glu Asn Ala His Lys His Leu Gln His Ile Asp Thr Arg Asp
355 360 365
Asn Thr Gln Arg Val Asn Ala Ile Met Gln Gly Val Lys His Val Gly
370 375 380
Gly Ala Ile Phe Phe Ala Leu Met Ile Ile Val Val Ser Phe Leu Pro
385 390 395 400
Ile Phe Ala Leu Thr Gly Gln Glu Glu Lys Leu Phe Ala Pro Leu Ala
405 410 415
Tyr Thr Lys Thr Phe Ala Met Leu Val Gly Ala Leu Leu Ser Ile Thr
420 425 430
Ile Val Pro Val Leu Met Val Trp Leu Ile Lys Gly Arg Ile Leu Glu
435 440 445
Glu Ser Glu Ser Pro Val Asn Ala Phe Phe Met Lys Ile Tyr Gly Val
450 455 460
Ser Leu Arg Val Val Leu Lys Phe Arg Tyr Ala Phe Leu Ile Ala Ser
465 470 475 480
Val Leu Gly Leu Gly Gly Leu Val Val Ala Tyr Lys Lys Leu Asn Trp
485 490 495
Glu Phe Ile Pro Gln Ile Asn Glu Gly Val Ile Met Tyr Met Pro Val
500 505 510
Thr Ile Asn Gly Val Gly Ile Asp Thr Ala Leu Glu Tyr Leu Lys Lys
515 520 525
Ser Asn Ala Ala Ile Lys Gln Leu Asp Phe Val Lys Gln Val Phe Gly
530 535 540
Lys Val Gly Arg Ala Asn Thr Ser Thr Asp Ala Ala Gly Leu Gly Met
545 550 555 560
Ile Glu Thr Tyr Ile Glu Leu Lys Pro Gln Asn Glu Trp Lys Glu Lys
565 570 575
Leu Ser Tyr Lys Glu Val Arg Asp Lys Leu Glu Lys Thr Leu Gln Leu
580 585 590
Lys Gly Leu Thr Asn Ser Trp Thr Tyr Pro Ile Arg Gly Arg Thr Asp
595 600 605
Met Leu Leu Thr Gly Ile Arg Thr Pro Leu Gly Ile Lys Leu Tyr Gly
610 615 620
Asn Asp Thr Asp Lys Leu Gln Glu Leu Ala Ile Leu Met Glu Gln Gln
625 630 635 640
Leu Lys Thr Leu Lys Glu Ser Leu Ser Gly Phe Ala Glu Arg Ser Asn
645 650 655
Asn Gly Tyr Tyr Ile Thr Leu Asp Leu Glu Arg
660 665

```

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

1168

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618

```

Arg Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr
1      5      10      15
Leu His Ala Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp
      20      25      30
Val Ala Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu
      35      40      45
Ser Thr Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys
      50      55      60
Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser
      65      70      75      80
Asn Ala Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
      85      90      95

```

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619

```

Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Ala Ser Leu Asn
1      5      10      15
Ser Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp Ala
      20      25      30
Phe Leu Asn Gly Asn Val Glu Ala Ile Val Gly Gly Phe Gly Ser Tyr
      35      40      45
Gly Tyr Ser Ser Phe Ser Asn Gln Ala Asn Ser Leu Asn Ser Gly Ala
      50      55      60
Asn Asn Ala Asn Phe Gly Val Tyr Ser Arg Phe Phe Ala Asn His Pro
      65      70      75      80
Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser
      85      90      95
Leu Asn Phe Lys Ser Thr Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn
      100      105      110
Tyr Leu Ala Tyr Ser Ala Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe
      115      120      125
Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val Ser
      130      135      140
Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln
      145      150      155      160
Val Ala Leu Lys Asn Gly Ala Ser Ser Gln His Leu Phe Asn Ala Asn
      165      170      175
Ala Thr Trp Lys Arg Val Ile Ile Met Gly Thr Leu His Thr Phe Ile
      180      185      190

```


1169

Cys Met Arg Glu Phe Tyr Lys Ser Ser Leu Thr Leu Asp Arg Met Met
 195 200 205
 Trp Arg Leu
 210

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620

Asn	Lys	Ile	Leu	Ala	Ser	Glu	Leu	Glu	Phe	Lys	Phe	Leu	Ile	Lys	Gly
1				5					10					15	
Val	Ile	Met	Ala	His	His	Glu	Glu	Gln	His	Gly	Gly	His	His	His	His
			20					25					30		
His	His	His	Thr	His	His	His	His	Tyr	His	Gly	Gly	Glu	His	His	His
		35					40					45			
His	His	His	Ser	Ser	His	His	Glu	Glu	Gly	Cys	Cys	Ser	Thr	Ser	Asp
	50					55					60				
Ser	His	His	Gln	Glu	Glu	Gly	Cys	Cys	His	Gly	His	His	Glu		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621

Gly	Val	Leu	Ile	Arg	Thr	Pro	Lys	His	Leu	Thr	Lys	Gln	Glu	Ser	Val
1				5					10					15	
Asn	Leu	Gly	Ala	Tyr	Tyr	Thr	Pro	Pro	Tyr	Leu	Val	Asp	Cys	Ala	Tyr
			20					25					30		
Lys	Leu	Leu	Lys	Lys	His	Val	Gly	Ile	Glu	Asn	Tyr	Thr	Leu	Leu	Asp
		35				40						45			
Thr	Ala	Cys	Gly	Asn	Lys	Glu	Phe	Leu	Lys	Leu	His	His	Pro	Lys	Lys

1170

```

      50              55              60
Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn Ala
65              70              75              80
Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu Pro
      85              90
Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe Ile
      100              105              110
Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn Asp
      115              120              125
Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala Ile
      130              135              140
Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu Ile
      145              150              155              160
Lys Glu Ala Asn Phe Lys Gln Leu Lys Leu Phe Lys Asp His Tyr Arg
      165              170              175
Leu Leu Asp Ala Phe Val Val Ser Ser Lys Ser Phe Thr Lys Ser Asn
      180              185              190
Glu Phe Pro Ile Val Ile Ala Leu Tyr Glu Arg Gly Arg Met Asp Tyr
      195              200              205
Ala Gly Ile Arg Arg Phe Val Phe Pro Thr Asp Cys Asp Thr Thr Leu
      210              215              220
Cys Leu Asn Asp Phe Asp Tyr Ile Ala Asn Tyr Val Asp Lys Tyr Pro
      225              230              235              240
Asn Ala Lys Lys Val Gly Ala Cys Val Gly Tyr Phe Phe Pro Met Arg
      245              250              255
Asp Ile Asn Ala Leu Lys Arg Asn Lys Thr Phe Leu Asn Ala Pro Ser
      260              265              270
Glu Asn Ala Val Arg Ile Ser Gln Asp Lys Leu Ile Tyr Tyr Gln Tyr
      275              280              285
Ile His Tyr Phe Lys Glu Ile Ala Pro Lys Ile Pro Tyr Tyr Phe Gly
      290              295              300
Asn Leu Asp Ile Ile Ile Asp His Phe Ala Phe Leu Glu Ile Lys Asp
      305              310              315              320
Ala Phe Leu Lys Asp Lys Arg Ala Arg Leu Glu Tyr Phe Lys Lys Leu
      325              330              335
Phe Gln Gly His Pro Cys Glu Phe Asp
      340              345

```

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622

```

Asn Ile Leu Lys Asn Cys Phe Lys Asp Thr Leu Val Ser Leu Ile Lys
1              5              10              15
Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser Ile Pro Leu Thr Ser
      20              25              30
Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His Ala Phe Ser Asp Tyr
      35              40              45

```

SUBSTITUTE SHEET (RULE 26)

1171

Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe Ser Leu Lys His Tyr
 50 55 60
 Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile Lys Asp Lys Glu Lys
 65 70 75 80
 Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr His Phe Leu Gly Ala
 85 90 95
 Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser Glu Met Ile Tyr Tyr
 100 105 110
 Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn Leu Glu Asn Thr Leu
 115 120 125
 Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu Asp Asn Phe Met Ile
 130 135 140
 Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly Gly Met Asp Phe Glu
 145 150 155 160
 Leu Leu Arg Ile Ser Tyr Pro Leu Leu Ile His Ser Phe Asp Asp Asn
 165 170 175
 Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln Tyr Gly Ser Lys Thr
 180 185 190
 Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu Glu Leu Lys Thr Ala
 195 200 205
 Thr Pro Leu Leu Asn Arg Thr Ala Met Pro Lys Glu His Ala Leu Leu
 210 215 220
 Ile Ile His Glu Thr Asn Ala Leu Val Phe Leu Glu Met Leu Lys Ile
 225 230 235 240
 Phe Gly Leu Leu Ser Gln Val His His Asn Asp Val Leu Lys Ile Leu
 245 250 255
 Glu Lys Ile Leu Gln Asn
 260

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
 1 5 10 15
 Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
 20 25 30
 Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
 35 40 45
 Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
 50 55 60
 Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
 65 70 75 80
 Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
 85 90 95
 Thr Leu Arg Asp Ala Asn Asn Thr Leu Ile Gln Ala Leu Ile Pro Ile
 100 105 110
 Ser Gln Asp Leu Gln Ile His Ile Tyr Lys Lys Gly Glu Asp Tyr Phe

SUBSTITUTE SHEET (RULE 26)

1172

```

      115      120      125
Leu Asp Phe Ile Pro Ile Val Phe Thr Arg Lys Glu Arg Thr Leu Leu
 130      135      140
Leu Ser Leu Gln Thr Ser Pro Tyr Gln Asp Ile Val Lys Ala Thr Asn
 145      150      155      160
Asp Pro Leu Leu Ala Asn Gln Leu Met Asn Ala Tyr Lys Lys Ser Val
      165      170      175
Pro Phe Lys Arg Leu Val Lys Asn Asp Lys Ile Ala Ile Val Tyr Thr
      180      185      190
Arg Asp Tyr Arg Val Gly Gln Ala Phe Gly Gln Pro Thr Ile Lys Met
 195      200      205
Ala Met Val Ser Ser Arg Leu His Gln Tyr Tyr Leu Phe Ser His Ser
 210      215      220
Asn Gly Arg Tyr Tyr Asp Ser Lys Ala Gln Glu Val Ala Gly Phe Leu
 225      230      235      240
Leu Glu Thr Pro Val Lys Tyr Thr Arg Ile Ser Ser Pro Phe Ser Tyr
      245      250      255
Gly Arg Phe His Pro Val Leu Lys Val Lys Arg Pro His Tyr Gly Val
 260      265      270
Asp Tyr Ala Ala Lys His Gly Ser Leu Ile His Ser Ala Ser Asp Gly
 275      280      285
Arg Val Gly Phe Ile Gly Val Lys Ala Gly Tyr Gly Lys Val Val Glu
 290      295      300
Ile His Leu Asn Glu Leu Arg Leu Val Tyr Ala His Met Ser Ala Phe
 305      310      315      320
Ala Asn Gly Leu Lys Lys Gly Ser Phe Val Lys Lys Gly Gln Ile Ile
      325      330      335
Gly Arg Val Gly Ser Thr Gly Leu Ser Thr Gly Pro His Leu His Phe
 340      345      350
Gly Val Tyr Lys Asn Ser Arg Pro Ile Asn Pro Leu Gly Tyr Ile Arg
 355      360      365
Thr Ala Lys Ser Lys Leu His Gly Lys Gln Arg Glu Val Phe Leu Glu
 370      375      380
Lys Ala Gln Tyr Ser Lys Gln Lys Leu Glu Glu Leu Phe Lys Thr His
 385      390      395      400
Ser Phe Glu Lys Asn Ser Phe Tyr Leu Leu Glu Gly Phe
      405      410

```

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624

```

Gly Cys Leu Met Lys Ser Ile Leu Leu Phe Met Ile Phe Val Val Cys
 1      5      10      15
Gln Leu Glu Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr
      20      25      30
Asn Tyr Tyr Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn
 35      40      45

```

SUBSTITUTE SHEET (RULE 26)

1173

```

Asp Leu Ser Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu
 50      55      60
His Ser Trp Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr
 65      70      75      80
Leu Gly Thr Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe
      85      90      95
Gln Trp Tyr His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe Lys
      100      105      110
Phe Gln Ile Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr
      115      120      125
Lys Gly Thr Leu Tyr Leu Ala Tyr Thr Gln Thr Asn Trp Phe Gln Ile
      130      135      140
Tyr Asn Asp Pro Gln Ser Ala Pro Met Arg Met Ile Asn Phe Met Pro
      145      150      155      160
Glu Leu Ile Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly Lys
      165      170      175
Ile Gly Asn Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser Asn
      180      185      190
Gly Val Gly Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly Asn
      195      200      205
Pro Glu Asn Gln Phe Pro Gly Gln Pro Val Ile Val Lys Asp Tyr Asn
      210      215      220
Gly Gln Lys Asp Val Arg Trp Gly Gly Cys Arg Ser Val Ser Ala Gly
      225      230      235      240
Asn Ala Leu Cys Phe Val Trp Cys Gly Lys Arg Glu Ala
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625

```

Met Asn Arg Ala Trp Ile Lys Lys Lys Met Lys Lys Ile Lys Leu Thr
 1      5      10      15
Lys Arg Met Ile Ala Thr Ala Lys Lys Ala Leu Ser Lys Ser Tyr Gly
      20      25      30
Tyr Cys Leu Val Gly Arg Phe Leu Ile Phe Phe Leu Arg Phe Cys Ile
      35      40      45
Phe Phe Trp His Ala Gly Lys Lys Ser Tyr Cys Pro Ser Leu Ala Val
      50      55      60
Lys Lys Thr Arg Lys Pro Gly Cys Arg Gly Ile Glu Ser Phe Tyr Gln
      65      70      75      80
Pro Ser Lys

```

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

1174

(A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626

```

Arg Ile Glu Trp Gly Asn Arg His Cys Gly Ala Leu Ser His Ala Asn
1           5           10           15
Ser Val Ser Met Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu
20           25           30
Gly Ile Leu Asn Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met
35           40           45
Leu Gly Val Val Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro
50           55           60
Ile Gln Asn Ala Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val
65           70           75           80
Met Phe Leu Gly Leu Phe Asn Asp Ile Thr Arg Leu Leu
85           90
  
```

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627

```

Asn Leu Gly Gly Ala Ala Asn Val Ala Asn Asn Leu Thr Ser Leu Lys
1           5           10           15
Ala Lys Val Phe Leu Cys Gly Val Val Gly Asp Asp Leu Lys Gly Lys
20           25           30
His Phe Ile Ser Thr Leu Asn Ser Ile Arg Ile Asp Thr Ser Gly Val
35           40           45
Leu Ile Asp Lys Thr Arg Cys Thr Thr Leu Lys Thr Arg Ile Ile Ala
50           55           60
Gln Asn Gln Gln Ile Val Arg Val Asp Lys Glu Ile Lys Asp Pro Leu
65           70           75           80
Asn Ala Asp Leu Arg Lys Asn Leu Leu Asp Phe Ile Ala Glu Lys Ile
85           90           95
Gln Glu Ile Asp Gly Val Ile Leu Ser Asp Tyr Asn Lys Gly Val Leu
100          105          110
  
```

1175

```

Asp Phe Glu Leu Thr Gln Thr Ile Ile Thr Leu Ala Asn Lys His His
      115              120              125
Lys Leu Ile Leu Cys Asp Pro Lys Gly Lys Asp Tyr Ser Lys Tyr Ser
      130              135              140
His Ala Ser Leu Ile Thr Pro Asn Arg Ala Glu Leu Glu Gln Ala Leu
      145              150              155              160
His Leu Lys Leu Asp Ser His Ala Asn Leu Ser Lys Ala Leu Gln Ile
      165              170              175
Leu Gln Glu Thr Tyr His Ile Ala Met Pro Leu Val Thr Leu Ser Glu
      180              185              190
Gln Gly Ile Ala Phe Leu Glu Lys Gly Glu Leu Val Asn Cys Pro Thr
      195              200              205
Ile Ala Lys Glu Val Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile
      210              215              220
Ala Ser Leu Thr Leu Ser Leu Leu Glu Ser Lys Ser Leu Lys Glu Ala
      225              230              235              240
Cys Glu Phe Ala Asn Ala Ala Ala Val Val Val Gly Lys Met Gly
      245              250              255
Ser Ala Leu Ala Ser Leu Glu Glu Ile Ala Leu Ile Leu Asn Gln Thr
      260              265              270
His Pro Lys Ile Leu Pro Leu Glu Lys Leu Leu Glu Thr Leu Glu Arg
      275              280              285
Asn Gln Gln Lys Ile Val Phe Thr Asn Gly Cys Phe Asp Ile Leu His
      290              295              300
Lys Gly His Ala Ser Tyr Leu Gln Lys Ala Lys Ala Leu Gly Asp Ile
      305              310              315              320
Leu Val Val Gly Leu Asn Ser Asp Asn Ser Ile Lys Arg Leu Lys Gly
      325              330              335
Asp Lys Arg Pro Ile Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala
      340              345              350
Ser Leu Ser Cys Val Asp Tyr Val Val Phe Gly Glu Asp Thr Pro
      355              360              365
Ile Lys Leu Ile Gln Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala
      370              375              380
Asp Tyr Leu Asn Lys Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr
      385              390              395              400
Arg Leu Ile Glu Phe Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu
      405              410              415
Lys Ile Lys Arg Thr His Asn Asp
      420

```

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628

```

Gly Ser Leu Met Val Asn Val Phe Phe Lys Gln Gln Lys Phe Val Ile
1           5           10           15
Lys Lys Arg Phe Asn Asp Phe Asn Gly Phe Asp Ile Glu Glu Asn Glu

```

SUBSTITUTE SHEET (RULE 26)

1176

```

      20      25      30
Val Leu Trp Phe Glu Leu Ile Asn Pro Thr Pro Asn Glu Leu Ala Thr
      35      40      45
Leu Ser Gln Glu Tyr Ala Ile His Tyr Asn Thr Asp His Ser Gln Arg
      50      55      60
Val Ser Ser Val Thr Lys Tyr Trp Glu Asp Ser Ser Ser Val Thr Ile
      65      70      75      80
Asn Ala Phe Phe Thr Asn Gln Asp Glu Asn Glu Thr Phe His Met Glu
      85      90      95
Met Ala Thr Phe Ile Leu Ser Asn Asn Ile Leu Phe Thr Ile Tyr Tyr
      100      105      110
Gly Thr Leu Glu Ile Phe Asp Ser Ile Gln Lys Lys Val Leu Ala Ser
      115      120      125
Pro Lys Lys Phe Glu Asp Gly Phe Asp Ile Leu Thr Lys Ile Phe Glu
      130      135      140
Val Tyr Phe Glu Lys Gly Val Glu Cys Leu Glu Trp Ile Asn Lys Gln
      145      150      155      160
Thr Ser Leu Leu Arg Lys Asn Ile Ile Phe Lys Glu Thr Ser Thr His
      165      170      175
Asp Asp Ile Leu Val Arg Leu Ser Asn Leu Gln Glu Phe Asn Val Ala
      180      185      190
Leu Arg Asp Ser Phe Phe Asp Lys Arg Arg Ile Ile Thr Ala Leu Leu
      195      200      205
Arg Ser Asn Lys Val Asp Ser Asp Thr Lys Asn Asn Leu Asn Ile Ile
      210      215      220
Leu Thr Asp Phe Ser Ser Leu Val Glu Ser Thr Thr Val Asn Leu Asn
      225      230      235      240
Ser Leu Asp Asn Ile Gln Asn Leu Phe Ala Ser Gln Val Asn Val Glu
      245      250      255
Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala Met Met
      260      265      270
Pro Pro Thr Leu Ile Gly Thr Ile Tyr Gly Met Asn Phe Lys Phe Met
      275      280      285
Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile Val Met
      290      295      300
Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys Gly Trp
      305      310      315      320
Leu

```

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629

```

Pro Phe Met Glu Phe Leu Ser Ser Leu Leu Asp Ala Leu Ser Thr Pro
1      5      10      15
His Gly Ile Val Ser Leu Ala Thr Leu Thr Leu Leu Glu Ile Val Leu
      20      25      30

```

SUBSTITUTE SHEET (RULE 26)

Gly Ile Asp Asn Ile Ile Phe Ile Thr Val Met Val Tyr Lys L
 35 40 45
 Lys His Gln Gln Asn Lys Val Met Ile Leu Gly Leu Gly Leu Ala Met
 50 55 60
 Ile Thr Arg Ile Gly Leu Leu Gly Ser Leu Phe Phe Ile Ser His Leu
 65 70 75 80
 Gln Lys Pro Leu Phe Ala Ile Ala Gly Met Ser Phe Ser Trp Arg Asp
 85 90 95
 Val Val Leu Leu Leu Gly Gly Ala Phe Leu Ala Phe Lys Ala Leu Val
 100 105 110
 Glu Leu Lys Glu Gln Ile Tyr Pro Lys Glu Lys Arg Gln Glu Lys Ala
 115 120 125
 Phe Gly Phe Phe Ile Thr Leu Ile Glu Ile Met Phe Leu Asp Ile Val
 130 135 140
 Phe Ser Leu Asp Ser Val Ile Thr Ala Ile Gly Ile Ala Lys His Leu
 145 150 155 160
 Glu Val Met Ala Leu Ala Ile Ile Leu Ser Val Ile Val Met Met Phe
 165 170 175
 Phe Ser Lys Ile Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys
 180 185 190
 Thr Leu Ala Phe Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu
 195 200 205
 Glu Gly Leu His Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile
 210 215 220
 Gly Phe Ala Leu Leu Ile Glu Cys Leu Asn Ile Phe Ile Glu Lys Lys
 225 230 235 240
 Met Lys Lys Ser

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630

Val Tyr Gly Phe Trp Ala Cys Val Leu Cys Gly Phe Lys Phe Gly Phe
 1 5 10 15
 Val Tyr Phe Ala Gln Thr Arg Ala Phe Gln Phe Arg Gln Asn His Ser
 20 25 30
 Phe His Arg Tyr Gln Asn Glu His Asp Phe Arg Pro Val His Ala His
 35 40 45
 Ser Arg Glu Phe Leu Arg Trp Gly Val Gly Glu Ile Leu Gly Ala Leu
 50 55 60
 Leu Gly Val Gly Pro Arg Asn Leu Gly Val Asp Phe Tyr Leu Arg Leu
 65 70 75 80
 Cys Leu Asp Leu Ala Phe Ala Phe Phe Arg Leu Ser Lys Leu Ala Leu
 85 90 95
 Tyr Phe Ser Glu Gln Gln Arg Ala Arg Val Leu Phe Gly Phe Asn Asp
 100 105 110
 Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys Arg

1178

```

          115          120          125
Arg Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser Asp Thr
    130          135          140
Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631

```

Arg Tyr Ser Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu
1      5      10      15
Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp
    20      25      30
Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser Leu Ala Glu Ile
    35      40      45
Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn Asp Val Ser Ser
    50      55      60
Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu Ser Asp Met Ser
    65      70      75      80
Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser Asn Leu Ser Ser
    85      90      95
Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr Ala Lys Ser Gly
    100     105     110
His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu Val Glu Lys Val
    115     120     125
Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu Asn Ile Ala Thr
    130     135     140
His Val Ser Gly Thr Thr Met Asn Leu Asp Lys Gln Val Asn Leu Phe
145     150     155     160
Lys Thr

```

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

1179

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632

```

Ile Cys Leu Lys Leu Asn Gln Gly Gly Val Tyr Gln Lys Arg Val Gly
1      5      10      15
Leu Leu Lys Val Ser Val Ile Thr Ala Cys Phe Asn Ser Glu Lys Thr
      20      25      30
Ile Glu Asp Thr Ile Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile
      35      40      45
Glu Tyr Ile Ile Ile Asp Gly Ala Ser Ala Ile Ala Leu
50      55      60

```

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633

```

Asn His Ile Val Arg Gly Val Asp Cys Asp Arg Gly Val Ser Ile Leu
1      5      10      15
Gly Val Ser Leu Asn Ser Arg Val Lys Glu Ile Leu Lys Glu Ser Ala
      20      25      30
Leu His Ser Met Gln Asp Ser Leu His Phe Lys Val Lys Glu Val Gln
      35      40      45
Ser Val Leu Glu Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met
50      55      60
Leu Pro Glu Asp Thr Lys Arg Glu Ile Lys Ile Gln Leu Leu Lys Asn
65      70      75      80
Phe Ile Leu Ala Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys
      85      90      95
Asp Arg Glu Asp Leu Arg Leu Thr Leu Leu Arg Asp Asn Asp Thr Ile
100      105      110
Lys Leu Met Glu Asn Pro Ser Leu Gly Ser Asn Pro Leu Val Gln Lys
115      120      125
Ala Met Lys Asn Lys Glu Ile Ser Lys Ser Leu Pro Tyr Tyr Arg Lys
130      135      140
Met Pro Asn Gly Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu
145      150      155      160
Phe Lys Glu Asn Thr Gln Glu Val Val Gly Val Leu Met Ile Phe Phe
165      170      175
Ser Ile Asp Ser Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu
180      185      190
Phe Leu Ile Gly Val Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser
195      200      205
Leu Gln Asp Lys Ser Ile Thr Glu Ile Tyr Lys Ser Val Pro Lys Ala
210      215      220
Thr Asn Glu Val Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu

```

SUBSTITUTE SHEET (RULE 26)

1180

225					230					235				240
Glu	Tyr	Leu	Asp	Pro	Phe	Ser	His	Lys	Glu	Asn	Phe	Leu	Ala	Val
				245					250					255
Thr	Phe	Lys	Met	Leu	Gly	Lys	Thr	Glu	Ser	Lys	Asp	Asn	Leu	Asn
			260					265					270	
Met	Ile	Ala	Leu	Ile	Ile	Glu	Lys	Asp	Lys	Val	Tyr	Glu	Gln	Val
		275				280					285			
Ser	Val	Arg	Phe	Val	Val	Val	Ala	Ala	Ser	Ala	Ile	Met	Val	Leu
	290					295					300			
Leu	Ile	Ile	Ala	Ile	Thr	Leu	Leu	Met	Arg	Ala	Ile	Val	Ser	Asn
305					310					315				320
Leu	Glu	Val	Val	Ser	Ser	Thr	Leu	Ser	His	Phe	Phe	Lys	Leu	Leu
				325					330					335
Asn	Gln	Ala	His	Ser	Ser	Asp	Ile	Lys	Leu	Val	Glu	Ala	Arg	Ser
			340					345					350	
Asp	Glu	Leu	Gly	Arg	Met	Gln	Thr	Ala	Ile	Asn	Lys	Asn	Ile	Leu
	355					360						365		
Thr	Gln	Lys	Thr	Met	Gln	Glu	Asp	Trp	Gln	Ala	Val	Gln	Asp	Thr
	370				375						380			
Lys	Val	Val	Ser	Asp	Val	Lys	Ala	Gly	Asn	Phe	Ala	Val	Arg	Ile
385					390				395					400
Ala	Glu	Pro	Ala	Ser	Pro	Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu
			405						410					415
Asp	His	Ala	Leu	Phe	Ala	Arg	Lys	Arg	Gly	Thr	His	Met	Pro	Ser
			420					425					430	
Phe	Lys	Ile	Phe	Glu	Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg
		435					440				445			
Gln	Asn	Ala	Ser	Gly	Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly
	450				455						460			
Glu	Ile	Gln	Lys	Met	Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp
465				470					475					480
Ala	Asn	Asp	Ser	Ala	Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu
			485					490					495	
Ala	Ser	Asn	Ser	Gln	His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr
			500					505					510	
Glu	Asn	Ile	Thr	Thr	Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu
	515						520					525		
Met	Ile	Glu	Gln	Gly	Lys	Asp	Ile	Lys	Ser	Ile	Val	Glu	Ile	Ile
	530					535					540			
Asp	Ile	Ala	Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Ile
545					550				555					560
Ala	Ala	Arg	Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val	Val	Ala
			565						570					575
Glu	Val	Arg	Lys	Leu	Ala	Glu	Arg	Thr	Gln	Lys	Ser	Leu	Ser	Glu
			580					585					590	
Glu	Ala	Asn	Ile	Asn	Ile	Leu	Val	Gln	Ser	Ile	Ser	Asp	Thr	Ser
	595						600				605			
Ser	Ile	Lys	Asn	Gln	Val	Lys	Glu	Val	Glu	Glu	Ile	Asn	Ala	Ser
	610					615					620			
Glu	Ala	Leu	Arg	Ser	Val	Thr	Glu	Gly	Asn	Leu	Lys	Ile	Ala	Ser
625					630				635					640
Ser	Leu	Glu	Ile	Ser	Gln	Glu	Ile	Asp	Lys	Val	Ser	Asn	Asp	Ile
			645					650					655	
Glu	Asp	Val	Asn	Lys	Lys	Gln	Phe							
			660											

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1181

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634

```

Arg Gly Glu Cys Tyr Phe Glu Arg Glu Ile Gly Leu Met Arg Lys Ile
1          5          10          15
Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile Gly Val Val Tyr Ala
20          25          30
Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly Arg Lys Gln Glu Ser
35          40          45
Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys Ser Lys Glu Leu Lys
50          55          60
Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn Lys Glu Glu Lys Lys
65          70          75          80
Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu Val His His Gly Asp
85          90          95
Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro Lys Ile Lys Gly Ser
100          105          110
Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn Asn Ala Pro Lys Pro
115          120          125
Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu Lys Asn Lys Glu Thr
130          135          140
Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly Asn Pro Asn Asn Ala
145          150          155          160
Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly Gly Ile Ser Leu Leu
165          170          175
Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile Gln Glu Glu Gln Glu
180          185          190
Lys Ser Lys Val Ser Lys Ala Gln Ala Arg Asp Arg Leu Ile Ala Glu
195          200          205
Arg Ile Lys Asn Gln Glu Ile Glu Arg Leu Lys Ile His Val Asp Asp
210          215          220
Asp Lys Leu Asn Gln Glu Met Ala Met Met Ala Gln Gln Gln Gly Met
225          230          235          240
Asp Leu Asp His Phe Lys Gln Met Leu Met Ala Glu Gly His Tyr Lys
245          250          255
Leu Tyr Arg Asp Gln Leu Lys Glu His Leu Glu Met Gln Glu Leu Leu
260          265          270
Arg Asn Ile Leu Leu Thr Asn Val Asp Thr Ser Ser Glu Thr Lys Met
275          280          285
Arg Glu Tyr Tyr Asn Lys His Lys Glu Gln Phe Ser Ile Pro Thr Glu
290          295          300
Ile Glu Thr Val Arg Tyr Thr Ser Thr Asn Gln Glu Asp Leu Glu Arg
305          310          315          320
Ala Met Ala Asp Pro Asn Leu Glu Val Pro Gly Val Ser Lys Ala Asn
325          330          335
Glu Lys Ile Glu Met Lys Thr Leu Asn Pro Gln Ile Ala Gln Val Phe
340          345          350
Ile Ser His Glu Gln Gly Ser Phe Thr Pro Val Met Asn Gly Gly Gly
355          360          365
Gly Gln Phe Ile Thr Phe Tyr Ile Lys Glu Lys Arg Gly Lys Asn Glu
370          375          380
Val Ser Phe Ser Gln Ala Lys Gln Phe Ile Ala Gln Lys Leu Val Glu
385          390          395          400
Glu Ser Lys Asp Lys Ile Leu Glu Glu His Phe Glu Lys Leu Arg Val
405          410          415
Lys Ser Arg Ile Val Met Ile Arg Glu

```

SUBSTITUTE SHEET (RULE 26)

1182

420

425

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635

```

Ile Val Gln His Phe Asn Phe Leu Tyr Lys Asp Ser Leu Phe Ser Ile
1      5      10      15
Ala Leu Phe Thr Phe Ile Ile Ala Leu Val Ile Leu Leu Glu Gln Ala
20      25      30
Arg Ala Tyr Phe Thr Arg Lys Arg Asn Lys Lys Phe Leu Gln Lys Phe
35      40      45
Ala Gln Asn Gln Asn Ala Tyr Ala Ser Ser Glu Asn Leu Asp Glu Leu
50      55      60
Leu Lys His Ala Lys Ile Ser Ser Leu Met Phe Leu Ala Arg Ala Tyr
65      70      75      80
Ser Lys Ala Asp Val Glu Met Ser Ile Glu Ile Leu Lys Gly Leu Leu
85      90      95
Asn Arg Pro Leu Lys Asp Glu Glu Lys Ile Ala Val Leu Asp Leu Leu
100     105     110
Ala Lys Asn Tyr Phe Ser Val Gly Tyr Leu Gln Lys Thr Lys Asp Thr
115     120     125
Val Lys Glu Ile Leu Arg Phe Ser Pro Arg Asn Val Glu Ala Leu Leu
130     135     140
Lys Leu Leu His Ala Tyr Glu Leu Glu Lys Asp Tyr Ser Lys Ala Leu
145     150     155     160
Glu Thr Leu Glu Cys Leu Glu Glu Leu Glu Val Pro Lys Ile Glu Thr
165     170     175
Ile Lys Asn Tyr Leu Tyr Leu Met His Leu Ile Glu Asn Lys Glu Asp
180     185     190
Ala Ala Lys Ile Leu His Val Ser Lys Ala Ser Leu Asp Leu Lys Lys
195     200     205
Ile Ala Leu Asn His Leu Lys Ser His Asp Glu Asn Leu Phe Trp Gln
210     215     220
Glu Ile Asp Thr Thr Glu Arg Leu Glu Asn Val Ile Asp Leu Leu Trp
225     230     235     240
Asp Met Asn Ile Pro Ala Phe Ile Leu Glu Lys His Ala Leu Leu Gln
245     250     255
Asp Ile Ala Arg Ser Gln Gly Leu Leu Leu Asp His Lys Pro Cys Gln
260     265     270
Ile Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys
275     280     285
Ala Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe
290     295     300
Pro Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met
305     310     315     320
Asp Met Val Leu Lys Ile Ser Lys Lys Thr His Ala Met Gly Val Asp
325     330     335

```

SUBSTITUTE SHEET (RULE 26)

1183

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636

```

Ile Arg Gly Ala Lys Thr Gly Gln Asn Asp His Leu Lys Gly Lys Met
1      5      10      15
Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp Asn
      20      25      30
Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp Lys
      35      40      45
Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala Leu
      50      55      60
Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu Val
      65      70      75      80
Ile Gly Glu Leu Leu Tyr His Lys Phe Tyr Gln Tyr Asp Glu Gly Lys
      85      90      95
Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr Lys
      100     105     110
Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser Ser
      115     120     125
Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser Ala
      130     135     140
Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala Lys
      145     150     155     160
Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg Leu
      165     170     175
Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu Leu
      180     185     190
Thr Gln Ala Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln Glu
      195     200     205
Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile Gln
      210     215     220
Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala Glu
      225     230     235     240
Gln Gln Cys Ala Tyr Gln Ala Leu Gln Lys Leu Lys Glu Val Lys
      245     250     255

```

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1184

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637

```

Ala His Gln Ser Ser Arg Gly Val Ser Met Ile Leu Ala Cys Asp Val
1      5      10      15
Gly Leu Lys Arg Ile Gly Ile Ala Ala Leu Leu Asn Gly Val Ile Leu
20      25      30
Pro Leu Glu Ala Ile Leu Arg His Asn Arg Asn Gln Ala Ser Arg Asp
35      40      45
Leu Ser Asp Leu Leu Arg Lys Lys Asp Ile Gln Val Leu Val Val Gly
50      55      60
Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala Arg Ile Glu His Phe
65      70      75      80
Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val Phe Ile Asn Glu Asp
85      90      95
Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu His Leu Gly Lys Lys
100     105     110
Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu Asp Ser Leu Ser Ala
115     120     125
Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val Leu Lys Lys Gly
130     135     140

```

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638

```

Lys Asn Glu Asn Phe Ile Lys Val Leu Ile Leu Asp Leu Lys Val Leu
1      5      10      15
Leu Gln Arg Ile Val Asp Phe Phe Ile Lys Leu Asn Lys Lys Gln Lys
20      25      30
Ile Ala Leu Ile Ala Ala Gly Val Leu Ile Thr Ala Leu Leu Val Phe
35      40      45
Leu Leu Leu Tyr Pro Phe Lys Glu Lys Asp Tyr Ala Gln Gly Gly Tyr
50      55      60
Gly Val Leu Phe Glu Arg Leu Asp Ser Ser Asp Asn Ala Leu Ile Leu
65      70      75      80
Gln His Leu Gln Gln Asn Gln Ile Pro Tyr Lys Val Leu Lys Asp Asp
85      90      95
Thr Ile Leu Val Pro Lys Asp Lys Val Tyr Glu Glu Arg Ile Thr Leu
100     105     110

```


1342

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813

```

Lys Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys
1      5      10      15
Ile Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile
20      25      30
Ser Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala
35      40      45
Pro Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile
50      55      60
Cys Asp Lys Gly Glu Trp Val Glu Val Gly Gly Ala Ala Asn Ala Ser
65      70      75      80
Lys Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe
85      90      95
Leu Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala
100     105     110
Gly Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val
115     120     125
Asn Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser
130     135     140
Ser Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His
145     150     155     160
Gly Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser
165     170     175
His Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn
180     185     190
Asp Tyr Ala Gly Gln Ala Phe Arg Gly Arg Gly Leu Lys Gly Leu Leu
195     200     205
Ser Lys Lys Ser Gly Ala Leu Pro Lys Gln His Ala Asn Phe Leu Val
210     215     220
Asn Leu Gly Gly Ala Glu Phe Glu Glu Ala Leu Asp Leu Ile Glu Leu
225     230     235     240
Ala Lys Thr Arg Val Leu Gln Glu Tyr Gly Ile His Leu Glu Glu Glu
245     250     255
Val Lys Ile Leu Arg
260

```

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814

SUBSTITUTE SHEET (RULE 26)

1341

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811

```

Thr Ser Ala Ser Arg Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn
1      5      10      15
Leu Cys Ala Arg Lys Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn
20     25     30
Glu Met Leu Ile Arg Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu
35     40     45
Leu Asp Glu Ala Ile Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val
50     55     60
Gln Asp Glu Asn Ala Leu Gln Pro Phe Glu Gln Ser Phe Gln Gln Leu
65     70     75     80
Glu Glu Ile Leu Arg
85

```

(2) INFORMATION FOR SEQ ID NO:1812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812

```

Asp Lys Arg Asn Ile Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu
1      5      10      15
Thr Tyr Lys Ile Thr Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly
20     25     30
Leu Val Val Gly Leu Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile
35     40     45
Asn Glu Met Thr Leu Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly
50     55     60
Val Leu Ile Leu Thr Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr
65     70     75     80
Thr Lys Thr Leu Ile Lys Leu Ile Pro Lys Ile Ile Gly
85     90

```

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

1340

```

      435              440              445
Phe Asn Leu Phe Lys Asp Lys Asp Ala Ile Val Phe Tyr Leu Ser Asp
  450              455              460
His Ala Gln Asp Ile Phe Glu Ser Gly Pro Thr Tyr Gly His Ser Cys
  465              470              475              480
Ser Lys Ala Gly Leu Glu Ile Pro Phe Met Ile Tyr Val Ser Asp Ile
      485              490              495
Phe Lys Glu Lys His Pro Glu Lys Val Lys Leu Ile Lys Asn Ala Leu
      500              505              510
Asn Lys Pro Phe Met Ser Asp Asp Leu Ile His Ser Leu Leu Pro Leu
      515              520              525
Val Gly Ile His Thr Lys Asp Glu Ile Glu Ser Lys Asn Leu Phe Ser
      530              535              540
Pro Gln Phe Asp Ala Gln Arg Lys Arg Ala Val Cys Tyr Gly Ser Met
  545              550              555              560
Asn Tyr Asp Arg Thr Lys
      565

```

(2) INFORMATION FOR SEQ ID NO:1810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810

```

Lys Ser Phe Met Pro Pro Thr Arg Pro Gln Ala Ser Ile Leu Arg Leu
1              5              10              15
Thr Leu Lys Asn Pro Leu Ser Met Leu Ser Arg Tyr Ser Leu Cys Leu
      20              25              30
Leu Lys Lys Thr Arg Leu Gln Thr Ser Asn Ser Ala Pro Lys Ala
      35              40              45
Cys Leu Ile Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn
      50              55              60
Thr Leu Lys Ile Arg Ser Leu Leu Lys Pro
  65              70

```

(2) INFORMATION FOR SEQ ID NO:1811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

1339

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809

```

Lys Lys Phe Ser Asn Ser Leu Lys Gly Gln Lys Lys Thr Met Lys Phe
1      5      10      15
Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys Phe Leu Met
20      25      30
Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn Ser Asp Leu
35      40      45
Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile Gly Phe Val
50      55      60
Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu Lys Tyr Ser
65      70      75      80
Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser Val Ala Glu
85      90      95
Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys Gly Leu Ile
100     105     110
Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala Phe Ile Lys
115     120     125
Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu Ile Ala Leu
130     135     140
Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val Pro Gly Val
145     150     155     160
Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly Ser Val Arg
165     170     175
Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys Arg Ser Leu
180     185     190
Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr Leu Ser Leu
195     200     205
Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu Asn Asn Leu
210     215     220
Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile Ser Asn Val
225     230     235     240
Val Leu Val Ile Gly Glu Ser Ala Ser Arg Asn Phe Met Gln Leu Tyr
245     250     255
Gly Tyr Ser Val Pro Asn Asn Pro Leu Cys Glu Arg Thr Arg Gln Ala
260     265     270
Arg Glu Arg Glu Arg Glu Ser Asn Asn Leu Phe Val Phe Ser Asp Thr
275     280     285
Ile Ser Lys Glu Ala His Thr Ser Asp Val Phe Glu Ser Leu Leu Asn
290     295     300
Tyr Ser Asp Ala Glu Thr Lys Pro Trp Tyr His Tyr His Asn Met
305     310     315     320
Ile Asp Ile Phe Lys Arg Ser His Tyr Glu Thr Phe Trp Leu Glu Lys
325     330     335
Gln Ile Val Asp Glu Trp Gly Ile Thr Gln Asn Leu Val Ser Asn Arg
340     345     350
Ser Lys Asn Arg Tyr Tyr Ile Leu Gly Asn Tyr Gly Ala Tyr Asp Glu
355     360     365
Glu Leu Val Lys Phe Tyr Ser Lys Asn Val Gln Pro Gln Leu Lys Ser
370     375     380
Lys Asn Phe Ile Val Phe His Leu Leu Gly Ser His Ser Trp Tyr Ala
385     390     395     400
Asp Arg Phe Pro Lys Ser Phe Ala Lys Phe Lys Pro Ser Asp Leu Ser
405     410     415
Phe Ser Asn Leu His Ala Ser Ser Asp Arg Asp Lys Gln Ile Val Ala
420     425     430
Asp Tyr Val Asn Ser Leu Tyr Tyr Asn Asp Phe Val Leu Asn Gly Ile

```

SUBSTITUTE SHEET (RULE 26)

1338

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808

```

Pro Leu Lys Ser Lys Ala Ser Lys Leu Leu Gly Ala Asn Ile Val Tyr
1      5      10      15
Lys Ile His Cys Leu Val Lys Gly Val Thr Leu Glu Gln Gln Asn Lys
20     25     30
Leu Leu Lys Thr Ile Glu Pro Phe Lys Lys Phe Ala Ser Leu Glu Phe
35     40     45
Ile Asp Ile Asn Ser Leu Asp Tyr Ser Ile Glu Ser Tyr Leu Asn Glu
50     55     60
Ser Cys Ser Lys Arg Tyr Gly Gly Leu Leu Val Leu Cys Arg Leu Leu
65     70     75     80
Leu Ala Ser Leu Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp Val
85     90     95
Asp Thr Val Phe Leu Gly Asp Val Ala Ser Ala Tyr Phe Ala Leu Asp
100    105    110
Asn Glu Pro Thr Lys Leu Leu Gly Met Val Arg Asp Thr Phe Ser His
115    120    125
Leu Pro Phe Glu Ala Phe Cys Asp Phe Cys Glu Arg Thr Cys Lys Asn
130    135    140
Phe Lys Ile Asp Leu Leu Arg Phe Ser Gln Asn Glu Leu Lys Arg Ile
145    150    155    160
His Gln Gly Phe Asn Met Gly Phe Leu Val Ala Asn Leu Asp Leu Trp
165    170    175
Arg Glu Asn Gly Phe Glu Lys Ile Ala Leu Glu Phe Leu Lys Thr Arg
180    185    190
Gly Lys Asp Leu Phe Tyr Pro Glu Gln Cys Leu Ile Asn Met Val Phe
195    200    205
Leu Glu Arg Ile Leu Glu Leu Pro Ile His Tyr Asn Cys Tyr Ser Asp
210    215    220
Phe Phe Lys Glu His Tyr Pro Lys Ser Ile Ile Met Leu His Phe Ile
225    230    235    240
Lys Tyr Lys Pro Trp Arg Ser Val Ser Ser Leu Asn Gly Arg Leu Ile
245    250    255
Cys Tyr Glu Ala Glu Ala Ser Phe Trp Leu Ala Asn Leu Phe Cys Thr
260    265    270
Pro Phe Lys Asn Asp Phe Phe Lys Glu Arg Leu Glu Met Ala Lys Asp
275    280    285
Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile Arg
290    295    300
Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe Glu
305    310    315    320
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:1809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

1337

```

Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala Val Asn Phe Val
65          70          75          80
Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser Gln Val Thr Pro
          85          90          95
Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr Tyr Lys Ile Phe
          100          105          110
Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys Ile Ser Gln Leu
          115          120          125
Glu Gln Lys Gly Val Met Met Glu Pro Gln Thr Leu Asn Phe Gly Glu
130          135          140
Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile Glu Ala Glu Ile
145          150          155          160
Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp Lys
          165          170

```

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807

```

Ile Ser Asn Met Glu Asn Thr Pro Lys Asp Arg Ala Arg Ile Leu Ile
1          5          10          15
Glu Glu Leu Lys Ile Leu Gln Gly Val Ile Asn Arg Met Ala Gln Asn
          20          25          30
Ser Leu Glu Cys Lys Lys Trp Thr Leu Ala Leu Ala Val Gly Val Leu
          35          40          45
Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly Leu Cys Val Leu
          50          55          60
Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala Tyr Tyr Leu Met
65          70          75          80
Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu Ile Lys Asn Arg
          85          90          95
Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro Ile His Gln Thr
          100          105          110
Cys Gln Ser Thr Gln Phe Leu Ser Ala Met Arg Ser Phe Ser Leu Phe
          115          120          125
Pro Tyr Trp Ala Leu Gly Leu Cys Leu Val Gly Tyr Gly Phe Cys Cys
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1336

100

105

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805

```

Ile Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile
1           5           10           15
Phe Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly
20           25           30
Tyr Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu
35           40           45
Ser Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys
50           55           60
Lys Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys
65           70           75           80
Lys Ala Cys Glu Glu Val Phe
85

```

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806

```

Arg Ala Ile Thr Thr Asn Gln Phe Val Gly Thr Asn Met Phe Phe Lys
1           5           10           15
Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala Leu Tyr Leu Val
20           25           30
Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val Glu Met Ile Ala
35           40           45
Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala Asp Ser Ile Thr
50           55           60

```

1335

```

Val Ser Val Val Asn Lys Gly Thr Leu Thr Arg Leu Ile Lys Glu Lys
      115      120      125
Gly Met Ile Tyr Lys Ile Ala Arg Leu Lys Asp His Tyr Val Ile Cys
      130      135      140
Tyr His Asn Glu Tyr Thr Ile Glu Leu Ser Lys Gln Phe Arg Ser Ala
      145      150      155      160
Gln Ile Pro Phe Val Val Val Asp Asn Asp Pro Asn Phe Glu Glu Glu
      165      170      175
Ala Ile Lys His Lys Tyr Pro Tyr Tyr Ile Ile Gly Asp Pro His Thr
      180      185      190
Asn Leu Ala Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val
      195      200      205
Ala Leu Ser Lys Ile Leu Pro Val Asn Val Ala Leu Met Val Ser Val
      210      215      220
Arg Leu Phe Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala
      225      230      235      240
Ser Ala His Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Leu Gly Ala
      245      250      255
Asp Met Val Val Ser Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala
      260      265      270
Met Ala Val Arg Pro Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn
      275      280      285
Lys Lys Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr
      290      295      300
Ser Trp Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile
      305      310      315      320
Ala Lys Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile
      325      330      335
Pro Met Pro Asp Gly Lys Arg Leu Leu Gln Ala Asn Pro Ser Tyr
      340      345      350

```

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804

```

Thr Lys Lys Leu Asn Asn Thr Leu Phe Asn Lys Gly Leu Ile Ile Phe
1      5      10      15
Lys Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly
      20      25      30
Phe Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr
      35      40      45
Pro Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile
      50      55      60
Ile Asn Arg Gln Lys Leu Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu
      65      70      75      80
Gly Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu
      85      90      95
Met Lys Asp Trp Met Pro Arg Ser Ile

```


1334

```

      50              55              60
Val Thr Pro Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro
65              70              75              80
Gln Asn His His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser
      85              90              95
Asp Asn Leu Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn
      100             105             110
Gln Ile Gln Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe
      115             120             125
Gln Asp Glu Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser
      130             135             140
Val Leu Asp Leu Lys Gly Trp Val Gly Ile Leu Glu Asp Leu Lys Met
      145             150             155             160
Asn Leu Lys Asp Pro Asn Ser Pro Asn Leu Asp Thr Leu Val Asp Gln
      165             170             175
Ser Ser Gly Ser Val Trp Phe Asn Phe Tyr Glu Pro Glu Ser Asn Arg
      180             185             190
Val Val His Asp Phe Ala Val Glu Val Gly Thr Phe Gln Ala Ile Thr
      195             200             205
Tyr Thr Tyr Thr Ser Thr Asn Asn Ala Ser Gly Gly Phe Asn Ser Ser
      210             215             220
Lys Ser Val Ile His Glu Asn Leu Asp Lys Asn Arg Glu Asp Ala Ile
      225             230             235             240
His Lys Ile Leu Asn Arg Met Tyr Ala Val Val Met Lys Lys Ala Val
      245             250             255
Thr Glu Leu Thr Lys Glu Asn Ile Ala Lys Tyr Arg Asp Ala Ile Asp
      260             265             270
Arg Met Lys Gly Phe Lys Ser Ser Met Pro Gln Lys Lys
      275             280             285

```

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803

```

Glu Leu Val Leu Phe Glu Lys Leu Lys Phe Phe Lys Ile Lys Lys Asp
1              5              10              15
Asp Glu Asn Gln Pro Glu Val Asn Leu Asn Ser Glu Ile Tyr Glu Gln
      20              25              30
Phe Lys Val Phe Arg Leu Pro Leu Ile Leu Ile Gln Leu Leu Val Leu
      35              40              45
Leu Gly Thr Leu Gly Tyr Phe Ala Leu Glu Asn Tyr Ser Leu Met Gln
      50              55              60
Ala Phe Phe Gln Thr Thr Tyr Thr Met Thr Ala Thr Gly Phe Gly Ala
      65              70              75              80
Leu Asn Glu Ser Gln Phe Gly Pro Ile Ser Ile Phe Leu Thr Ser Ile
      85              90              95
Leu Met Phe Cys Gly Thr Gly Ile Ile Ala Phe Ser Val Ala Ile Leu
      100             105             110

```

SUBSTITUTE SHEET (RULE 26)

1333

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801

```

Phe Leu Leu Trp Ala Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr
1      5      10      15
Gly Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro
20      25      30
Val Val Phe Gly Gln Met Gly Ala Ile Gly Val Leu Val Ser Ile Leu
35      40      45
Phe Leu Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val Ala Leu
50      55      60
Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln Tyr Ser Arg
65      70      75      80
Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val Gly Val
85      90      95
Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu Thr Phe
100     105     110
Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser Thr Ile
115     120     125
Ile Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly Trp Val
130     135     140
Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe Leu Gly Pro
145     150     155     160
Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr Pro Leu
165     170     175
Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
180     185

```

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802

```

Glu Ser Phe Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr
1      5      10      15
Ser Lys Met Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys
20      25      30
Ala Met Asn Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn
35      40      45
Gln Gln Pro Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His

```

1332

```

65          70          75          80
Pro Lys Lys Arg Trp Lys Tyr Ala Gly Ile Met Leu Ile Ser Gly Pro
      85          90          95
Leu Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr
      100        105        110
Leu Val Ser Ile Ser Phe Asn Leu Pro Ser Ser Ile Gln Glu Ser Glu
      115        120        125
Gln Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly
      130        135        140
Leu Phe Ser Val Leu Phe Ile Thr Gly Trp Ile Val Ser Arg Gly Ile
      145        150        155
Lys Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe
      165        170        175
Ala Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe
      180        185        190
Ser Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp Leu Thr
      195        200        205
Ser Gln Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser
      210        215        220
Ile Gly Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr
      225        230        235
Gln Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu
      245        250        255
Ile Ser Leu Val Gly Arg Ala Tyr Asp Phe His Phe Cys Val
      260        265        270

```

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800

```

Cys Leu Thr Arg His Arg Val Asn Leu His Phe Phe Thr Gly Gly Phe
1          5          10          15
Trp Pro Asn Gly Ser Asp Arg Arg Ser Cys Phe Asn Ser Phe Leu Ala
      20        25        30
Arg Ala Arg Phe Cys Trp His His Phe Tyr Gly Gly Phe Ile Arg Ala
      35        40        45
Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe
50          55          60

```

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1331

Lys Ala Tyr Pro Leu Ile Tyr Leu Leu Ile Asn Val Glu Ala Asp His
 165 170 175
 Leu Thr Trp His Cys Asn Phe Glu Asn Tyr Leu Asn Ala Lys Leu Lys
 180 185 190
 Val Leu Thr Leu Met Pro Lys Thr Ser Leu Ala Ile Leu Pro Leu Lys
 195 200 205
 Phe Lys Glu His Pro Ile Val Gln Asn Ser Gln Ala Gln Lys Ile Phe
 210 215 220
 Phe Asp Lys Ser Glu Glu Val Leu Glu Cys Leu Lys Ile Pro Ser Asn
 225 230 235 240
 Ala Leu Phe Phe Lys Gly Ala Phe Leu Leu Asp Ala Ala Leu Ala Leu
 245 250 255
 Leu Val Tyr Glu Gln Phe Leu Lys Ile Lys Asn Leu Lys Trp Gln Asp
 260 265 270
 Tyr Arg Glu Asn Ala Leu Lys Arg Leu Asn Ala Phe Lys Ile Gly Ser
 275 280 285
 His Lys Met Glu Glu Phe Arg Asp Lys Gln Gly Arg Leu Trp Val Asp
 290 295 300
 Asp Ser Lys Ala Thr Asn Ile Asp Ala Thr Leu Gln Ala Leu Lys Thr
 305 310 315 320
 Phe Lys Asn Gln Lys Ile His Leu Ile Leu Gly Gly Asp Ile Lys Gly
 325 330 335
 Val Asn Leu Thr Pro Leu Phe Glu Glu Phe Lys Asn Tyr Lys Ile Ser
 340 345 350
 Leu Tyr Ala Ile Gly Ser Ser Ala Ser Ile Ile Gln Ala Leu Ala Leu
 355 360 365
 Glu Phe Asn Val Ser Cys Gln Val Cys Leu Lys Leu Glu Lys Ala Val
 370 375 380
 Gln Glu Ile Lys Ser Val Leu Leu Gln Asn Glu Val Ala Leu Leu Ser
 385 390 395 400
 Pro Ser Ala Ala Ser Leu Asp Gln Phe Ser Ser Tyr Lys Glu Arg Gly
 405 410 415
 Glu Lys Phe Lys Ala Phe Val Leu Lys Asp
 420 425

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799

Asp Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu
 1 5 10 15
 Gly Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr
 20 25 30
 Gly Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser
 35 40 45
 Leu Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln
 50 55 60
 Ser Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn

SUBSTITUTE SHEET (RULE 26)

1330

```

      115      120      125
Asp Leu Glu Gln Ala Lys Met Gln Phe Ser Met Leu Gln Asn Gly Ser
130      135      140
Leu Ile Trp Pro Val Ile Gly Phe Ser Ala Cys Leu Leu Pro Thr Ile
145      150      155      160
Trp Phe Val Ser Arg Gly Ile Glu Glu Gly Ile Glu Lys Leu Asn Val
      165      170      175
Val Leu Met Pro Leu Leu Phe Val Ile Phe Ile Gly Leu Leu Ile Tyr
      180      185      190
Ala Met Thr Leu Glu Ser Met Pro Lys Ala Leu Arg Phe Leu Phe Asn
      195      200      205
Phe Glu Ile Gln Lys Ile Asp Phe Lys Val Val Met Asp Ala Leu Gly
      210      215      220
Gln Met Phe Phe Ser Leu Ser Leu Gly Val Gly Thr Ile Ile Thr Tyr
      225      230      235      240
Ser Ala Phe Thr Pro Lys Lys Glu Asn Leu Leu Lys Ser Ser Leu Phe
      245      250      255
Ile Val Leu Pro Gly Ile Leu Ile Ser Leu Ile Ala Gly Val Met Ile
      260      265      270
Phe Thr Phe Val Phe Glu Tyr His Ala Asp Val Ser Gln Gly Pro Gly
      275      280      285
Leu Val Phe Ile Ser Leu Pro Leu Thr Phe Ala Lys Met Gly Ser
      290      295      300

```

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798

```

Arg Cys Val Lys Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr
1      5      10      15
Leu Ala Leu Gly Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe
      20      25      30
Phe Asp Asp Lys Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu
      35      40      45
Cys Tyr Pro Ser Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile
      50      55      60
Val Ser Pro Gly Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys
      65      70      75      80
His Leu Met Ser Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser
      85      90      95
Phe Thr Pro Thr Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr
      100      105      110
Thr Thr Glu Met Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser
      115      120      125
Gly Gly Asn Ile Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser
      130      135      140
Pro Leu Trp Val Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn
      145      150      155      160

```

SUBSTITUTE SHEET (RULE 26)

1329

```

Ile Val Ser Val Leu Leu Ser Leu Lys Gly Leu Asp Thr Phe Leu Tyr
      165      170      175
Ala Pro Phe Leu Lys Asn Pro Leu Phe Glu Met Pro Thr Met Leu Ala
      180      185      190
Val Gly Phe Trp Val Leu Val Phe Leu Ser Thr Ser Asn Ala Val Asn
      195      200      205
Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser Val Pro Ser Ile Phe Thr
      210      215      220
Leu Leu Ser Leu Ser Ile Phe Val Tyr Val Ala Gly Asn Ala Glu Phe
225      230      235
Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile Asp Val Gly Glu Leu Phe
      245      250      255
Val Ile Ser Leu Ala Leu Val Gly Ser Leu Phe Gly Phe Leu Trp Tyr
      260      265      270
Asn Cys Asn Pro Ala Ser Val Phe Met Gly Asp Ser Gly Ser Leu Ala
      275      280      285
Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile Val Ser His Asn Glu Ile
      290      295      300
Leu Leu Val Leu Met Gly Ser Ile Phe Val Ile Glu Thr Leu Ser Val
305      310      315
Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg Lys Lys Arg Leu Phe Leu
      325      330      335
Met Ala Pro Ile His His His Phe Glu Gln Lys Gly Trp Ala Glu Asn
      340      345      350
Lys Val Ile Val Arg Phe Trp Ile Ile Ser Met Leu Ser Asn Leu Val
      355      360      365
Ala Leu Leu Ser Leu Lys Val Cys
      370      375

```

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797

```

Ala Arg Phe Ile Lys Ile Phe Gly Met Gly Lys Phe Ser Lys Leu Gly
1      5      10      15
Phe Ile Leu Ala Thr Leu Gly Ser Ser Ile Gly Leu Gly His Ile Trp
      20      25      30
Arg Phe Pro Tyr Met Val Gly His Asn Gly Gly Ser Ala Phe Val Leu
      35      40      45
Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu Leu Val
      50      55      60
Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser Asn Tyr
      65      70      75      80
Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr Ser Phe
      85      90      95
Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val Val Leu
      100      105      110
Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu Pro Lys

```

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